

## (2) INFORMATION ON SEQ ID NO. 83:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

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ggcttgtggc ggctctgcc caggggcagg tgttgagggg ctcccgggtcc ggctgcccgc 60
gctccccgcg tccggaccgc gggctcccc tagcgccgct gaggagccgc ctctgcccgc 120
caggagggcg caggagcggg actgagagcg cctggaggct cgagcagagg atagaaggac 180
aaggacagaa tcaccagcac tggctgaagg taccttaaca tggggaatct tcttaaagtt 240
ttgacatgca cagacctga gcaggggcca aatTTTTTcc ttgattttga aaatgccag 300
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cagcatccag cagatgagaa gttgcaagag aaggcatggg gtgcagttgt tccactagta 480
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acaaatcctg ccatacagaa tgatttcagc tattatagaa gaacattgag tcgtatgagg 720
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ttctaaaaaa aaaaaaaaaa aaaaaaaaaa

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1890

## (2) INFORMATION ON SEQ ID NO. 84:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1829 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

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gaccaacctg acgcagatcg agctgcgggg caaccggctg gagtgcctgc ctgtggagct 60
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ctgccacccg aggtgaagga gcggtgtgg agggctgaca aggagcaggc ctgagcgagg 180
ccggcccgac acagcaagca gcaggaccgc tgcccagtc tcaggcccgg aggggcaggc 240
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tgccaccaga ggtcctggga cctcacttt agttcttggg atttattttt ctccatctcc 540
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caaataaaat ctataacaga aaaaaaaaaa
1829

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## (2) INFORMATION ON SEQ ID NO. 85:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2358 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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cgaaacgcgc cgagtgagg cagttccgct ggctagtgtg tacgcggcga gcttctccc 60
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actccgcgcg ccaagatata aacctgaatt ctccctaaca aggtctgctg tctgactcca 180
tgacggatgt tcctgtcgac acaggtgtgg ctgcccggac tcctgctgtt gagggctga 240
cagaggctga ggaggaggag ctgagggtct agcttaccaa ggtggaagag gaaattgtca 300
ctctgcgcca ggtcctggca gccaaaggaga ggactgtgtg agagctcaag aggaggctgg 360
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aaaaaaaaa aaaaaaaaaa

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2358



## (2) INFORMATION ON SEQ ID NO. 86:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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cagctgcgga actgcgcgat tgtggttccc gccgtatttc ccgttcccca tctagtaact 60
cccatctcag ccacgtatc tccctgagtg gaaatctcgg gcccagacc agtcgattgg 120
gaggtccgcc ctccccttca gcgacttggt ctgtgttttg gcagttgccg cgacaacagt 180
cacttccggg aagggggtct gcgaatctcc ttccgtcggg ccgctcagaa tcagctgtcc 240
tctcagactg tgtgggtggt ttccccggcc gcagctccgt acgggcttgg attgctgggc 300
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ttttctttta gtgtgaattt ttaaaatagc agttattcaa ggttttagaa cttaataaat 1620
acctagtcag aagaaaaaaa aaaaaa

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## (2) INFORMATION ON SEQ ID NO. 87:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3096 base pairs
- (B) TYPE: Nucleic acid.
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

gcggggtgacg	cgacgacggc	tcgacacttt	gctacggagt	gcatcggacg	tcgaagccta	60
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cgccgccacc	atgaacaaga	agaagaaacc	gttcctaggg	atgcccgcgc	ccctcggcta	180
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atgtggaagg	gctctgagct	gtgtcctcct	tcattaaaag	tttttatgtc	tcgtgtcaga	3060
aaaaaaaaa	aaagaaaaaa	gggggcgccc	gggggc			3096

## (2) INFORMATION ON SEQ ID NO. 88:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1906 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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aggtctcttc ttgggatgca gtcctgtcca gccagagcct gttttagtaa atcccagatg 480
gattattagc tgatgggagc aaagaaggat tgtagcact gctagagttt gctgaagaga 540
agatgaaagt gaactatgtc ttcatctgct tcaggaaggg ccgagaagac agagctccac 600
tcctgaagac cttcagcttc ttgggctttg agattgtacg tccaggccat ccctgtgtcc 660
cctctcggcc agatgtgatg ttcatggttt atccctgga ccagaacttg tccgatgagg 720
actaatagtc atagaggatg ctttacccaa gagccacagt gggggaagag gggaagttag 780
gcagccctgg gacagacgag agggctcctc gctgtctagg gaaggacact gaggggctca 840
gggtgagggt tgctatttgt gttctcggag ttgactcgtt gaaattgttt tccataaaga 900
acagtataaa catattatc acatgtaatc accaatagta aatgaagatg tttatgaact 960
ggcattagaa gctttctaaa ctgcgctgtg tgatgtgttc tatctagcct aggggaggac1020
attgcctaga gggggaggga ctgtctgggt tcaggggcat ggcttgagg gctggtgggc1080
agcactgtca ggctcagggt tccctgctgt tggctttctg ttttggttat taagacttgt1140
gtattttctt tctttgcttc ctgtcaccct aggggctcct gagtataggc ttttcagtccl1200
ctgggcagtg tccttgagtt gttttttgac actcttacct gggcttctct gtgtgcatttl1260
gcgtctggcc tggagtaagc aggtccgacc cctccttctt tacagcttag tgttattctg1320
gcatttggtt aagctggctt aatctgttta atgttatcag tacattttaa ataggggcat1380

tgaaatttac tcccaccacc agggcttttt tgggggatgc ctgggccttt aaaacactag1440
ccaaactcta attaattctc aaatcactgc caggagtctt tgctcctggc tgcaggccca1500
ggccccaagg tctccttctt ggggtcaca acagcagtaa ggaagaggaa tatatagca1560
ctcagggcct gggaattgtg gggcaatccg ttcttaggga ctggatactt ctggctggct1620
gagtatagta ctagctgcct ccccaccagg ttccagtag tgctctgagac tctgctgctc1680
agggcctagg gtagcgctgg gagtgtagaa gtggcctgcc cttaactgtt ttcactaaac1740
agctttttct aagggggagag caagggggag agatctagat tgggtgaggg ggacggggat1800
gtcaggggag caagtgtgtt gtgttactgt gtcaataaac tgatttaaag ttgtaaaaaa1860
aaaagaaaagg ggggggggtg aggggaggga gggggaaaag aaaaaa 1906

```

## (2) INFORMATION ON SEQ ID NO. 90:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 349 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

gctaagagga caagatgagg cccggcctct catttctcct agcccttctg ttcttccttg 60
gccaagctgc aggggatttg ggggatgtgg gacctccaat tcccagcccc ggcttcagct120
ctttcccagg tggtgactcc agctccagct tcagctccag ctccaggteg ggctccagct180
ccagccgcag cttaggcagc ggaggttctg tgtcccagtt gttttccaat ttcaccggct240
ccgtggatga ccgtgggacc tgccagtgtc ctgtttccct gccagacaac aactttccc300
tggacagagt ggaacgttgg aattcacagc tcatagttat ttctcagag 349

```

## (2) INFORMATION ON SEQ ID NO. 91:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2142 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

cagacccaga aagtagtgac cagccctcct cggattaccc ttcattggct cctcccttgc 60
gccgcccacc ctccagattt gcataaaaaa ggccaagaaa actctggctg tgccccagca 120
acggctcatt ctgctccccg gggtcggagc cccccggagc tgcgcgcggg ctgacagcgc 180
ctcgcccgcg ctgtcctccc ggtgtcccg cttctccgcg cccagccgcc ggtgccagc 240
ttttcggggc cccgagtcgc acccagcgaa gagagcgggc ccgggacaag ctcgaaactcc 300
ggcgccctcg ccttcccccg gctccgctcc ctctgcccc tgggggtcgc gcgcccacga 360
tgctgcaggg ccttggtcgc ctgctgctgc tcttctcgc ctgcactgc tgctgggct 420
cggcgcgcg gctcttcctc tttggccagc ccgacttctc ctacaagcgc agaattgcaa 480
gccccatccc gccaacctgc agctgtgcca cggcatcgaa taccagaaca tgcggtgcc 540
caacctgctg ggccacgaga ccatgaagga ggtgctggag caggccggcg cttggatccc 600
gctggctcatg aagcagtgcc acccggacac caagaagttc ctgtgctcgc tcttcgcccc 660
cgtctgcctc gatgacctag acgagacctc ccagccatgc cactcgctct gcgtgcaggt 720
gaaggaccgc tgcgccccgg tcatgtccgc cttcggcttc ccctggcccg acatgcttga 780
gtgcgaccgt ttcccccgag acaacgacct ttgcatcccc ctcgctagca gcgaccacct 840
cctgccagcc accgaggaag ctccaaaggt atgtgaagcc tgcaaaaata aaaatgatga 900
tgacaacgac ataattgaaa cgctttgtaa aaatgatttt gcaactgaaa taaaagtga 960
ggagataacc tacatcaacc gagataccaa aatcatcctg gagaccaaga gcaagaccat 1020
ttacaagctg aacggtgtgt ccgaaaggga cctgaagaaa tcggtgctgt ggctcaaaga 1080
cagcttgtag tgacactgtg aggagatgaa cgacatcaac gcgccctatc tggatcatggg 1140
acagaaacag ggtggggagc tggatgacac ctcggtgaag cgggtggcaga aggggcagag 1200
agagttcaag cgcactctcc gcagcatccg caagctgcag tgctagtccc ggcacctga 1260
tggctccgac aggcctgctc cagagcacgg ctgaccattt ctgctccggg atctcagctc 1320
cogttcccca agcacactcc tagctgctcc agtctcagcc tgggcagctt cccctgcct 1380
tttgcaagtt tgcaccccca gcatttctct agttataagg ccacaggagt ggatagctgt 1440
tttcaacctaa aggaaaagcc caccgaatc ttgtagaaat attcaaacta ataaaatcat 1500
gaatattttt atgaagttta aaaatagctc actttaagc tagttttgaa taggtgcaac 1560
tgtgacttgg gtctggttgg ttggtgtttg ttgttttgag tcagctgatt ttcacttccc 1620
actgaggttg tcataacatg caaattgctt caattttctc tgtggcccaa acttgtgggt 1680
cacaaacct gttgagataa agctggctgt tatctcaaca tcttcatcag ctccagactg 1740
agactcagtg tctaagtctt acaacaattc atcattttat accttcaatg ggaacttaaa 1800
ctgttacatg tatcacattc cagctacaat acttccattt attagaagca cattaacct 1860
ttctatagca tgatttcttc aagtaaaagg caaaagatat aaattttata attgacttga 1920
gtactttaag ccttggttta aacatttctt acttaacttt tgcaaatata acccattgta 1980
gcttacctgt aatatacata gtagtttacc tttaaaagtt gtaaaaatat tgctttaacc 2040
aacactgtaa atatttcaga taaacattat attctgttat ataaacttta catcctgttt 2100
tacctataaa aaaaaaaaaa aaaaaaaaaa aaaaaaggg aa 2142

```

## (2) INFORMATION ON SEQ ID NO. 92:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cgtggggogaa catgggagct gttcctcgcg ggccgcccggg tgctggtcac cggggcaggc 60
aaaggtatag ggcgcggcac ggtccaggcg ctgcacgcga cgggcgcgcg ggtgggtggc 120
gtgagccgga ctcaggcgga tcttgacagc cttgtccgcg agtgcccggg gatagaacct 180
gtgtgcgtgg acctgggtga ctgggaggcc accgagcggg cgctgggcag cgtgggcccc 240
gtggacctgc gcggagactg cgcgcacatg gagctgttcc tcgcgggccc ccgggtgctg 300
gtcaccgggg caggcaaagg tataggcgcg ggcacgggtcc aggcgctgca cgcgacgggc 360
gcgcgggtgg tggctgtgag ccggactcag gcggatcttg acagccttgt ccgcgagtgc 420
ccggggatag aaccogtgtg cgtggacctg ggtgactggg aggccaccga gcgggcgctg 480
ggcagcgtgg gccccgtgga cctgctgggtg aacaacgcgg ctgtcgccct gctgcagccc 540
ttcctggagg tcaccaagga ggcctttgac agatcctttg aggtgaacct gcgtgcggtc 600
atccaggtgt cgcagattgt ggccaggggc ttaatagccc ggggagtccc aggggccatc 660
gtgaatgtct ccagccagtg ctcccagcgg gcagtaacta accatagcgt ctactgctcc 720
accaaggggtg ccctggacat gctgaccaag gtgatggccc tagagctcgg gcccacaag 780
atccgagtga atgcagtaaa cccacagtg gtgatgacgt ccatgggcca ggccacctgg 840
agtgaccccc acaaggccaa gactatgctg aaccgaatcc cacttgcaa gtttgctgag 900
gtagagcacg tgggtgaacgc catcctcttt ctgctgagtg accgaagtgg catgaccacg 960
ggttccactt tgccggtgga agggggcttc tgggcctgct gagctccctc cacacacctc 1020
aagcccatg ccgtgctcat cctaccccca atccctccaa taaacctgat tctgctgccc 1080
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa g 1111

```

## (2) INFORMATION ON SEQ ID NO. 93:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 657 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

atttaaagcc tggattgtaa ccagattttc ttttttcccc cttctcagct gtagatatga 60
tatctccttt cagggcccca gcttaagggc aaagtgaagt aatgtgtaga caaaggcgag120
ggacaagaga gagttaacat ctagacagtg gaaaaagcca tgggtgtgtg tttctgggaa180
ccaccaacac ttgcagggtt agctttttcc cagggttgac tacaagaaag aaaaccatgt240
ttttgcaaga ttaaaatgtg gttgagtgtg cctaaattaa ccatcccat ttttatcata300
tttccaccat cacttcaggg ttttaagagt cagtgtcac ctgggcggac tggtagtaca360
ttttgcttct tagaaagcta agtcctgggt tccgtctgat tttaggttcc aggaacttcc420
tgagaacacc cgatcgacaga gggtaatttt ctggagtttg ttttgcaggg atagctggga480
gtatggccac cctgctccac gatgcggtaa tgaatccagc agaagtgggt aagcagcgct540
tgcagatgta caactcgacg caccggtcag caatcagctg catccggacg gtgtggagga600
ccgagggggtt gggggccttc taccggagct acaccacgcc gagccctatc tcgtgcc 657

```

## (2) INFORMATION ON SEQ ID NO. 94:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 863 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

gcggtcggta gtgcggcgct gtttaaagat ggcggcggag gaacctcagc agcagaagca 60
ggagccgctg ggcagcgact ccgaagggtg taactgtctg gcctatgatg aagccatcat120
ggctcagcag gaccgaattc agcaagagat tgctgtgcag aacctcttgg tgtcagagcg180
gctggagctc tcggctctat acaaggagta tgctgaagat gacaacatct atcaacagaa240
gatcaaggac ctccacaaaa agtactcgta catccgcaag accaggcctg acggcaactg300
tttctatcgg gctttcggat tctccactt ggaggcactg ctggatgaca gcaaggagtt360
gcagcgggtc aaggctgtgt ctgccaaag caaggaagac ctggtgtccc agggcttcac420
tgaattcaca attgaggatt tccacaacac gttcatggac ctgattgagc aggtggagaa480
gcagacctct gtcgcccacc tgctggcctc cttcaatgac cagagcacct ccgactacct540
tgtggtctac ctgcccgtgc tcacctcggg ctacctgcag cgcgagagca agttcttcga600
gcacttcacg gaggggtggac ggactgtcaa ggagttctgc cagcaggagg tggagcccat660
gtgcaaggag agcgaccaca tccacatcat tgcgctggcc caggccctca gcgtgtccat720
ccaggtggag tacatggacc ggcggcaggg cggcaccacc aatccgcaca tcttccctga780
gggcttccga gcccaaggtc ttacctgtt ttaaccggct tggggcaatt taggtattgc840
ttttacaaa taggggtttg gtt

```

863

## (2) INFORMATION ON SEQ ID NO. 95:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1015 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

aattcgggaac gagggcgccct gcaagccatg atgacccacc tgcattgtgaa gtctacagaa 60
cccaaagctg cccctcagcc cctgaatctg gtatcaagtg tcaccctctc caagtccgca 120
tcggaggctt ctccacagag cttacctcat actccaacga cccaaccgc cccctgact 180
cccgtcaccc aaggcccctc tgtcatcaca accaccagca tgcacacggt gggacccatc 240
cgcaggcggt actcagacaa atacaacgtg cccatttcgt cagcagatat tgcgcagaa 300
caagaatttt ataagaacgc agaagttaga ccaccattta catatgcatc ttttaattagg 360
caggccattc tcgaatctcc agaaaagcag ctaacactaa atgagatcta taactgggtc 420
acacgaatgt ttgcttactt ccgacgcaac gcggccacgt ggaagaatgc agtgcgtcat 480
aatcttagtc ttcacaagtg ttttgtgcga gtagaaaacg ttaaaggggc agtatggaca 540
gtggatgaag tagaattcca aaaacgaagg ccacaaaaga tcagtggtaa cccttccctt 600
attaaaaaca tgcagagcag ccacgcctac tgcacacctc tcaatgcagc tttacaggct 660
tcaatggctg agaatagtat acctctatac actaccgctt ccatgggaaa tcccactctg 720
ggcaacttag ccagcgcaat acgggaagag ctgaacgggg caatggagca taccaacagc 780
aacgagagtg acagcagtc aggcagatct cctatgcaag ccgtgcatcc tgtacacgtc 840
aaagaagagc ccctcgatcc agaggaagct gaaggggccc tgtccttagt gacaacagcc 900
aaccacagtc cagattttga ccatgacaga gattacgaag atgaaccagt aaacgaggac 960
atggagtgcac tatcgggggc ggccaacccc gagaatgaag attggaaaaa aaaaa 1015

```

## (2) INFORMATION ON SEQ ID NO. 96:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2532 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

gctcgatgtg caagtgaagg atgattccag ggccctgact ttaggagcac tgacgctgcc 60
tctggccccg ctgctgactg cccagaaact catcctggac cagtgggtcc agctcagcag 120
ctctggtcca aactccagac tctatatgaa actagtcagt aggatcctgt acttggattc 180
atcagaaaata tgcttcccca cggcgccctg ttgtcctggg gcttgggacg tggacagtga 240
gaatccccag agaggcagca gtgtggatgc cccacctcga ccctgtcaca cgactcctga 300
tagccagttt gggactgagc atgtgcttcg gatccatgta ttagaggccc aggacctgat 360
tgccaaagac cgtttcttgg ggggactggg gaagggcaag tcagaccctt atgtcaaaact 420
aaagttagga ggacgaagct tccggagcca tgttgttcgg gaagatctca atccccgctg 480
gaatgaggtt tttgaggtga tcgtcacatc agttccaggc caagagctag aggttgaagt 540
ctttgacaag gacttggaca aggatgattt tctgggcagg tgtaaagtgc gtctcaccac 600
agtcttaaac agtggccttc ttgatgagtg gctgacctg gaggatgtcc catctggccg 660
cctgcacttg cgcctggagc gtctcaccac ccgtccact gctgctgagt tagaggaggt 720
gctgcaggtg aatagtttga tccagactca gaagagtgcg gagctggctg cggccctgct 780
atccatctat atggagcggg cagaggacct cccgctgcga aaaggcacca agcacctcag 840
cccttatgct actctcactg tgggagatag ttctcataaa accaagacta tttcgcaaac 900
ttcagccccct gtctgggatg agagtgcctc ctttctcatc aggaaaccac aactgagag 960
cctagagttg caggttcggg gtgagggcac tggcgtgctg ggctcattat ccctgccccct 1020
ctcagagctc ctgctgggctg accagctctg cttggaccgc tggtttacac tcagcagtggt 1080
tcaggggcag gtgctactga gagcacagct agggatcctg gtgtcccagc actcgggagt 1140
ggaagctcat agccacagct acagccacag ctctcatcgt ctgagtgaag aaccagagct 1200
ctcgggggga cccctcaca tcacctctc agccccagag ctccggcagc gcctaacaca 1260
tggtgacagt ccccttgagg ctccagccgg gcctctgggc caggtgaaac tgactctgtg 1320
gtactacagt gaagaacgaa agctggtcag cattgttcat ggttgccggt cccttcgaca 1380
gaatggacgt gatcctcctg atccctatgt gtcactgttg ctactgccag acaagaaccg 1440
aggcaccaag aggaggacct cacagaagaa gaggacctg agtcctgaat ttaatgaacg 1500
gtttgagtgg gaactcccc ttgatgaggc ccagagacga aagctggatg tctctgtcaa 1560
gtctaattcc tcttcatgt caagagagcg tgactgctgg ggaaggtgca gctggacctal 1620
gctgagacag acctttccca ggggtgagcc cgggtggtatg acctgatgga caacaaggac 1680
aagggcagct cctaggagct ggcgagtccc agcctgactg ctctgtcttc ctgccttcgt 1740
ctcgtctccat caccgcctca atgtgatgag cctaaagcta ggggtccaagg gcagagcctg 1800
tgcccttcag ccccttcacc taacaggccc atattcgggc ctttgccctga ccaaagagaa 1860
gaaccgtatg ttccctttac tgcacggcct ttatccttct gggccctgg ggcggggacc 1920
tgagctggct gtttctctgt ttgctgcac attgttctcc ctctctccca actcctcagg 1980
gccttctgta tctgtgctg gccagtggca gcactagcag tggatttagc ttatgccaaa 2040
tacagctttg gaaggatctt ttttcttta actagatggg cacttcttc cctaccacac 2100
atgggtggga aggtggacag gctaacctct ccagctgtga gcctcttaga ctactgcatg 2160
tagcaaatgt tcagcagctc agggccccc atgtccagttc gtccccactg tcctcaaccc 2220
tgtcctgaaa attctactgc tttgatggct ggggccagtc tcttgtcact ttggaaactg 2280
aggacgcgtg gattctactc aagcctccaa gtagtggcat atcagtcttg gagctcctag 2340
ctggtgatac ggagagggct ttggaggact tgggacagca gggccaattt ttttgcccaa 2400
gtgcctagga tgctaactca ctgactagaa cttaatctgg tactttacag ttttgacca 2460
actctgccaa gccactggat cttacattaa acatcatact caaaaaaaaa aaaaataaaa 2520
ataaaaaaaaa aa

```

2532

## (2) INFORMATION ON SEQ ID NO. 98:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 776 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

tttttttttt tttttttttt tttttttttt ttttgagaca aagtctcact gtgtcaccca 60
gactggaatg cagtgcacac atctcggtc actgaaacct ctgccttcca gggtcaagct120
attctcatgc ctcagcctct caagtagctg ggactacaga tgtgggccac catgtctggc180
taattttttt ttttttttgt agagacaggg ttctgccatg ttgacgagac tgggtctcgaa240
ctcctggcct caagtgatct gccgcctcag cttctcaaag tactgggatt atataggcat300
gagccactga gcctggccct gaagcgtttt tctcaaaggc cctcagttag ataaattaga360
tttggcatct cctgtcctgg gccagggatc tctctacaag agcccctgcc cctctgttgg420
aggcacagtt ttagaataag gaggaggagg gagaagagaa aatgtaaagg agggagatct480
ttcccaggcc gcaccatttc tgtcactcac atggacccaa gataaaaagaa tggccaaacc540
ctcacaaccc ctgatgtttg aagagttcca agttgaaggg aaacaaagaa gtgtttgatg600
gtgccagaga ggggctgtc tccagaaagc taaaatttaa tttctttttt cctctgagtt660
ctgtacttca accagcctac aagctggcac ttgctaacaa atcagaaata tgacaattaa720
tgattaaaga ctgtgattgc caccaaaaaa aaaaaaaca gccaggaaaa aaaggg 776

```

## (2) INFORMATION ON SEQ ID NO. 99:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 629 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

cggtcgact tccgttactt gctgctggagg accgtgggca gccaggggtcg gtgaaggatc 60
ccaaaatggc tgggcgaaaaa cttgctctaa aaaccattga ctgggtagct tttgcagaga120
tcatacccca gaaccaaaag gccattgcta gttccctgaa atcctggaat gagaccctca180
cctccaggtt ggctgcttta cctgagaatc caccagctat cgactgggct tactacaagg240
ccaatgtggc caaggctggc ttggtggatg actttgagaa gaagtttaat gcgctgaagg300
ttcccgctgcc agaggataaa tatactgccc aggtggatgc cgaagaaaaa gaagatgtga360
aatcttgtgc tgagtgggtg tctctctcaa aggccaggat tgtagaatat gagaaagaga420
tgagagaagat gaagaactta attccatttg atcagatgac cattgaggac ttgaatgaag480
ctttcccaga aaccaaatta gacaagaaaa agtatcccta ttggcctcac caaccaattg540
agaatttata aaattgagtc caggaggaag ctctggccct tgtattacac attctggaca600
ttaaaaataa taattataca aaaaaaaaaa

```

629

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 757 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ggcgggggagc aggggggacac caggggtgaat caggaagacc cgaggggtgg cccccaccct 60
ttctccaccc acgcggcagg ttccaggtgc cctggctgga gtcagtcctc atcgtagtca120
gcaacaacat tgacgaggag gcgctggccc gactggccca ggagggcagt gaggtgaatg180
tcattggcat tggcaccagt gtggtcacct gcccccaaca gccttccctg ggtggcgtct240
ataagctggt ggccgtgggg ggccagccac gaatgaagct gaccgaggac cccgagaagc300
agacgttgcc tgggagcaag gctgctttcc ggctcctggg ctctgacggg tctccactca360
tggacatgct gcagttagca gaagagccag tgccacaggc tgggcaggag ctgaggggtgt420
ggcctccagg ggcccaggag ccctgcaccg tgaggccagc ccaggtggag ccactactgc480
ggctctgcct ccagcaggga cagctgtgtg agccgctccc atccctggca gagtctagag540
ccttgggcca gctgtccctg agccgactca gccctgagca caggcggctg cggagccctg600
cacagtacca ggtggtgctg tccgagaggg tgcaggccct ggtgaacagt ctgtgtgcgg660
ggcagtcctc ctgagactcg gagcggggct gactggaaac aacacgaatc actcactttt720
ccccacagga agaggagggt agggaagagg gggggcg 757

```

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1262 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aatttggtga agagtgattc tccctcatcc tctgcaaaca ttccataggc gataggaaga 60
actatgcctc tgccaagctt tctgagttgc tgccagaaga agttgaagca gaagtgaag 120
cagctgcaga gatatcaatg ggaacagagg tttcagaaga agatatttgc aatattctgc 180
atctttgcac ccaggtgatt gaaatctctg aatatcgaac ccagctctat gaatatctac 240
aaaatcgaat gatggccatt gcacccaatg ttacagtcac gggtggggaa ttagttggag 300
cacggcttat tgctcatgca ggttctcttt taaatttggc caagcatgca gcttctaccg 360
ttcagattct tggagctgaa aaggcacttt tcagagccct caaatctaga cgggataccc 420
ctaagtatgg tctcatttat catgcttcac tcgtgggcca gacaagtccc aaacacaaaag 480
gaaagatttc tcgaatgctg gcagccaaaa ccgttttggc tatccgttat gatgcttttg 540
gtgaggattc aagttctgca atgggagttg agaacagagc caaattagag gccaggttga 600
gaactttgga agacagaggg ataagaaaaa taagtggaaac aggaaaagca ttagcaaaaaa 660
cagaaaaata tgaacacaaa agtgaagtga agacttacga tccttctggt gactccacac 720
ttccaacctg ttctaaaaaa cgcaaaatag aacaggtaga taaagaggat gaaattactg 780
aaaagaaaagc caaaaaagcc aagattaaag ttaaagttga agaagaggaa gaagaaaaag 840
tggcagaaga agaagaaaca tctgtgaaga agaagaagaa aaggggtaaa aagaaacaca 900
ttaaggaaga accactttct gaggaagaac catgtaccag cacagcaatt gctagtccag 960
agaaaaagaa gaaaaagaaa aaaaagagag agaacgagga ttaacagaaa ggaattacga 1020
ttatatcacc cggacacaca tcatgcttaa gattcaactg ggagcatacc agggatgctc 1080
tctaacgtaa tcaagggaag gttcagtaag acaaagtgat ttatcatcta taacttcaa 1140
cctatttgtc ttgacatcaa ctctgttaac cttatgtcat catttcttag agtctttgat 1200
atacaataa aattttcttt gtatttttaa acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
aa

```

## (2) INFORMATION ON SEQ ID NO. 102:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ggcggaagta gccgcaggca tggcggcggc tatgccgctg ttgctctgct cgtcctgttg 60
ctcctggggc ccggcgggctg gtgccttgca gaacccccac gcgacagcct gcgggaggaa 120
cttgtcatca ccccgctgcc ttccggggac gtagccgcca cattccagtt ccgcacgcgc 180
tgggattcgg agcttcagcg ggaaggagtg tcccattaca ggctctttcc caaagccctg 240
gggcagctga tctccaagta ttctctacgg gagctgcacc tgtcattcac acaaggcttt 300
tggaggaccc gatactgggg gccacccttc ctgcaggccc catcagggtg agagctgtgg 360
gtctggttcc aagacactgt cactgatgtg gataaatctt ggaaggagct cagtaatgtc 420
ctctcaggga tcttctgcgc ctctctcaac ttcctcgact ccaccaacac agtcaactcc 480
actgcctcct tcaaaccctt gggctgccc aatgacactg accactactt tctgcgctat 540
gctgtgctgc cgcgggaggt ggtctgcacc gaaaacctca cccctggaa gaagctcttg 600
ccctgtagtt ccaaggcagg cctctctgtg ctgctgaagg cagatcgctt gttccacacc 660
agctaccact cccaggcagt gcatatccgc cctgtttgca gaaatgcacg ctgtactagc 720
atctcctggg agctgaggca gacctgtca gttgtatttg atgccttcat cacggggcag 780
ggaaagaaag actggtcctt cttccggatg ttctccgaa ccctcacgga gccctgcccc 840
ctggcttcag agagccgagt ctatgtggac atcaccacct acaaccagga caacgagaca 900
ttagagggtg accaccccc gaccactaca tatcaggacg tcatcctagg cactcggaag 960
acctatgcca tctatgactt gcttgacacc gccatgatca acaactctcg aaacctcaac1020
atccagctca agtgggaagag acccccagag aatgaggccc cccagtgcc cttcctgcat1080
gcccagcggt acgtgagtggt ctatgggctg cagaaggggg agctgagcac actgctgtac1140
aacaccacc cataccgggc cttccgggtg ctgctgctgg acaccgtacc ctggtatctg1200
cggtgttac atccactacc agcctgccc ggaccggctg caaccaccac tcctggagat1260
gctgattcag ctgccggcca a

```

## (2) INFORMATION ON SEQ ID NO. 103:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 716 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

gggccccaga aagagaccaa tgtgttgtgc gacgggtggg tggcagtggc agtggcagat 60
ggtaccaggc gccccagaac tctaaggggc ctcaagtagt ttaaaacctc ggaggctgcc120
tgacttgggg ccaagggttt ctatgctcag gcctgacccc tcatggatta gtttctgctg180
gaaaaacttt ttctgccctc ggccaggtct ctatctcctt ctgccttaac atattttgga240
aggtttggtt ccagcagaga cggggccatg ggctcacact ctgacctctc ccacggcatt300
agccctgtct cagcctctgg gctgttacgc aagttaattc ctgcacaaga ctcaaacag360
ggctgtggag gaagcaaagg agcccttttt atgcctctgt agtaggactg agagaggccc420
tctggccagc gtgagcctgc tggttcttcc cggactgtac caggccttga ggcggggtat480
ggaaacgccc cactctgggg cctggcttgg ggaaggggag gcggcagggg ttctttgggc540
ttctcgaggg tataatctga gctctctggg gaacgtgtgt ccattttagt gcagtagtcc600
gacacgtcgg gggactcaac tttaacttgg gacaatctgt gtgtggtctg tttttagtaa660
attcatccac acaagagagt ggaggcatga acaggggtgg cttcctcgg atctca 716

```

## (2) INFORMATION ON SEQ ID NO. 104:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

tttgttgttg gagaaaggag agaaaggaaa gcgcgagggg ccgcccgcac caccagcgca 60
gagtcctgga gctgtgagga gattcgggcc gtcacctgct cccccctgct tcccgccacc 120
ggccgcttct gtcctcggac ccattccaac aatctcgtaa aacatgggtg attactatga 180
agttctaggc gtgcagagac atgcctcacc cgaggatatt aaaaaggcat atcgaaaact 240
ggcactgaag tggcatccag ataaaaatcc tgagaataaa gaagaagcag agagaaaatt 300
caagcaagta gcggaggcat atgaagtgtc gtcggatgct aagaaacggg acatctatga 360
caaatatggc aaagaaggat taaatgggtg agggaggagt ggaagtcat ttagacagtcc 420
atttgaattt ggcttcacat tccgtaaccc agatgatgtc ttcagggaat tttttggtgg 480
aagggaacca ttttcatttg acttctttga agaccctttt gaggacttct ttgggaatcg 540
aaggggtccc cgaggaagca gaagcogagg gacggggctg tttttctctg cgttcagtgg 600
atttcctgtt tttggaagtg gattttcttc ttttgataca ggatttactt catttggtgc 660
actaggtcac gggggcctca cttcattctc ttccacgtca tttggtggta gtggcatggg 720
caacttcaaa tcgatatcaa cttcaactaa aatggttaat ggcagaaaaa tcaactacaaa 780
gagaattgtc gagaacggtc aagaaagagt agaagttgaa gaagatggcc agttaaagtc 840
cttaacaata aatggtgttg ccgacgacga tgccctcgtc gaggagcgca tgcggagagg 900
ccagaacgcc ctgccagccc agcctgccgg cctccgcccc ccgaagccgc cccggcctgc 960
ctcgtctgtg agacacgcgc ctactgtct ctctgaggag gaggcgagc aggaccgacc1020
tggggcaccc gggccctggg accccctcgg cgtccgcagc aggattgaaa gaaggtggca1080
agaggaagaa gcagaagcag agagaggagt ttgaaggagg aaggaagttg gaccaaaggc1140
attgattaga ccggaatttt

```

## (2) INFORMATION ON SEQ ID NO. 105:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agcatccgct tccggttccc agactgaatt gtcagtgagc ggagtctgag gtcgctgtgg 60
actgcccact gggccttgcc cgagatggac agccggattc cttatgatga ctaccggtg 120
gttttcttgc ctgcctatga gaatcctcca gcatggattc ctctcatga gaggggtacac 180
caccgggact acaacaatga gttgacccag tttctgcccc gaaccatcac actgaagaag 240
cctcctggag ctcaagtggg atttaacatc cgaggaggaa aggcctcca gctaggcatc 300
ttcatctcca aggtgattcc tgactctgat gcacatagag caggactgca ggaaggggac 360
caagttctag ctgtgaatga tgtggatttc caagatattg agcacagcaa ggctgttgag 420
atcctgaaga cagctcgtga aatcagcatg cgtgtgcgct tctttcccta caattatcat 480
cgccaaaaag agaggactgt gcactagaaa gttgcagccc acagcccttc atgtggactc 540
tgtcatgaca tgctaactag acttcagggg agccacttct gttttcagcc cctccctgga 600
atagtgaagt gggaggatgg ggagacagct aaccaactgc attaccctaaa ccatattgca 660
cttttagttc cctagttttc taggtgagct tcattccctg aaaggaggat gatgatattc 720
aggcataacc tagcctgtga ggaacctagt taggaaagac aactgacatt tattgaatat 780
catgcactag tcccttacat atgtcatatt ttaattatag aaatcagtag caaaaagaat 840
cttggggatt ttccatctga ctcccctggc catcttatcc catccttgca ctaccagaag 900
attcatacac ttttgagact ccagtgaagc gctgttttca ccccttctc ctctagcct 960
ctctcccaa aagtaaaaca caatgctgaa gaaaaaaaaa aaaaaaaaaa aaaaaggggg 1020
gggcgggccg gtgggtggtc

```

1040

## (2) INFORMATION ON SEQ ID NO. 106:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

cgagggacag aacctggtgc aggaggagtt ggcgggccgc gggacccagc ccccgctccat 60
ccgcaacggc ctggacaaaag ccgcgaggtc cgcttcgagc gagctgagca ggccctgctc 120
cggttcagcc agggcccccac acccgctgcc gctgtccccc agggcacggc agccgagggc 180
gctcccaggc aggaaaactg tgggtgccag caggtccccc caggccgggc actagcacc 240
ctcccagcag ccccgctgctg acctgcgggc ccctgacgga tgaggacgtg gtcaggctgc 300
ggccctgtga gaagaagcgg ctggacatcc gtggcaaaact ttacctggcc cccctcacca 360
cgtgtgggaa cctgcccttc cgacggatct gcaagcgctt cggggcggtat gtgacatgtg 420
gagagatggc cgtctgcacc aacctgctgc agggccagat gtccgagtgg gccctactca 480
aacgccacca gtgtgaggac atctttggcg tccagctgga gggcgccctc cccgacacca 540
tgaccaagtg tgccgagctg ctgagccgca ccgtggaggt ggactttgtg gacatcaacg 600
tcggctgccc catcgacctc gtgtacaaga aggggtgggg ctgtgccctc atgaatcgct 660
ccaccaagtt ccagcagatc gtccgtggca tgaaccaggt gctggatgtg ccgctgactg 720
tgaagatccg cacaggcgct caggagcgtg tgaacctggc gcaccgcctg ctgcccgagc 780
tgccggactg gggcgtggca ctgctcacgg aatggggac atcttgtcat ttgaggatgc 840
caaccgcgcc atgcagactg gtgtcaccgg gatcatgatt gcccgaggcg ccctgctcaa 900
gccgtggctc ttcacggaga tcaaggagca gcggcactgg gacatctcgt cgtccgagcg 960
cctggacatc ctgcgggact tcaccaacta cggcctggag cactggggct cggacacgca 1020
ggcggtggag aagacccggc gctttctgct cgagtggctg tccttcctgt gccggtacga 1080
tcccgtgggg ctgctggagc ggctcccaca gaggatcaac gagcgggcgc cctactacct 1140
gggccgcgac tacctggaga cgctgatggc cagccagaag gcagccgact ggatccgcat 1200
cagcgagatg ctccctgggc cagtgcctcc cacctcgctt tcttgccgaa gcacaaggcc 1260
aacgcgtaca agtagcctca ggctttccca ggggcaccct ggggcgagga gagtacaata 1320
aattttattc ttttaa

```

1336

## (2) INFORMATION ON SEQ ID NO. 107:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 812 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

ggcagcccaa tgtctcctgc acgtgcaatg caaacgctct ttgttccaga gcatggagat 60
cacggagctg gagtttgttc agatcatcat catcgtggtg gtcacgtgcc tgctgagcca120
ctacaagctg tctgcacggc cttcatcag ccggcacagc caggggcgga ggagagaaga180
tgccctgtcc tcagaaggat gcctgtggcc tcggagacac agtgtcaggc aacggaatcc240
cagagccgca gtcttacgcc ccgcctcggc ccaccgaccg cctggccgtg cgcccttcgc300
ccagcggagc gttttccacc gttgccagcc caatgtctcc tgcacgtgca actgcaaacc360
ctctttgttc cagagcatgg agatcacgga gctggagttt gttcagatca tcatcatcgt420
ggtggtcacg tgccctgtga gccactacaa gctgtctgca cggtccttca tcagccggca480
cagccagggg cggaggagag aagatgccct gtcctcagaa ggatgcctgt ggccctcgga540
gagcacagtg tcaggcaacg gaatcccaga gccgcaggtc tacgccccgc ctcgccccac600
cgaccgcctg gccgtgccgc cttcgccca gccggagcgc ttccaccgct tccagcccac660
ctatccgtac ctgcagcacg agatcgacct gccgcccacc atctcgctgt cagacgggga720
ggagcccca ccctaccagg gccctggac cttcaagggt cgggaccccg aggaggagtt780
ggaaattgaa cggggattgg gtgcggagac cc
812

```

(2) INFORMATION ON SEQ ID NO. 108:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 2681 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gatgcttggt atcatcatca tgatgacgct gtgtgaccag gtggatattt atgagtgcct 60
cccatccaag cgcaagactg acgtgtgcta ctactaccag aagttcttcg atagtgcctg 120
cacgatgggt gcctaccacc cgctgctcta tgagaagaat ttggtgaagc atctcaacca 180
gggcacagat gaggacatct acctgcttgg aaaagccaca ctgcctggct tccggaccat 240
tcactgctaa gcacaggctc ctcaactctc tccatcaggc attaatgaa tggctctctg 300

gccaccccag cctgggaaga acattttcct gaacaattcc agcctgctcc ttttactcta 360
ggggcctctg tcagcaagac catggggact tcaagagcct gtggtcagga aatcagggtcc 420
agccttcctt gtagccagac agtttatgag cccagagcct cctgccacac acatgcacac 480
atatctagca ttctttccag acagcatcct cccgccttc caccttggtg gatgcaagggt 540
ctatctctcc catcagggtc gccaaagctg ggctttgttt ttcccagcag aatgatgcca 600
ttctcacaaa ccaatgctct atattgcttg aagctctgcat ctaaaatttg atttcacgtt 660
ttaaagaaat tctcttaaat tacaattgtg cccaatgcag ggtggctctg gggggcaagt 720
aggtggtaca ggggattgga aacatgctcc gcgcctccag agaaaagttg ctcccagggt 780
ccatgccccct ggaacgtgtt cctatcactc tggctgggtg ggctggctct tagactgggt 840
gcttatgatt aaagggctct ggtagccca ctttccctct ccatgtggag atggaaggta 900
gagaaggata cagtgtctat cctcaagttg ctacggttca gtgagagagg cagacatctg 960
aacaggcagg taggattcag tgtgctcagt gcactgggga tttggagaga gatgggcttg1020
ctctctctgt gcacccagga gggccacgca cttaaaactg tgtttgtgga tcagagaagg1080
ctttatagca cagggggcat tcagatgagt cttagaggaa gagaagaaac atggcaagca1140
gattacatct gagcggtttg aattgtgttt ttctttcttc ccatgtttat tttctaagat1200
ctacctgaac tttagagactc aagatatttt tttaggaaac ctctacccta tgtctgagggt1260
agcaagtgca gcctcacgac agataccagg caatccagag ccacaaaacg tgattcctcc1320
aggctctgcc tggcctgacc ctgtcctgtc agctgggttt acataccagt cccattcttc1380
cttttcaata aataccccca aatcttctcc taaccacat taaagcattt tttgctttaal1440
aagcatcctg accccaattt ctttgagctc acgggccttt tgctgaagggt ctctcagggt1500
gtagtgggtg ggctctctgg acttaacgtc actctcagag gtcagaacct tggagatcag1560
aactgattct caccagggtg gagagggtgt gtagcagatt gcaatgctct gcacctcttc1620
cttgcaagtg agcaacttca ggctctctgg gcagaggctg gccactgtga gtttgagac1680
atgctctcca gatggtttta ctaagtcctc tctcctgat agggaaatcct gctggaccag1740
cgcagcctgg gtgtggagag gttaaaagac ttgcacagga tcaccaagtc atgctgtaga1800
gccaggattc ctagaccag ggctctgcac tctcaaggct ggccccatgt gctcaagggt1860
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ccctcagctt atgtagctag aaagggccct ggagtgaaga agcctggatt ttcaaattga1980
tgctccccta ctgactagct gtgccactct gggcaaatgc tcttccttga gcctgtttcc2040
acacctgtaa agtggggatg atgacccat ctcaactgct ttgtgaggat tacaggaaag2100
cacctgtcct ggctctgtac ctggcacgta gtaggtgctc agttcatgct ggtttccttc2160
ctgcctttag tagggacctg ctctgtgtct acacctcggc tgcattgcacc ctgctgtgac2220
ggaggctagt gtggaagagg tcctgtcctc agggaattaa ctgtcttatt gggagacaac2280
aactgtcctc cttggaacac ccaagaaacc atgcaaagca gtggacaaca cagaacacgc2340
cctcctcctc gctgcctgca gctccaatct gattctgctt gggaaatggc ggagcacgtg2400
ggctgcttaa ctgctgtata ggacaagccc cttacccctc tctgggcccc tgaattcctg2460
gcttgggtta tgttctgatt tgacacactg attttaatct tcgaatcatg acactgagtg2520
cagaggaggt ggcattccga cagcaggaca tacatgttgg tgtgaagact gggacgacac2580
tgggtagaat ctagttttta attattatta atataaagga tcaaattaat ttaaatatga2640
atccgaagtc cacagaactt taagtgtgtg gccggccatg t

```

2681

## (2) INFORMATION ON SEQ ID NO. 109:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1407 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

cttgggacgg aagcctagct ggggtggggg cgccgggctg gagccttcgc aggggagcgg 60
gctcagtcac caccctgcgc ccagagtgga ctacagcccc acgtcccccac ccatccccgg 120
ggagccaggg ccgcagaggg aggtagataa gtgggggtggc agcctgggtc ggccagagag 180
ttcaggccac cccggccgga cgctgccac ttgctgtcac tgtgccgctg tcatggcacg 240
ctccgggagt gccacgccac ctgccgggc tccgggagcc cctccacgga gcccacccca 300
gaggctggta caggatgtca gtgggcccct gagggagctg cgccctcggc tctgccacct 360
gcgaaaggga cctcagggtc atgggttcaa cctgcatagt gacaagtccc ggcccggcca 420
gtacatccgc tctgtggacc cgggctcacc tgccgcccgc tctggcctcc gcgcccagga 480
ccggtcatt gaggtgaacg ggcagaatgt ggagggactg cgccatgctg aggtggtggc 540
cagcatcaag gcacgggagg acgaggcccg gctgctgttc gtggaccccc agacagatga 600
acacttcaag cggcttcggg tcacacccac cgaggagcac gtggaaggte ctctgccgtc 660
acccgtcacc aatggaacca gccctgccc gctcaatggt ggctctgctg gctcgtcccc 720
aagtgcctg cctggttccg acaaggacac tgaggatggc agtgccctga agcaagatcc 780
cttccaggag agcggcctcc acctgagccc cacggcggcc gaggccaagg agaaggctcg 840
agccatgcga gtcaacaagc gcgcgccaca gatggactgg aacaggaagc gtgaaatctt 900
cagcaacttc tgagccccct cctgcctgtc tcgggaccct gggacccctc ccgcacggac 960
cttgggcctc agcctgcccc gagctcccc agcctcagtg gactggaggg tggctctgcc 1020
attgcccaga aatcagcccc agccccggtg agcccccatc ctgcccctgc ccaccaggta 1080
ctgggggcct gtggcagcaa gataggggga gagagacca gagatgtgag agagagtcag 1140
agacagagac agagagagag agagagagac acagagagag acagagagag agcgagcgag 1200
cgcgcggcag ccgcggggcg agggcctttg ctgctctgcc ggggcctgct gactgaaagg 1260
aatttggtt tttgcttttt ttccaaaaag atctccagct ccacacatgt ttccacttaa 1320
taccagagac ccccccgctc aaagcccccc tccccggccc cttgggacgc gctctaaata 1380
attgcaataa aacaaacctt tctctgc

```

1407

## (2) INFORMATION ON SEQ ID NO. 110:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1376 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

cgaagaagcc ccgccccgtc ccgcttagac aatgccccgg agccgccaga ccgtcgcgcc 60
cctgccccat cgtagtatat gagctcgcc acacaaggac ccccgctaaa agccagagct 120
cccagtcgcc gaggcttgaa gacggggact cccttctcca ccaactctgt cctcgggggg 180
tgggggcccca gccgagatca cagcgcgaca ggagtggggg tggccgctgg agacaggtga 240
agaaacaaga aaactaagaa atccgagcgg ttggaggggg agtctgtgtg gatgggatgg 300
ggacgccggg ggaggggctg ggccgctgct cccatgccct gatccgggga gtcccagaga 360
gcctggcgct cgggggaagg ggcggggctg gccttcccgc tctggatctg gccaaagctc 420
aaagggagca cggggtgctg ggaggtaaac tgaggcaacg actggggcta cagctgctag 480
aactgccacc tgaggagtca ttgccgctgg gaccgctgct tggcgacacg gccgtgatcc 540
aaggggacac ggccctaate acgcggccct ggagccccgc tcgtaggcca gaggtcgatg 600
gagtcgcaa agccctgcaa gacctggggc tccgaattgt ggaaatagga gacgagaacg 660
cgacgctgga tggcactgac gttctcttca ccggccggga gtttttcgta ggctctcca 720
aatggaccaa tcaccgagga gctgagatcg tggcggacac gttccgggac ttcccgctct 780
ccactgtgcc agtctcgggt ccctcccacc tgcgcggtct ctgcggcatg gggggacctc 840
gcactgttgt ggcaggcagc agcgacgctg cccaaaaggc tgtccgggca atggcagtgc 900
tgacagatca cccatatgcc tccctgaccc tcccagatga cgcagctgct gactgtctct 960
ttcttcgtcc tgggttgccct ggtgtgcccc ctttctcctt gcaccgtgga ggtggggatc1020
tgcccaacag ccaggaggca ctgcagaagc tctctgatgt caccctggta cctgtgtcct1080
gctcagaact ggagaaggct ggcgcggggc tcagctccct ctgcttggtg ctccagcacac1140
gccccacag ctgagggcct ggccttgggg tactgctggc caggggtagg atagtatagg1200
aagtagaagg ggaaggaggg ttagatagag aatgctgaat aggcagtagt tgggagagag1260
cctcaatatt gggggagggg agagtgtagg gaaaaggatc cactgggtga atcctccctc1320
tcagaaccaa taaaatagaa ttgacctttt aaaaaaaaaa aaaaaaaaaa agttct 1376

```

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

acgtatagtc gggtcggctg gtggagtagc tcagagtagg gggagcgccg taattgacac 60
atctcttatt tgagaagtgt ctggtgccct cattaggttt aattacaaaa tttgatcacg120
atcatattgt agtctctcaa agtgctctag aaattgtcag tggtttacat gaagtggcca180
tgggtgtctg gagcaccctg aaactgtatc aaagtgttac atatttccaa acatttttaa240
aatgaaaagg cactctcgtg ttctcctcac tctgtgcact ttgctgttg tgtgacaagg300
catttaaaga tgtttctggc attttctttt tatttctaag gtggtggtaa ctatggttat360
tggctagaaa tcctgagttt tcaactgtat atatctatag tttgtaaaaa gaacaaaaca420
accgagacaa acccttgatg ctcttgctc ggcgttgagg ctgtggggaa gatgcctttt480
gggagaggct gtagctcagg gcgtgcactg tgaggctgga cctgttgact ctgcaggggg540

catccattta gcttcaggtt gtcttgtttc tgtatatagt gacatagcat tctgctgcc600
tcttagctgt ggacaaaggg gggtcagctg gcatgagaat attttttttt ttaagtgcgg660
tagtttttaa actgtttgtt tttaaacaaa ctatagaact cttcattgtc agcaaagcaa720
agagtcaact catcaatgaa agttcaagaa cctcctgtac ttaaacacga ttcgcaacgt780
tctgttattt tttttgtatg tttagaatgc tgaaatgttt ttgaagttaa ataaacagta840
ttacattttt aaaa

```

854

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1681 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

ttcagctttt gccgaaatgg gtagtgatca cacacagtca tctgcaagca aaatctcaca 60
agatgtggac aaagaggatg agtttgggta cagctggaaa aatatcagag agcggttatgg 120
aaccctaaca ggcgagctgc atatgattga actggagaaa ggcatagtg gtttgggctt 180
aagtcttgct gggaacaaag accgatccag gatgagtgtc ttcatagttg ggattgatcc 240
aaatggagct gcaggaaaag atggctgatt gcaaatgtca gatgagcttc tagagatcaa 300
tggtcagatt ttatatggaa gaagtcatca gaatgcctca tcaatcatta aatgtgcccc 360
ttctaaagtg aaaataatth ttatcagaaa taaagatgca gtgaatcaga tggccgtatg 420
tcctggaaat gcagtagaac ctttgccttc taactcagaa aatcttcaaa ataaggagac 480
agagccaact gttactactt ctgatgcagc tgtggacctc agttcattta aaaatgtgca 540
acattctgga gcttcccaag gaggcagggg gggttgggta ttgctatcag cgaagaagat 600
cgactcagtg gagtcacatc aaagagctta acagagcatg gggtagcagc cagggatgga 660
cgactcaaag tcggagatca gatactggct gtagatgatg aaattgttgt tggttaccct 720
attgaaaagt ttattagcct tctgaagaca gcaaagatga cagtaaaact taccatccat 780
gctgagaatc cagattccca ggctgttctt tcagcagctg gtgcagccag tggagaaaaa 840
aagaacagct cccagtctct gatggtccca cagtctggct cccagaacc ggagtccatc 900
cgaaatacaa gcagatcatc aacaccagca atttttgctt ctgatcctgc aacctgcccc 960
attatccctg gctgcgaaac aaccatcgag atttccaaag ggcgaaacagg gctgggcctg1020
agcatcggtg ggggttcaga cacgctgctg ggtgccatta ttatocatga agtttatgaa1080
gaaggagcag catgtaaaga tggaagactc tgggctggag atcagatctt agaggtgaat1140
ggaattgact tgagaaaggc cacacatgat gaagcaatca atgtcctgag acagacgccal200
cagagagtg cactgacact ctacagagat gagggcccat acaaagagga ggaagtgtgt1260
gacaccctca ctattgagct gcagaagaag ccgggaaaag gcctaggatt aagtattgtt1320
ggtaaaagaa acgatactgg agtattttgt tcagacattg tcaaaggagg aattgcagat1380
gccgatggaa gactgatgca gggagaccag atattaatgg tgaatgggga agacgttcgt1440
aatgccaccc aagaagcggg tgccgtttgg ataaaagtgt ttccctaggg cacagttaac1500
cttgggaagt tgggaaggat tcaaagctgg gtcccgttcc gtttcaggag gagggagggc1560

cgttttttcaa aggcagccca gggttgagtt tgaaggggca gcctctttcg tcttttttca1620
cgttttttccc acttttttgg ggatccccgt ttacattttg agttccactt ggggaagtta1680
g

```

1681

## (2) INFORMATION ON SEQ ID NO. 113:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 852 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ggcaatttcc gttaggtgct gaaggctgtg ggcgcgggct gtccccattc ccacgtgaag 60
cgctacgcta gcatcgctcg gctggcggct cccagctcgc cgcggagcag tcccggcagc120
agcgggggac cggaagtggc tcgcggaggc tcagaagcta gtcccggagc ccggcgtgtg180
gcgcctcgga gcacggtgac ggcgccatgt ccctaattctg ctccatctct aacgaagtgc240
cggagcaccc atgtgtatcc cctgtctcta atcatgttta tgagcggcgg ctcatcgaga300
agtacattgc ggagaatggt accgaccca tcaacaacca gcctctctcc gaggagcagc360
tcacgacat caaagttgct cacccaatcc ggcccaagcc tccctcagcc accagcatcc420
cggccattct gaaagctttg caggatgagt gggatgcagt catgctgcac agcttcactc480
tgcgccagag ctgcagacaa cccgccaa ga gctgtcacac gctctgtacc agcacgatgc540
cgctgccgt gtcattgcc gtctcaccaa ggaaactgtg aaggggatgg gcaggagggc600
ttgtgcaggg ttttctaagc agtgatctag ttctattaaa aaaagaaaac aataaaaaag660
ccctgcacaa ggcctacagc ccctctccct tccgtcgtt caatggacgt ggtggtggct720
gttccacacc cattttgttg cagttcctgt gagacaggag aggctgagcc aagggaactg780
tgaaggggat gggcaggagg gcttgtgcag ggttttgtaa gcagtgatct agtttcatta840
aaaaaagaga ac

```

852

## (2) INFORMATION ON SEQ ID NO. 114:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1739 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

gaagccccggg gcctggcgac ggcacgcgg agcggagcgg cagcgcacgc gggcgatcgc 60
ttcacggatg cggacgacgt agccatcctt acctacgtga aggaaaatgc ccgctcgccc 120
agctccgtca cgggtaacgc cttgtggaaa gcgatggaga agagctcgct cacgcagcac 180
tcgtggcagt ccctgaagga ccgctacctc aagcacctgc ggggccagga gcataagtac 240
ctgctggggg acgcgcgggt gagccccctc tcccagaagc tcaagcggaa ggcggaggag 300
gacccggagg ccgcggatag cggggaacca cagaataaga gaactccaga tttgcctgaa 360
gaagagtatg tgaaggaaga aatccaggag aatgaagaag cagtcaaaaa gatgcttgtg 420
gaagccaccc gggagtttga ggaggttgtg gtggatgaga gccctcctga ttttgaaata 480
catataacta tgtgtgatga tgatccaccc acacctgagg aagactcaga aacacagcct 540
gatgaggagg aagaagaaga agaagaaaaa gtttctcaac cagaggtggg agctgccatt 600
aagatcattc ggcagttaat ggagaagttt aacttggtac tatcaacagt tacacaggcc 660
ttcctaaaaa atagtgggtg gctggaggct acttccgcct tcttagcgct tggtcagaga 720
gctgatggat atcccattht gtcccacaaa gatgacatag atttgcaaaa agatgatgag 780
gataccagag aggcatttgt caaaaaattt ggtgctcaga atgtagctcg gaggattgaa 840
tttcgaaaga aataattggc aagataatga gaaaagaaaa aagtcattgg aggtgagggtg 900
gttaaaaaaa attgtgacca atgaacttta gagagttctt gcattggaac tggcacttat 960
tttctgacca tcgctgctgt tgctctgtga gtcctagatt tttgtagcca agcagagttg 1020
tagaggggga taaaaagaaa agaaattgga tgtatttaca gctgtccttg aacaagtatc 1080
aatgtgttta tgaaaggaag atctaaatca gacaggagtt ggtctacata gtagtaatcc 1140
attgttgtaa tggaaccctt gctatagtag tgacaaagtg aaaggaaatt taggaggcat 1200
aggccatttc aggcagcata agtaatctcc tgtccttttg cagaagctcc tttagattgg 1260
gatagattcc aaataaagaa tctagaaata ggagaagatt taattatgag gccttgaaca 1320
cggattatcc ccaaaccctt gtcatttccc ccagtgaact ctgatttcta gactgctttg 1380
aaaatgctgt attcattttg ctaacttagt atttgggtac cctgctcttt ggctgttctt 1440
tttttgagc cttctcagt caagtctgcc ggatgtcttt ctttaacctac ccctcagttt 1500
tccttaaaac gcgcacacaa ctctagagag tgtaagaat aatgttactt ggtaaatgtg 1560
ttattttatt agtattgttt gtgctaagca ttgtgttaga ttttaaaaaa tagtggattg 1620
actccacttt gttgtgttgt tttcattgtt gaaaataaat ataactttgt attcgaaaaa 1680
aaaaaaaaa aaaaaaaaaa gaggagaaaa agagggggaaa ggggggaagag gagcaaaaga 1739

```

## (2) INFORMATION ON SEQ ID NO. 115:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 805 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

ataggcgcac cccaagggtca gggtcacctc gagcctccag acaactgogt caccttgacg 60
accaactgaa aaaaccggaa gggatggaag cagcggatca tctcgcgata tctggagcgt120
ctgcgcctgc cttcctgacc tgggacttgt ttccagctct cgcgagactt tcaggggtcg180
gagcgcgggg gccggccgag aggaaagctg gaggcgcggg tggggaacat gtctgagtcg240
gagctcggca ggaagtggga cgggtgtctg gcggatgcgg tcgtgaagat agaatcctgg300
taattgatgt ccaccgcgaga aatccctgca gatgttccag cctctgtcta gtccagatag360
ccacaggaag ggtactggtt ttggattagg aattgttttc tcaattacct tctttaaaag420
aagaatgtgg ccattagcct tcggttcttg catgggatta ggaatggctt attccaactg480
tcagcatgat ttccaggctc catatcttct acatggaaaa tatgtcaaag agcaggagca540
gtgacttcac ctgagaacat ccagcggga ggacaagaga aatcatgttt attcctcagg600
aatactgaag tgccctggag taagctgcca ttcttctgta acaatgttat cagtaatgct660
ttaaactcca gcacctggtt atgcatttga aaccaagtct gtttcttggt ttgtattttc720
tctctggaag ttgtaaggag gtggtcttaa ataaattaaa caaaaatagg aagtccaaa780
aaaaaaaaa aaaaaaaaaa aaaaa

```

805

## (2) INFORMATION ON SEQ ID NO. 116:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1483 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

tgaaaaagac ccaacgceaa cacctggtgc cttttgcagc cagcgccac ccacccgtgc 60
ccggaccctt gggaatgccc gcggctccag aggaaaaagc ccagggacgg ggcctccgtt 120
gcgggggggtc ggctgcttct tgggaacttt gtgctttccg gcgctggctg gctggctggc 180
tgtaaagcac tgaagcccc cgcccgccaa cccctgaaag cagaacctgg cctccctggc 240
cacagcagcc ttaccaccgg ctctacgtgt cccgggcact tcccgagcc ttcccgcccc 300
tttctcatcg gccttgtagt tgtacagtgc tgttggttg aaaaggtgat gtgtggggag 360

tgcggtcat cactgagtag agaggtagaa tttctattta accagacctg tagtagtatt 420
accaatccag ttcaattaag gtgatttttt gtaattatta ttattttggt gggacaatct 480
ttaattttct aaagatagca ctaacatcag ctcatagcc acctgtgcct gtccccgcct 540
tggcccggtt ggatgaagcg gcttccccgc agggccccc cttcccagtg gctgcttcc 600
ggggacccag ggcaccccg caccctcagg cacgctcctc agctggtcac ctcccggtt 660
tgccgttcag atggggctcc tgaggctcag gagtgaagat gccacagagc cgggctcccc 720
taggctgcgt cgggcatgct tggaagctgg cctgccagga ccttccaccc tggggcctgt 780
gtcagccgccc ggccctccgc accctggaag cacacggcct ctgggaagga cagccctgac 840
cttcggtttt ccgagcacgg tgtttcccaa gaattctggg ctggcgccct ggtggcagt 900
ctggagatga ccccgagccc ctcccgtgg ggcacccagg agggccctgc cggaatgtgc 960
agcctgtggg tagtcggctg gtgtccctgt cgtggagctg ggggtgcgtga tctggtgctc 1020
gtccacgcag gtgtgtggtg taaacatgta tgtgctgtac agagagacgc gtgtggagag 1080
agccgcacac cagcgccacc caggaaaggg ggagcgggta ccagtgtttt gtgtttattt 1140
ttaatcaaga cgtttccctt gtttccctat aaatttgctt cgtgtaagca agtacataag 1200
gaccctcctt tgggtgaaatc cgggttcgaa tgaatatctc aaggcaggag atgcatctat 1260
tttaagatgc tttggagcag acagctttag ccgttcccaa tccttagcaa tgccttagct 1320
gggacgcata gctaatactt tagagaggat gacagatcca taaagagagt aaagataaga 1380
gaaaatgtct aaagcatctg gaaaggtaaa aaaaaaaaaa tctatttttg gacaaatgta 1440
attttatccc ccattgggatg cttgggtatg gcggggggga ggc 1483

```

## (2) INFORMATION ON SEQ ID NO. 117:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

tgaggtcttc catgactgca agtgttatat tggactggat ggcatgaag tccctttcat 60
agccagagat tttgtgtggc tgctaaaatg cttacatctc tggctatgaa agggacttca 120
tgaccatcca gtccaatata acactgcag acagagaaac tgaggtcttc catgacttgc 180
ctagtctccc agctagtttg aggcaaaact ggattccac tctggtattc tttcttccct 240
ttacatcatt ttccctcctt tataatgtcc tgagagacca gaactcacac cagaatcgat 300
tattctcag gtgaagcata gactctttca tggtagacag atttcacgac tcagagatag 360
aaatctcttg ctatcatcag gtcacgggca gtcctgtgg agtcctgccc aacttatgtg 420
gcttcataa aatggcaaca gtccaggctc cttgccta attagagcat taactcccta 480
attgccagta agcaaggagg tggatctctg caaacctaca ctgtctatga cagctctagt 540
tgtacttggg gtgactaaat acctcaaagg caacctgctt ctgcagggtt tgaagtgtca 600
gcttcataag aactgaggt ttagaattgt ttgattctag accataactg aagggcataa 660
atggaaacag gatatgaagg gaaacaagta gcatcatgga gctgaaaagt ggtgcatcac 720
ccaatggcta gcacaaacaa ggatcacact gtccattctc ttgtctgcta aattaagcat 780
tttcttgctt cctttgcttc atcttttcac aacagctgga tagagggatc agaaatgact 840
gtgtcatggt gctcattcac tgcaaaactc cagttgcaag ctcttggct cccccggagg 900
gagcaagaat ctcatagttc agagacacag agggcctttt agccctaag accttttgga 960
tgggactgca actcatgact atcctgatat tggaagaaag gactttgtta atcttctccc1020
ccatagctct gctgcgtagg tctacatctt actcagaatc actacacatt cctttagtct1080
tcctccaagc tccagagcca ttggtacaaa tgctttattg aaactaaata cataatacac1140
acaatgagat gaagacaata tagaagtccg catagtcac ataatcccgt tccttggccg1200
gttgaggcag ctcaagggt gagcccagtc aagccaaccc gcagcttcac tcacgacttc1260
aagatttgat gctaattctt ttggatttct acagttatta aataagtgtc tgagtggaaa1320
aaaaaaaaa aaaaaaaaaa aaaaaat

```

1347

## (2) INFORMATION ON SEQ ID NO. 118:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1683 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

aattcggcac gatgggggga atctccgacc ccgacaccct acacatctgg aagaccaaca 60
gccttcctct ccggttctgg gtgaacatcc tgaagaaccc ccagtttgtc tttgacatcg 120
acaagacaga ccacatcgac gcctgccttt cagtcacgcg gcaggccttc atcgacgcct 180
gtccatctc tgacctgcag ctgggcaagg attcgccaac caacaagctc ctctacgcca 240
aggagattcc tgagtaccgg aagatcgtgc agcgctacta caagcagatc caggacatga 300
cgccgctcag cgagcaagag atgaatgccc atctggccga ggagtcgagg aaataccaga 360
atgagttcaa caccaatgtg gccatggcag agatttataa gtacgccaag aggtatcggc 420
cgcagatcat ggccgcgctg gaggccaacc ccacggccccg gaggacacaa ctgcagcaca 480
agtttgagca ggtggtggct ttgatggagg acaacatcta cgagtgcctac agtgaggcct 540
gagacacatg gagagtgggt caggctgctg ctgggagaaa tggacgcccc ctgggcctca 600
acttgatctt ctaccccgct cctgtgactc agactgggaa atactgagca gagacggctg 660
gggcgggggc aggaggaggg gctgctctct gagacagggg ccccccgcc ttgaccctg 720
ggcacctcca tccctccca cctgtcccca gatcagtcctc tgggatggag gccagagagc 780
tggtcaggct ccccatctg cccagcacgg cctgcactgt gcccacccac ttgctccaca 840
acgtccagtt ggtcctgctg ccaagagccc cgtgcaccca ggccgccaag cacaaactgg 900
gggagaggag gccgccagcc cggaggctgc agcccagaaa ctctacctca tccacactgg 960
tgcagggagc cctccttgaa ctgacctttg attggtttct gcttcaacta ccaaaatggt1020
atctccactt cccctcacc cgtagaggat cctggccaca gacagtttca agtagtgtca1080
gatttttggt gcttgggcgg ctggtggtag agtgggcagt gcccgcgcca tggggtgctc1140
tgtgggcttc tccaggagca gggaggggtg aggggagggg tggggggcac aggagctggg1200
agccccgtct ccaggaaaag gagaggggtt aagatgcacc gaggctgtag ctgggctact1260
tgatcttgct gaaagtgtt ctaaagatag caccactttt ttttttaaag cttttatata1320
ttaaaaaacg tatcatgcac caactgtgaa tagctgccgc ttgcgcagag gacccgggga1380
ggggtcccga gaggtcctcc atgcaacact ggaaatgact gttccagaga gcgggcagac1440
ctggcagagc gccctggcg cctgagacta ccaccactc cgttcctgcc agaaacgacc1500
ctctgtggc gatgggcat gcggggccct cgcagccaac tcagccagtg ttgggactgg1560
ctcagagccc atgggggctg gaggggggca gctgggactc tggaatcttc ttataataa1620
aagccttacg gacaaaccta aaaaaaaaaa aacaagacaa gagagggaaa gggaaagaag1680
ggg

```

1683

## (2) INFORMATION ON SEQ ID NO. 119:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

acaagcatgg aagctttact gtttcggctc ttcaaacttc cagcaactac actgcggtgc 60
atcggacttc gacgcccgtt ggtgacgcac acgctgcgcc ggaagtgtga acacaaagcc 120
tccaggcttt gtcattggcg ctgctgctgc acgctggaac catgtgtggg tcggcaccga 180
gactgggatc ttgaaagggg taaatcttca gcgaaaacag gcggcgaact tcacggccgg 240
aggacagccg cggcgcgagg aggcagtga cgcctgtgt tggggcaccg gcggcgagac 300
ccagatgctg gtgggctgcg cggacaggac ggtgaagcac ttcagcaccg aggatggcat 360
attccagggt cagagacact gcccgggcgg ggagggcatg ttccgtggcc tcgcccaggc 420
cgacggcacc ctcatcacat gtgtggattc tgggattctc agagtctggc atgacaagga 480
caaggacaca tcctctgacc cactcctgga actgagagtg ggccctggg tgtgtaggat 540
gcgccaagac ccagcacacc cccatgtggt tgccacaggt gggaaagaga atgctttgaa 600
gatatgggac ctgcagggt ctgaggaacc tgtgttcagg gccaaagaacg tcggaatga 660
ctggctggac ttgcgggttc ccatctggga ccaggacata cagttttctc caggatcaca 720
gaagcttgtc acctgcacag ggtaccacca ggtccgtgtt tatgatccag catcccccca 780
gcgcccggca gtcctagaga ccacctatgg agagtaccca ctaacagcca tgaccctcac 840
tccgggaggg aactcagtga ttgtgggaaa cactcatggg cagctggcag aaattgacct 900
tcggcaaggg cgtctactgg gctgtctgaa ggggctggca ggcagtgtgc gtgggttgca 960
gtgccaccct tcaaagcctc tactagcctc ctgtggcttg gacagagtct tgaggataca 1020
caggatccag aatccacggg gtctggagca taagggttat ctcaagtctc aattgaactg 1080
cctcctcttg tcaggcaggg acaactggga ggatgagccc caagagcctc aagaacccaal 1140
caaggtgccc ctagaagaca cagagacaga tgaactttgg gcaccccttg aggcagctgc 1200
caagcggaag ctctcgggtt tggagcagcc ccaaggagct ctccaaacga gacggagaaa 1260
gaagaagcgg cctgggtcca ccagcccctg acgcccctgt gccactttg taaataaaact 1320
gctgaacacc caaaaaaaaaa gaaaaaaaaa agggg

```

1355



## (2) INFORMATION ON SEQ ID NO. 120:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1816 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggtcagagag attctgaaaa gtaatccaaa gtgttcgcta gctaaacatg gtgcagggtc 60
gttgtagcac tgcaaccgac tgacgttact gtagttccta gaatgctgtg agggcggggg 120
gttcagatca acataaagcc taacttgctg gagttgtagt ctcaaggctt tctctcttgc 180
ttaactaaaa cctaaggacc actgtttttg gtagcaatta tatggttact atccactgca 240
gtcctcagtt gttggggtaa atcccacatg gcagagtaag gcacccca gaaattaact 300
tggagagcct gagaaattcc cagtggcctt ggcatagctg tctagaacac catctctagg 360
aaaatttaat tctgtccctg gccagctatt gttcttccac ttcgttttct gctgtcccaa 420
ggccagatga gtggaatcac catctgactg ttgtcaataa aatgtatctg gcgtgaacag 480
caggataacc catgttctcc acataaggat aaccttacgt gaaaccttcc tgctgacaac 540
catgcagagg aatttttcca cttaagtcag agccttcctc cccatctgga attcacagct 600
gttccctggc agcacacagg aggtatttaa ggaccttgtt gaggctaggt acaactgtcca 660
cacctctttg gggaaagttac gatttttttt ttccatcata attcagtctc ttcttattct 720
acagtgtgca ctttatgcct ctcgcctttt gataatagtt gttcagtga ggaagtcagc 780
tgccagaata ttaagaaggg tctcccttta tgtcagtaca actgttaggg cggccttccc 840
atttacttta ggtttcaaga ggattcaccg gaagcacatg ccccggtcta gtcccatttg 900
aaacagttct gctttactga gaccctaggc cggctcctt gctgacccta gcgtgctgc 960
ctaggtgcca tttcctttcc tctcagtc aatacaggct gcacattttg tcacttaatg1020
ccagtacaat ctgtgttact cctaaggact tttgggattt tgatgagacc tgcgaggag1080
aagacactga gaagccagtg atctgcaagc atttgctctt gtttccacat cacctctggg1140
atatttcagc tggtgtttcc aaatggcaaa tcatcaacta aaagcacttg tttcaagttt1200
tgttctgcac tcccacgact gaagttgtag attgagctga ataaccatgg gaagtgacca1260
agcaaagaca ctcgattgga gtcagttgaa tatttgtagc ctcaaggagg ccttctggt1320
cttttcttcc acttctgcag aatttctctt agcaaatact tctttctcct tgcttgcctc1380
caccatgata tttgaataag agatggccag aggataacac ttgtctctta aaaactaagc1440
taaaaagaac ctagaacctt caattgagca gttgtgaaaa ttgctaattg tgccaaggcc1500
aagcaaagag tttcagaaaa tgactgagaa ggagcgataa ccccagaat gcaaaatcag1560
gggcatcatt atccggtgct tgaacaagga gctccgctct acaactgggt ttttaggac1620
ttgtgaggaa cacagcaacg gaaatccatc cacaaaggat gcagtgcctc aacttgtaact1680
gcgcctgaat agtcatgtga taatttactg aagaaatcta gtgtacttta aatttttttc1740
ataaaaagtt acattgtatt gtaggttaac attaaatgtt ttatagcaaa aacttcaaaa1800
aaaaaaaaa aaaaaa

```

1816

## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 740 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

tttagaattc agcataggtt gaggtcagaa agcaattcag gcatgagcca ccgtgcccgg 60
cttcacaccc atttctttaa aaaggatccc gtagcaggca gaaaagcccc ttccatcctg120
ctcctctgat actgtgcccc cttggagata tttccgtcct ccaccacgt gtctgtggct180
ggaactgccc agcctgtctc tggccccctg gaagcctccc cacagctggt aatctggact240
taaggattgc tgggccaccg cctctctgcc taccaccatt ccatatttaa gtggagcccc300
tacgtagaaa ggccccgggg ctttatttta gtctcctttt cagggatgtc gtggcggggg360
gaggggggtc ttggtgctac agccctctcc ccacccttaa agggacgccg acgctgtttg420
ctgccttcac cacatattag tgcttgacct tggcagggga ccccatggaa aagatgggga480
agagcaaaat acatggagac gacgcacct ccaggatgct cgctgggatt ccacgcca540
ccactgtccc ccaccccatg gctgggaggg gcctctgaac ggaacagtgt cccacagag600
cgaataaagc caaggcttct tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aagatagggt660
agttaaggcg gccgaaagtt tttttccctt tagtaagggt tagtttttag tttgggggtg720
gccttcgttt ttaagaacgt

```

740

## (2) INFORMATION ON SEQ ID NO. 124:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1493 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

aacacctgcc ctggttcagc gcttttaggga gggcggtca ggcgccccg agcaggcaga 60
gtgctgtggag ctgctgtctgg ccctgggcca gcctgcggag gagctgtgcg aggagttcct 120
ggcgcacgcc cgcggccggc tggagaagga gctgagaaac ctggaggccg agctggggcc 180
ctcacctccg gctcccgcg tgtagagtt caccgacct ggaggcagt gcttcgtggg 240
cggcctctgc cagggtggcg cggcctacca ggagctgttt gcggcccagg gccagcagg 300
tgccgagaag ctggcgccct tgcggcgca gctgggcagc cgctattttg cgctggtgga 360
gcgcgcgctg gcgcaggagc aggggtggtg tgacaactca ctgctggtgc gggcgctgga 420
ccgcttccac cggcgcttgc gggctcccg ggcctgctg gccgctgccg ggctcgaga 480
cgctgccacg gagatcgtgg aacgagtggc ccgcgagcgc ctgggccacc acctgcaggg 540
tctccgggcg gccttctctg gctgcctgac agacgtccgc caggcgctgg cagcacctcg 600
cgtggctggg aaggagggcc ctggcctggc cgagttgctg gccaatgtgg ccagctccat 660
cctgagccac attaaaggct ctctggcagc agtgcacctt ttcaccgcca aagggtgtc 720
cttctccaac aagccctact tccgggtga gttctgcagt cagggtgtcc gtgaggccct 780
catcgtgggc ttcttccact ctatgtgcca gacggtcag agcttctgcg acagccctgg 840
ggagaagggg ggtgccacac cacctgccct gctcctgctg ctctcccgc tctgctgga 900
ctacgagacg gccaccatct cctacatct cactctcact gatgaacagt ttctggtgca 960
ggatcagttc ccagtgcgc ccgtgagcac gctgtgtgca gaggccaggg aaacggcgcg1020
gcggtgctg acccactacg tgaaggtgca gggcctggtc atatcacaga tctgctgca1080
gagcgtggag actcgcgact ggctcagcac tctggagccc cggaatgtgc gggccgtcat1140
gaagcgggtg gtggaggata ccaccgccat cgacgtgcag gtggggctcc tgtacgaaga1200
gggtgttcgc aaggcccaga gcagcgactc cagcaagagg actttctccg tgtacagcag1260
ctctcggcag cagggccgct acgccccag ctatacccc agtgccccga tggacacca1320
cctcttgagc aatatccaga agctattctc tgaacgtatt gatgtgttca gccctgtgga1380
gttcaacaag gtgtcggtgc tgaccggcat catcaagatc agcctgaaga cgcttgctgg1440
gagtgtgtgc gggctgcgaa cctttttggc cctttgcggg cttcaacaag ggg 1493

```

## (2) INFORMATION ON SEQ ID NO. 125:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 250 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ccagactgaa ttgtcagtga gcggatctga gggcggtgtg gagtggccag tggggccttgg 60
ccgagatgga caaccggatt ccttatgatg actagccggt ggtttccttg ctgcctatga120
gaatcctcca gcatggaatc ctctcatga gagggtagac agccggacta caacgatgag180
ttgacccagt tttggcccga accatcacac tgaagaagcc tcttgagtc attgggatta240
agatcgaggg
                                         250

```

## (2) INFORMATION ON SEQ ID NO. 126:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

tcgggggggag cggcgcgggcg gcgcggggagt tggttctaaa gagtgggtgag tcagaagaga 60
cgtcaggcag caagcgactt gggccatggc ctctgacctt gacttctcac ctccggaggt 120
gcccagagccc actttcctgg agaacctgct acggtagcga ctcttcctgg gagccatctt 180
ccagctcatc tgtgtgctgg ccatcatcgt acccattccc aagtcaccac aggcgagggc 240
tgaaccgtct gagcccagaa gtgctgaggt gacgaggaag cccaaggctg ctgttccttc 300
tgtgaacaag agggccaaga aagagactaa gaagaagcgg tagaagagga ggcctgagga 360
gctgggcggg cagggagagg gtcttgggga cagccctcct gggaatctac attgtgttcc 420
cccgcatctc aggtcagggt tctgaggagg ctgtgacgcc ctatgaccgc agagatctag 480
acagtcgtaa cagtcctccag gctccagctg ggcaatccac cacttcctct tccttctgct 540
tctgtgacgg tttagagtca agggggctga aacacactgt gagcatagac tgtattaggt 600
ttgttcagaa gccgggtcag ctccacagagt cacattttct tgcttagtca tgtgtccctc 660
cttgagttgc cccctccttg tgggtttaca ctacattttg gagtcatgtt ctaatgctga 720
caagcacacc ctctcccatc atttgtgcac tacagatctc ctgctgatca gtcacctttg 780
ttgctgctgt gtagacagag ccaggcctca cctgtttggt taggccaaga tgccatggac 840
atgcagcggt agtgatccca ctagctgtga cagccaggcc cagaaaatgc ctggcgtgag 900
agccagcaga cagccaggcc aggggtaggc agtgctgct tctgctccat cagggtgcagg 960
ggatttggtc gaaggcgtgc atatttctct ggcacaaact tcctgagcct ctgaaatggg 1020
aggctcgtca atttcagacc aacctctttt caaccatca tagcacgttc aaggtgtgcc 1080
ttttacttct acctgtacat ccccatccc ttcaattctt tcattccctg accagtgag 1140
gggttcctgg gggaagtatg gtgaataaac tgacatgcat gcttcagaaa aaaaaaaaaa 1200
aa

```

1202

## (2) INFORMATION ON SEQ ID NO. 127:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

cccttttttt ttctttttga gatgggggga aagtcctagc aaaaggcagg agttagcatt 60
ttccttttaac aagactttct aatgctaaac aaagaccaac ttctttttaa aggggttggt 120
ttggttggtg gtgaaaaata ctgtactgta atgatctgct tggtttttaa gcaaaagaga 180
tcctgacatg tgaaaccaat acaccaaatt gccaaagtcca caaatgaaca aaacaagtgc 240
ttaaaaaaaaa aattcttctg ctcttatatt tttggaggaa gctgctgatt ttggctgtca 300
gatttcactt agaaatggtc actttctgag atgctttttc ctacacagaat ctgtagataa 360
actcattaaa agattgtccc atttcaaaat ccccccaag tctagcagca ctgttttttt 420
tttttttagt ttttgtttta aaattacaaa ccaagtaaga agtccaacat cctcttccat 480
gaacagcttt gtgacagagc tcctgagtgt gtgcagcccc cactgtgctc tgaatacagt 540
ctctgcagct ccagtgtgtc ctcttttcag gaaggaaagc atattcaata cattcactat 600
ctgtaccccc tggaacttgc acatgctgac gagctattat aagccaactc atccccagct 660
ctcttcgggg actggtcacc ccttgtaaaa ccattctgta taagttctct ttgaaatttc 720
tgatcttgag cagcatattc agaaagttca gattccaccg cgggaggagg aatgtttgga 780
ataaatttag aaaatagagt tggagccatc tgaacccact ctggtctgag ggtatacagg 840
cctttcaciaa tatttgccat agttgaaggt gtgacctgaa atggtgttga ctgggcttct 900
aaaagtaaag gcattaggcc gtaaatgtgc ttttctgcaa catgttccgt aaacagcttt 960
ataagggcac ctttaagccc gggtaagctg gtccatggga acctatcggt tttg 1014

```

## (2) INFORMATION ON SEQ ID NO. 128:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

caccaaatta atcagggttta cagacaggggt cccaccggta ttcacattct tgtagtgat 60
cagatgggttc agaattttca agatgagagt tgttttttat tctccacagt aaaagctgaa 120
agtagtgatg gcatccacat aattttgaaa tgatgtctta tatagactga actgtattca 180
gtaccaaata gtcacgctta aaagtgtgtg aagactgaat ccaagaagtc ttgggattgg 240
attttaccat atgaaatgtt tcatattgaa aacacaagat gacctttcta atgagctgta 300
tgagagggtga atctcctcac tgtcactgcc atagccaagc atcctcatga gagtgagcac 360
atcggcacag catgcatcca gctctggagg ccacgggtgca ggcatagctg cctgctgctc 420
tggcagaggc cagtaaaatac agttcctaga agcagccttt gctgtctttt tacactgtat 480
gcggttttga aatgaatgta gaaacttact gtgggcattt acctttctgt gccagtttgg 540
cttttattgc ctgaacctta tgctgacctg gagaggagat gggggacagt gctgttgg 600
ggccagcagt gaatctgtat gcggagagtt gtgttgtgct gatgtggccg ttggtggtca 660
ggtaagaggc tcggcacctt cttggaagaa atcatgtctg aggggtgtacg tttgatatga 720
tcatgccaga ttggagaaga tccaagccag gaagatgggc ttgaagcaaa ctgcattatc 780
aggagtacct tgggtgagagg atcagtgtaa atcctaatag gtacaaagac ttttgtgttt 840
tggttttgtc acagatttat tgaaaaactt ttttgcttct gcttccattt ttagcatttt 900
agtttctggt tttcattttt ggagattcct tgccttttaa actcgtggtt tttctctcat 960
tttcttccct ctctccctcc atctctgacc acccccacc taacccccca ccccaccat1020
cctattaaac atttttaaag ccctacccca gacattggga aataggtgga cccaagtagg1080
gggggaggaa agtattgatt tgtttgata ggcttggga ttaggggtgtt aagggggttct1140
tggattatgg aacaaggtgg aatttttttt g                                     1171

```

## (2) INFORMATION ON SEQ ID NO. 129:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 353 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cdna library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

ggccgggacg cagggcaaag cgagccatgg ctgtctacgt cgggatgctg cgccctgggga 60
ggctgtgctg cgggagctcg ggggtgctgg gggcccgggc cgccctctct cggagttggc120
aggaagccag gttgcagggt gtccgcttcc tcagttccag agaggtggat cgcatggtct180
ccacgccccat cggaggcttc agctacgttc aggggtgcac caaaaagcat cttaacagca240
agactgtggg ccagtgcctg gagaccacag cacagagggg cccagaacga gaggccttgg300
tcgtcctcca tgaagacgtc aggttgacct ttgcccaact caaggaggag tgg                                     353

```

## (2) INFORMATION ON SEQ ID NO. 130:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 205 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

cggctgagcg gccccgcagc caacccccga ggagcggccg gctggcgtgc cgctggcgcc 60
caggagttag ggatgtccta caaacccatg cgcccctggc tgcccagcag caccacctgg120
tctgccaggc accccctggg gcccggggca ccccggttcc ctgacaggga ggcgtgcgcg180
tgcgccgtgc ggggctgcag tgtcc
                                         205

```

## (2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 211 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

aaatcacctt acaacccatt tctcagaaca tgtttctatt gttaaacaac acacaactat 60
tttatttatg tgttttattt atgcctgac accaatatca ataactgaaa cacagcagtt120
tagtaataat ttaatacaca ccataacctg cctattgaga atggcattat atttgtttct180
attgtagtgg ctccatccaa aataaaatga t
                                         211

```

## (2) INFORMATION ON SEQ ID NO. 132:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 867 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

gtcttcccaa gatggagatg ctaacgaaac tgagaagggg gcgtatgttt gacgaaggtt 60
tgtgcaagtc aggcccttct ggaacacagc agggcctaca acgaggggccc tttgcgatgg120
gctgtgagga tgggggtggt gggagaatt ggccacgtta gagaccccat gccacccac180
catggtgagt gctctgtgcc tctgtctcac ctgtggtgag tgggcgagct gggcgagctg240
ggcgagctgg gctggggaga gcctgtgagg accgagagga gaaatgagaa gaaggaacaa300
aaatattatt tctatgtaat ttatatTTTA cttatgccaa attatttatg ataatttgcc360
attgctatac tgtaccagtg tcaaagtctg cagcctgcca agctgtgatt ttgtgaggct420
tgtccctatg taggatgcac cgcaggcccc tggccactga aagagtgtgc agtggactgt480
gggtctccca tatgcggtgc cgcccaaagg tggctttgcc tcaagcaacc taccctgatg540
ttttactcat tggaatgttt ttccccgatt gtggatgact tcttttctga tggagagagt600
ccaggaggga tggaaaacgc ctggatttaa gctcagcatc cccacatgg gcttttcgat660
catcttcagg cctgaagctg cagcaoctga agttcgctg catttatcag ccctctttgt720
gctgctcctt gccaccttgg ggttctgct ggggaacctg tgtggttgtg gcatgtgtga780
gcagaaggga ggatgaggaa aaaagagaa gaaacccccg ttagtgacaa gtgttttttt840
gagttgccag gttttgccat cattaaa
                                         867

```

## (2) INFORMATION ON SEQ ID NO. 133:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 257 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

aattcagact cccattctta acttggcatt tttgtagctt acaggaacca gcttgggtgta 60
ccttctctta tgagatgcag ctggaaagcc atttatgcaa gaggtgggtt cacttttgtc120
gctcctccat tcattgaccc ttcagccctt aaaaaattag aatgtgaaaa ttagtagcaal80
agagtgcaga gatattagct taagggataa ataaatgaaa gtagcaagta gtcattatt240
tatgaagagt aataatt
                                         257

```

## (2) INFORMATION ON SEQ ID NO. 134:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 204 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

gactggctca tggcctctgt aaatggctgc tggcgggact gtctgcctag cgggtgccct 60
tggaacctag cccttggtgg gttttgagga aatgattcct gaatgaggag tcgattgccg120
tgtgaagggc tggtaggcacg gcacccgcgt gagctacgcg tgcctcagt gcgcttctgg180
attgactggc catgggtgct caca

```

204

## (2) INFORMATION ON SEQ ID NO. 135:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 245 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ttgcaccatg gtaaactgtg ataatacagt atcatttttg agcagttttt taaatgtaaa 60
tctgtatctt actcagagtg tgtgtctgaa gttattaagg acatttccca acgttactgg120
cccatttccc tttgtaatca gaggaattct gtttcaagat tattgttggtg tgtgatctgt180
ggctcttgat cagaatgaag ttaaattggc acaggaggat taagctatga ggttggcatt240
tttca

```

245

## (2) INFORMATION ON SEQ ID NO. 136:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1637 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

ggggaggggac gagtatggaa ccctgaaggt agcaagtcca ggcactggcc tgaccatccg 60
gctccctggg caccaagtcc caggcaggag cagctgtttt ccatcccttc ccagacaagc 120
tctattttta tcacaatgac ctttagagag gtctcccagg ccagctcaag gtgtcccact 180
atccccctctg gaggggaagag gcaggaaaat tctccccggg tccctgtcat gctactttct 240
ccatcccagt tcagactgtc caggacatct tatctgcagc cataagagaa ttataaggca 300
gtgatttccc ttaggcccag gacttgggcc tccagctcat ctgttccttc tgggccatt 360
catggcagggt tctgggctca aagctgaact ggggagagaa gagatacaga gctaccatgt 420
gactttacct gattgccctc agtttggggt tgcttatttg gaaagagaga gacaaagagt 480
tacttggttac gggaaatatg aaaagcatgg ccaggatgca tagaggagat tctagcaggg 540
gacaggattg gctcagatga cccctgaggg ctcttccagt cttgaaatgc attccatgat 600
attaggaagt cgggggtggg tgggtgggtgg gggctagttg ggtttgaatt taggggccga 660
tgagcttggg tacgtgagca ggggtgttaag ttagggctg cctgtatttc tgggtccctt 720
ggaaatgtcc ccttcttcag tgtcagacct cagtcccagt gtccatatcg tgcccagaaa 780
agtagacatt atcctgcccc atcccttccc cagtgcactc tgacctagct agtgccctgg 840
gcccagtgac ctggggggagc ctggctgcag gccctcactg gttccctaaa ccttggtggc 900
tgtgattcag gtccccaggg gggactcagg gaggaatatg gctgagttct gtagtttcca 960
gagttggctg gtagagcctt ctagagggttc agaattattg cttcaggatc agctgggggt 1020
atggaattgg ctgaggatca aacgtatgta ggtgaaagga taccaggatg ttgctaaagg 1080
tgagggacag tttgggtttg ggacttacca ggggtgatgt agatctggaa cccccaagt 1140
aggctggagg gagttaaggt cagtatggaa gatagggttg ggacagggtg ctttggaatg 1200
aaagagtgac cttagagggc tccttgggcc tcaggaatgc tcctgctgct gtgaagatga 1260
gaagggtgctc ttactcagtt aatgatgagt gactatattt accaaagccc ctacctgctg 1320
ctgggtccct tgtagcacag gagactgggg ctaagggcc ctcaggga agggacacca 1380
tcaggcctct ggctgaggca gtagcataga ggatccattt ctacctgat ttcccagagg 1440
actagcagga ggcagccttg agaaaccggc agttcccaag ccagcgcctg gctgttctct 1500
cattgtcact gccctctccc caacctctcc tctaaccac tagagattgc ctgtgtcctg 1560
cctcttgct cttgtagaat gcagctctgg ccctcaataa atgcttcctg cattcatctg 1620
caaaaaaaaa aattttc
1637

```

## (2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 260 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

aaaagcatag ctcaactctgt aataggctat tttcatgatt tcaagtgggt ttatgaagaa 60
acagaaagca gtgatgatgt tgaagtgctg actctcaaga aattcaaagg agacctggcc120
tacagacgac aagagtatca ggtagaattc aacatatggt gcttgaagtg ggctcttggt180
ttatcagtta tggcatatgt aaataacagt gtaccaagtt agtgtggtgt ttatgaagat240
gagtttaatc ttttgtgatg
                                         260

```

## (2) INFORMATION ON SEQ ID NO. 138:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 957 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

ggggaatttg tctttggaaa gcttgtgcaa cctctacaac tggcgataca agaatctagg 60
aaacttacct catgtgcagc tcttgccaga gttagtaga gcaaagtctg gcttactgta120
tgacttccag ctcattaatg ttgaagattt tcaaggagtg ggagaatctg aacctaatcc180
ttactttctat cagaatcttg gagaggcaga atatgtagta gcacttttta tgtacatgtg240
tttacttggt taccctgctg acaaaatcag tattctaaca acatataatg gccaaaagca300
tcttattcgc gacatcatca atagacgatg tggaaacaat ccattgattg gaagaccaa360
caaggtgaca actgttgata gatttcaagg tcaacagaat gactatattc ttctttctct420
ggtacgaacc agggcagtgg gccatctgag ggatgtccgt cgcttggtag tggccatgtc480
tagagccaga cttggacttt atatcttcgc cagagtatcc ctcttccaaa actgttttga540
actgactcca gctttcagtc agctcacagc tcgccccctt catttgcata taattccaac600
agaacctttc ccaactacta gaaagaatgg agagagacca tctcatgaag taaaaataat660
aaaaaatatg cccagatgg caaactttgt atacaacatg tacatgcatt tgatacagac720
tacacatcat tatcatcaga ctttattaca actaccacct gctatggtag aagaggggtga780
ggaagttcaa aatcaagaaa cagagttgga aacagaagaa gaggccatga ctgttcaagc840
tgacatcata cccagtccaa cagacaccag ctgccgtcaa gaaactccag cctttgagcg900
tgagagccgc cccggtgggg aaggggcaat tgcgttgggg gggcttgggt gtttttt 957

```

## (2) INFORMATION ON SEQ ID NO. 139:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 760 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

gtggaataca atagatatta atttgtggtt ggtttttctg cctgotttaa atgaaatgta 60
ttatgtttct gggttccttt tttagctgta aaaatacttc gtcactaaag catgaaattt120
aatcagcagt tgttcttcaa gttcctgaaa gctataaaag tttctcatga cttgagtgg180
tttttcctg cccaccagag gagaaagccc ttgtagaatt ctgcagtggt acaagtgttc240
cctacaaaaa ctgaaacat cagctcctct ttaacaagtt ggctttttta aagcacgtaa300
ttacaattta atggtattct gttaaagtgg gctctaggca taatttaa at tctttttaat360
gactatattt cttcaaaact ttgaaagaaa aatgtgttct ttttgctgca tcctttgtaa420
gaagactgcc aacagaggaa aaaggacttt acaaattaag accatcttgg tttcatttcc480
acaaagatga gaacaaatca tgggtgttag aaaggatcct tagaagaaca caagaatttg540
aaagcccttg gtggttatca ctactatatt tcatatttcc acagaagtga cttagccaag600
ctctgcattt tgagcctgct gactttcatt taaaaggaat gaaaggctga aaatccaggc660
tgctgtgtct gtagataaag gtcaaaccat gtttgagttc ttcactgttg tgtccaccta720
aataaaaactg agtaagtaat gaaaaaaaaa aaaaaaaaaa 760

```

## (2) INFORMATION ON SEQ ID NO. 140:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 260 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

aggaaccctc cggcctagaa gtccagatgt cttgccata tatctgtgct tcacaacttg 60
cctactctct ctgacccta acattttcac atacttttcc aattctgcct gtcataaatt120
tgctgcttcc ccctaagtag aatgttgatt cctgtcaaac acacagccta gccctgattc180
ctcctcttct ctcaagcagt gatattgtca acaatgataa acaactacta tgtactgagt240
gtttttttat gtgctgctca cactttatac acatgtatag 280

```

## (2) INFORMATION ON SEQ ID NO. 142:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 461 base pairs
- (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

gcgggccgctc gaggggaagca cccgccgggtt ggccgaagtc cacgaagccg ccctctgcta 60
gggaaaaccc ctggttctcc atgccacacc tctctccagg tgccctctgc ctcttcaccc120
cacaagaagc cttatcctac gtccttctct ccatctatcg gaccccagtt tccatcacta180
tctccagaga tgtagctatt atgcgcccgt ctacaggggg tgcccgcgca tgacggtgcc240
ttcgcagtca aattactctt cgggtcccaa ggtttggtt tcacgcgctc cattgccccg300
gcgtggcagg ccattccaag cccttccggg ctggaactgg tgcggagga gcctcgggtg360
tategtacgc cctggtgttg gtgttgctc actcctctga gctcttctt ctgatcaagc420
cctgcttaaa gttaaataaa atagaatgaa tgataccccg g 461

```

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 436 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

caaagatgtc atgtggccag aatcatcttt tagtctcacc actccacact gatggtcaca 60
tagaggtgtg agttgggaag ttgttaaata caagagggtt tgagcttctg gagaagagga120
aaatgtaaaa gtattttttc ctttaagaaa gataaaaagg taagcctaaa ccttggcggc180
caccgaagtc agctgttacg catgtgtagt taaatttcac tgtaaattt tcataagggt240
tcttagaatg gagccagggt gacatcacag cccaactgt accaaaggaa ccatttcatt300
caaataagcc aacatttcca aagaaacacg aatgtctatg gcagagttaa cataagggtca360
gaaaatcctc tggaagaaat ttcgggtatca atgtttataa tctctgcatt taggggtttg420
ccagtttggg caaaaaa                                     436

```

## (2) INFORMATION ON SEQ ID NO. 144:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 287 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

ctttaaagta gggctgtgga agggggatat agtagagggg gagagggctg ttttatacac 60
gtataaatgg tataccat ttatacacgg tggtcagaga agctctgatc aggtgacgtal20
tgtacagaaa gtcactgtgg cctgagtaga gtcaaggaga aggagcagca agagttgagcl80
ttagggaggt ggagaagggg tggaatagat caagcaagac cttggccctg gtagggatct240
gggattttaa gtgagaggac aaccgttggg atgttgtgag cacagaa                287

```

## (2) INFORMATION ON SEQ ID NO. 145:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 555 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ggcgacgcct cggtactgac ctctgcagag ccgggtggag cccattgacg tccagcgaac 60
gaggagcagc gatggacggt cgggtgcagc tgataaaggc cctcctggcc ttgccgatcc120
ggcctgcgac gcgtcgctgg aggaaccgga ttccctttcc cgagacggtt gacggcgata180
ccgaccgact cccggagtgc atcgtgcaga cgggtccta catgttcgtg gacgagaaca240
cgttctccag cgacgccctg aaggtgacgt tcctcatcac ccgcctcaca gggcccgccc300
tgcaagtggg gatcccctac atcaagaagg agagccccct cctcaatgat taccggggct360
ttctggccga gatgaagcga gtctttggat gggaggagga cgaggacttc taggccggga420
gaccctcggg cctggggggc ggtgctctgg ggaggggccg ctgtgttact ggccgccgcc480
agggctcgcca ccggcgccct ccctccgcga gtccctcccc ctcgaaaccg ccgcgaagtc540
ccctgcggtg ctgtt
555

```

(2) INFORMATION ON SEQ ID NO. 146:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1790 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

agtgagaaaag cagggactct tcggcctagg cagccgggac ccagccagcc ctgcgcctcg 60
cgccgtcgcg catgcgtcct ggtctttctc tagagttgta tatatagaac atcctggagt 120

ccaccatgaa cggacagttg gatctaagtg ggaagctaata catcaaagct caacttgggg 180
aggatattcg gcgaattcct attcataatg aagatattac ttatgatgaa ttagtgctaa 240
tgatgcaacg agttttcaga ggaaaacttc tgagtaatga tgaagtaaca ataaagtata 300
aagatgaaga tggagatcct ataacaattt ttgatagttc tgacctttcc tttgcaattc 360
agtgcagtag gatactgaaa ctgacattat ttgttaatgg ccagccaaga ccccttgaat 420
caagtcaggt gaaatatctc cgtcgagaaac tgatagaact tcgaaaataaa gtgaatcggt 480
tattggatag cttggaacca cctggagaaac caggaccttc caccaatatt cctgaaaatg 540
atactgtgga tggtagggaa gaaaagtctg cttctgattc ttctggaaaa cagtctactc 600
aggttatggc agcaagtatg tctgcttttg atcctttaaa aaaccaagat gaaatcaata 660
aaaatgttat gtcagcgttt ggcttaacag atgatcaggt ttcagggcca cccagtgtct 720
ctgcagaaga tcgttcagga acaccogaca gcattgcttc ctctcctca gcagctcacc 780
caccaggcgt tcagccacag cagccaccat atacaggagc tcagactcaa gcaggtcaga 840
ttgaagggtca gatgtaccaa cagtaccagc aacaggccgg ctatggtgca cagcagccgc 900
aggtoaccac tcagcagcct caacagtatg gtattcagta ttcagcaagc tatagtcagc 960
agactggacc tcaacaacct cagcagttcc agggatatgg ccagcaacca acttcccagg 1020
caccagctcc tgctttttct ggtcagcctc aacaactgcc tgctcagccg ccacagcagt 1080
accaggcgag caattatcct gcacaaactt acactgcca aacttctcag cctactaatt 1140
atactgtggc tcctgcctct caacctggaa tggctccaag ccaacctggg gcctatcaac 1200
caagaccagg ttttacttca cttcctggaa gtaccatgac ccctcctcca agtgggccta 1260
atccttatgc gcgtaaccgt cctccctttg gtcagggtca taccacaacct ggacctgggt 1320
atcgataagg aggtccctct acaccaatta atgtagctgc tagctattgg cctcccaaaa 1380
gactccagta ctattttaat ttgtattgaa gaagttcaga aattttaaaag cagagcattt 1440
tttatgatat cattgttggg gttaattgaa agtataattt gctggaacac aaagaccaaa 1500
atgaaagttt tttcctccct gcttaaaaaa gtagcagctt cttagttaact ttggaacact 1560
actcttacat gtataaagtg attgacttga ctttctagct tcccttgctc ggaggatatt 1620
aaaatgcttg ggtgaggttt agccatctta cttggctttt tactattaac atgatgtact 1680
aaagttagag cctttgagaa tacaagatat tatgtataaa atgtaacact gatgatagg 1740
taataaagat gattgaatcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaca 1790

```

## (2) INFORMATION ON SEQ ID NO. 147:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2357 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

ctcgagccga atcggtctga ggcgagacct gcagcgggca aagagctccc gaggaagcac 60
agcttgggtc aggttcttgc ctttcttaat gttagagaca gctaccggaa ggaggggaac 120
aaggagttct ctccgcagc ccctttcccc acgcccaccc ccagtctcca gggacccttg 180
cctgcctcct aggtcggaag ccatggtccc gaagtgtagg gcaaggggtgc ctcaggacct 240

tttgggtcttc agcctccctc agccccccag atctgggtta ggtggccgct cctccctgct 300
cctcatggga agatgtctca gagccttcca tgacctcccc tccccagccc aatgccaaagt 360
ggacttggag ctgcacaaaag tcagcaggga ccactaaatc tccaagacct ggtgtgcgga 420
ggcaggagca tgtatgtctg cagggtgtctg acacgcaagt gtgtgagtgt gagtgtgaga 480
gatggggcgg ggggtgtgtct gtagggtgtct ctgggcctgt gtgtgggtgg ggttatgtga 540
gggtatgaag agctgtcttc ccctgagagt ttctcagaa cccacagtga gaggggagg 600
ctcctggggc agagaagttc cttaggtttt ctttggaatg aaattcctcc tccccccat 660
ctctgagtag aggaagccca ccaatctgcc ctttgagtg tgcagggtgg aagtaagag 720
gttgggtgtg agttggggct gccatagggg ctgcagcctg ctggggctaa gcggtggagg 780
aaggtctctg cactccaggc atatgtttcc ccatctctgt ctggggctac agaatagggt 840
ggcagaagtg tcacctgtg ggtgtctccc tggggggtc tccccctaga cctccccctc 900
acttacataa agctcccttg aagcaagaaa gaggggtccc gggctgcaa actggaagca 960
cagcctcggg gatggggagg gaaagacggg gctatatcca gttcctgctc tctgctcatg 1020
ggtggctgtg acaacctggt cctcacttga ttcatctctg gttttcttgc caccctctgg 1080
gagtecccat cccattttca tctgagccc aaccaggccc tgccattggc ctctgtctcc 1140
ttggcacact tgtaccaca ggtgaggggc aggacctgaa ggtattggcc tgttcaacaal 1200
tcagtcatca tgggtgtttt tgtcaactgc ttgttaattg atttggggat gtttgccccg 1260
aatgagaggt tgaggaanaa actgtgggtg gggaggccct gcctgacca tcccttttcc 1320
tttctggccc cagcctaggt ggaggcaagt ggaatatctt atattgggcg atttgggggc 1380
tcggggaggc agagaatctc ttgggagctt tgggtggcgc tgggtgcattc tgtttcctct 1440
tgatctcaaa gcacaatgtg gatttgggga ccaaaggtca gggacacatc cccttagagg 1500
acctgagttt gggagagtgg tgagtggaa gaggagcag caagaagcag cctgttttca 1560
ctcagcttaa ttctccttcc cagataaggc aagccagtca tggaatcttg ctgcaggccc 1620
tccctctact cttcctgtcc taaaaatagg ggccgttttc ttacacaccc ccagagagag 1680
gagggactgt cacactggtg ctgagtgacc gggggctgct gggcgctctg tctttaccaal 1740
aaccatccat ccctagaaga gcacagagcc ctgaggggct gggctgggct gggctgagcc 1800
cctggtcttc tctacagttc acagaggtct ttcagctcat ttaatcccag gaaagaggca 1860
tcaaagctag aatgtgaata taacttttgt ggaccaatac taagaataac aagaagccca 1920
gtggtgagga aagtgcgttc tcccagcact gcctcctgtt ttctccctct catgtccctc 1980
cagggaaaat gactttattg cttaatttct gcctttcccc cctcacacat gcacttttgg 2040
gccttttttt atagctggaa aaaacaaaat accacctac aaacctgtat ttaaaaagaa 2100
acagaaatga ccacgtgaaa tttgcctctg tccaaacatt tcatccgtgt gtatgtgtat 2160
gtgtgtgagt gtgtgaagcc gccagttcac ctttttatat ggggttgttg tctcattttg 2220
gtctgttttg gtccctccc tcgtgggctt gtgctcggca ccaaagagaa aaacgttttg 2280
ggggcttgta atttatcctg aaaaatttaa ctttgagcga aaagggggag tgttttaccg 2340
tgggggggta aaataaa
2357

```

## (2) INFORMATION ON SEQ ID NO. 148:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 907 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
gttcattgtc tggcaccaag ctcccttgggg tgaattttct tccaaaagag tccgggggagt 60
ccagggtcctt cttccttggtt actcataacg cgccccatt tctcactccc attgggcgtc120
gggtttctag agaagccaat cagtgtcgcc gcagttccca ggttctaaag tcccacgcac180
cccgcgggac tcatattttt cccagacgcg gaggttgggg tcatggcgcc ccgaagcctc240
ctcctgctgc tctcaggggc cctggccctg accgatactt gggcggtga gtgcggggtc300
cagagagaaa cggcctctgt ggggaggagt gaggggcccc cccggtggg gcgcaggact360
cagggagccg cgcccgagg aggtctggc ggtctcagc ccctcctcg ccccaggctc420
ccactccttg aggtatttca gcaccgctgt gtcgcggccc ggccgcggg agccccgcta480
catcgccgtg gagtacgtag acgacacgca attcctgcgg ttcgacagcg acgccgcgat540
tccgaggatg gagccgcggg agccgtgggt ggagcaagag gggccgcagt attgggagt600
gaccacaggg tacgccaagg ccaacgcaca gactgaccga gtggccctga ggaacctgct660
ccgccgtac aaccagagcg aggtggtga gtgaaccgg ccggggggcg aggtcacgag720
caccccccat ccggcacggg accgccggg tccttcagag ttccgggtgc gaaatgtacc780
ccgagggagg ggagggcgtt gattgctgga gtggatactg ggggggtttt acgcaggttc840
attttcagtt taggccaata tccccgcggg ttgggcgggg atgggggggg gttaggtggg900
cggggtt
```

907

## (2) INFORMATION ON SEQ ID NO. 149:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

aggaggcgtg gggggggggg cgggggagtc aggggaagagc accatcgtca agcagatgaa 60
gatcatccac gaggatggct actccgagga ggaatgccgg cagtaccggg cggttgtcta 120
cagcaacacc atccagtcca tcatggccat tgtcaaagcc atgggcaacc tgcagatcga 180
ctttgccgac cctccagag cggacgacgc caggcagcta tttgactgt cctgcaccgc 240
cgaggagcaa ggcgtgctcc ctgatgacct gtccggcgtc atccggaggc tctgggctga 300
ccatggtgtg caggcctgct ttggccgctc aagggaatac cagctcaacg actcagctgc 360
ctactacctg aacgacctgg agcgtattgc acagagtgc tacatcccca cacagcaaga 420
tgtgtacgg acccgcgtaa agaccacggg gatcgtggag acacacttca ccttcaagga 480
cctacacttc aagatgtttg atgtgggtgg tcagcgggtc gagcgggaaga agtggatcca 540
ctgctttgag ggcgtcacag ccatcatctt ctgcgtagct tgagcgccta tgacttggtg 600
ctagctgagg acgaggagat gaaccgcatg catgagagca tgaagctatt cgatagcatc 660
tgcaacaaca agtgggtcac agacacgtcc atcatcctc tcctcaacaa gaaggacctg 720
tttgaggaga agatcacaca cagtcccttg accatctgct tccctgagta cacagggggc 780

aacaatatg atgaggcagc cagctacatc cagagtaagt ttgaggacct gaataagcgc 840
aaagacacca aggagatcta cagcacttc acgtgcgcca ccgacaccaa gaacgtgcag 900
ttcgtgtttg acgccgtcac cgatgtcatc atcaagaaca acctgaagga ctgcccctc 960
ttctgagggg cagcggggcc tggcgggatg ggccaccgcc gactttgtac cccccaaccc1020
ctgaggaaga tgggggcaag aagatcacgc tccccgcctg ttccccgcgc gcttttctcc1080
tctttcctct ctttgttctc agctccccct gtccctcag ctccagacgt aggggagggg1140
ttgccacagg cctccctgtt tgaagcctgc ccttgtctga gatgctggtg atggccatgg1200
taccoccttc tgggcatctg ttctggtttt taaccattgt cttgttctgt gatgagggga1260
ggggggcaca tgctgagtc cccaaggctg cgtctggagg ggcccctgct tctccagcct1320
ggacccccag ctttgcccaa caccagcccc tgccccagcc caagtccaaa tgtttacagg1380
gagcctcctg cccagtcccc caaccccagc cgctcggagg ccccaaagga aaaagcaca1440
gaagcgtgag acgccaccat tccctggaaac cacagtccac ctgctcattc tcgtagcttt1500
ttaaaaaaat gaaagtaaa gaaaaaaa aaactgcaaa tctagaaaac tttttagaga1560
aaaactattt aaaactgtca gatcctgacc agcaagcgcc cccccagccc cccttccaag1620
tgactccgtg ccttgagtg gtctgcgtgt ttacacccgt cctctgctg gccgcccccg1680
tgcgagcggc acccctgccc tgccctccac agaattgggt tccaagggct gttccagaca1740
actgccaacg tctactgagg ccctgcccc ggggcccctg cccagggctc tattaacct1800
aaatgtagct ccctagcgt aacctaggaa ccgcccgtgc ctgctggggg gccacgcccc1860
tcatgccctt gtcccaggcc cggggccttc agcgttgaac acttccctgc ttttttcaca1920
tgttttatgg aattgttcac ctggtttgaa ataataaat gtagaaagga aaaaaaaaaa1980
aaaaaaa

```

1987

## (2) INFORMATION ON SEQ ID NO. 151:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2906 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

gtccagaagc	aaaaattaag	ttccccaagt	tttccatgcc	caagatcggc	atcccaggtg	60
tgaaaatggg	gggtggggga	gccgaggtcc	atgccagct	accctctctt	gaaggagact	120
tgagaggacc	agatgttaag	ctcgaagggc	ccgatgtttc	tctaaagggg	ccaggagtag	180
acttgccctc	agtgaacctc	tctatgccaa	aagtctctgg	gcctgacctt	gatctgaact	240
tgaaaggacc	aagtttgaag	ggagacctgg	atgcatctgt	tcccagcatg	aagggtgcatg	300
ctccagggct	caacctcagt	ggtgtcgggt	gcaaaatgca	ggtgggagga	gacgggtgtga	360
aagtgccagg	gatcgatgcc	acaacaaagc	ttaacgttgg	ggcaccagat	gtgacactga	420
ggggaccaag	cctgcaggga	gatctggctg	tctctggtga	catcaaatgc	cctaaagtat	480
ccgtaggagc	tcctgatcta	agcttggagg	catccgaagg	cagcattaaa	cttcccaaaa	540
tgaagctgcc	ccaatttggc	atctctactc	cgggggtccg	cttgacagtc	aatgccaaag	600
ggccacaggt	ttctggcgaa	ctgaaggggc	caggtgtgga	tgtgaacctg	aaagggcctc	660
ggatttcagc	accgaatgtg	gactttaact	tgggaaggacc	aaaagtgaag	gggagccttg	720
ggggccactg	tgagatcaaa	ggccccactg	toggaggagg	tcttccaggc	attggtgttc	780
aaggccatga	aggaaacctc	cagatgcctg	gaattaaagt	ctctggatgt	gatgtgaacc	840
tgccaggcgt	gaatgtgaaa	ctcccaactg	ggcagatttc	tgggcctgaa	atcaaaggtg	900
gtctgaaagg	ttcagaagta	ggtttccatg	gggctgctcc	tgatatcagt	gtgaaggggc	960
ctgcctttta	tatggcatct	cctgagtcag	attttggcat	caacttgaag	ggcccaaaaa	1020
tcaaaggagg	tgcgatgtt	tcaggggggt	tcagtgcctc	agacatcagc	cttgggtgaag	1080
ggcattttgag	tgttaaaggt	tcgggggggt	agtggaaagg	acccaagtc	tcctctgtctc	1140
tcaacttggg	cacatctaag	tttgctgggg	gccttcattt	ctcaggacca	aagggtgaag	1200
gaggtgtgaa	aggaggtcag	attggactcc	aggctcctgg	gctgagtggt	tctgggcctc	1260
aaagtcactt	ggaaagtggg	tctggaaaag	taacattccc	taaaatgaag	atcccaaaat	1320
ttaccttctc	tgccgtgag	ctgggtggca	gagaaatggg	ggtggatgtt	cacttcccta	1380
aagcagaggc	cagcatccaa	gctggtgctg	gagacggcga	gtgggaagag	ctgaagtca	1440
aactgaaaaa	gtccaagatc	aaaatgccca	agtttaattt	ttccaaacct	aaagggaag	1500
gtggtgtcac	tggtcacca	gaagcatcaa	tttctgggtc	caaaggtgac	ctgaaaagtt	1560
caaaggccag	cctgggctct	ctggaaggag	aggcagaggc	cgaagcctct	tcaccgaaag	1620
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aaagagagtt	ctctggacct	tcacccccga	cggggacgct	ggagtttgaa	ggtggggaag	1740
tgtctctgga	aggtgggaaa	gttaaaggga	aacacgggaa	gctgaaattc	ggtacctttg	1800
gtggattggg	gtcaaagagc	aaaggtcatt	atgaggtgac	tgggagcgat	gatgagacag	1860
gcaagttaca	ggggagtggg	gtgtccctgg	cctctaagaa	gtcccgaact	tcctcctctt	1920
ctagcaatga	cagtgggaat	aaagttggca	tccagcttcc	cgaggtggag	ctgtcagttt	1980
ccacaaagaa	agagtagcag	gcctttgtag	aacaaaacat	cagccttggg	tggtgtgttc	2040
ctatataaac	tccaaaggga	aacacaccga	ctgcctcagc	aatcatgcaa	agaccttgcc	2100
tggcccggtg	gcaagcgctg	aaaaaccgac	cgctgtagg	ctcctggaac	tatacagata	2160
ggtaaagagt	tccaagtctg	tccagcccat	gtgcaaagtc	aacagtattt	gccttaagat	2220
ttcatatata	tatatTTTTT	tgcattgact	gctgagagct	cctgtttact	aagcaagctt	2280
ttgtgtttat	tatcctcatt	tttactgaac	attgttagtt	ttggggtaat	ggaaaccac	2340
tttttcattg	taatgacttt	gggggctttt	gttagtaagg	gtgggtggg	tgatgggttg	2400
cagacggagg	tcaggtcttc	ctctttcctg	agactggatc	tgttcaaaac	gcaaaccgcc	2460
acagatggcc	cagaggtggg	ggtagtcagg	gtgtgtgggt	gttttttagg	ttcttttagt	2520
ttgtttcttt	caccagggg	tggtggtccc	agccagtttg	gtgctgacgg	tgagaggaaa	2580
ttagaatctg	tttgcaatt	gtccaaccca	ccccctcaac	atgaggggct	tccattttct	2640
gtgttttgta	agggaactgt	ttccttcag	ccgccatgtt	cctgatatta	gttctgattt	2700
ctttttaaca	aatgttatca	tgattaagaa	aatttccagc	actttaatgg	ccaattaact	2760
gagaatgtaa	gaaaattgat	gctgtacaag	gcaataaag	ctgtttatta	accttgaaaa	2820
aaaaaaaaaa	aaggaggagg	ggggggggag	gggggagggg	gggggggggt	aggggggggg	2880
agggagggaa	agggggggcg	gggagg				2906

## (2) INFORMATION ON SEQ ID NO. 153:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

gcctcccgcc cgccgcctct gtctccctct ctccacaaac tgcccaggag tgagtagctg 60
ctttcggtcc gccggacaca ccggacagat agacgtgagg acggcccacc accccagccc 120
gccaactagt cagcctgcgc ctggcgccct ccctctccag gtccatccgc catgtggccc 180
ctgtggcgcc tcgtgtctct gctggccctg agccaggccc tgccctttga gcagagaggc 240
ttctgggact tcacctgga cgatgggcca ttcatgatga acgatgagga agcttcgggc 300
gctgacacct cgggcgctct ggaccggagc tctgtcacac ccacctacag cgccatgtgt 360
cctttcggtc gccactgcca cctgcgggtg gttcagtgtc ccgacctggg tctgaagtct 420
gtgccc aaag agatctcccc tgacaccacg ctgctggacc tgcagaacaa cgacatctcc 480
gagctccgca aggatgactt caagggtctc cagcacctct acgccctcgt cctggtgaac 540
aacaagatct ccaagatcca tgagaaggcc ttcagcccac tgcggaagct gcagaagctc 600
tacatctcca agaaccacct ggtggagatc ccgccc aacc taccagctc cctggtggag 660
ctccgcatcc acgacaaccg catccgcaag gtgccc aagg gagtgttcag tgggctccgg 720
aacatgaact gcatcgagat gggcggg aac ccactggaga acagtggctt tgaacctgga 780
gccttcgatg gcctgaagct caactacctg cgcattctcag aggccaa gct gactggcatc 840
cccaaagacc tccctgagac cctgaatgaa ctccacctag accacaacaa aatccaggcc 900
atcgaactgg aggaactgct tcgctactcc aagctgtaca ggctgggcct aggccacaac 960
cagatcagga tgatcgagaa cgggagcctg agcttcctgc ccacctccg ggagctccac 1020
ttggacaaca acaagttggc cagggtgccc tcagggtctc cagacctcaa gctcctccag 1080
gtggtctatc tgactccaa caacatcacc aaagtgggtg tcaacgactt ctgtcccatg 1140
ggcttcgggg tgaagcgggc ctactacaac ggcacagcc tcttcaacaa ccccgctgcc 1200
tactgggagg tgcagccggc cactttccgc tgcgtcactg accgcctggc catccagttt 1260
ggcaactaca aaaagtagag gcagctgcag ccaccgaggc gcctcagtgg ggtctctgg 1320
ggaacacagc cagacatcct gatggggagg cagagccagg aagctaagcc agggcccagc 1380
tgctccaac ccagccccc acctcgggtc cctgacccca gctcgatgcc ccatcaccgc 1440
ctctccctgg ctcccaaggg tgcaggtggg cgcaaggccc ggccccatc acatgttccc 1500
ttggcctcag agctgcccc ctctctccac cagagccacc cagaggcacc ccatgaagct 1560
ttttctcgt tcaactccaa acccaagtgt ccaaggctcc agtcctagga gaacagtccc 1620
tgggtcagca gccaggaggc ggtccataag aatggggaca gtgggctctg ccagggtctg 1680
cgcacctgtc cagacacaca tgttctgttc ctctctca tgcatttcca gcctttcaac 1740
cctccccgac tctgcggtc ccctcagccc ccttgcaagt tcatggcctg tccctccaag 1800
acccctgctc cactggccct tcgaccagtc ctcccttctg ttctctcttt ccccgctcct 1860
cctctctctc tctgtgtgtg tgtcgtgtgt gtgtgtgtgt gtgtgtgtgt gtcttgtgtg 1920
tcctcagacc tttctcgctt ctgagcttgg tggcctgttc cctccatctc tccgaacctg 1980
gcttcgctctg tccctttcac tccacacctt cctggccttct gccttgagct gggactgctt 2040
tctgtctgtc cggcctgcac ccagccctg ccacaaaaac ccaggggaca gcggtctccc 2100
cagcctgccc tgcctaggcc ttgccccaa acctgtactg tcccggagga ggttgggagg 2160
tggaggccca gcatcccgcg cagatgacac catcaaccgc cagagtccca gacaccggtt 2220
ttcctagaag cccctcacc ccactggccc actggtggct aggtctcccc ttatccttct 2280
ggtccagcgc aaggaggggc tgcttctgag gtcggtggct gtctttccat taaagaaaca 2340
cogtgcaacg tgaaaaaaaa aaaaaaa

```

2367

## (2) INFORMATION ON SEQ ID NO. 154:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

cacacacctg cacatactca tgcattgcaca tgtacacacg cagtcacaca tgcactcacg 60
cagttgcaca cacacgcattg ctactcccca cactgtgtgc actcaggtgg ctgtgttgga 120
cagttggggcc caggggtccc ctgctgtcct gtggggccgg catctgctct ccttctttct 180
ccccaggtag ttctactccc gaaggattga catcaccctg tcgtcagtca agtgcttcca 240
caagctggcc tctgcctatg gggccaggca gctgcagggc tactgogcaa gcctctttgc 300
catcctcctc cccaggacc cctcgttcca gatgcccctg gacctgtatg cctatgcagt 360
ggccacaggg gacgcccctg tggagaagct ctgcctacag ttccctggct ggaacttcga 420
ggccttgacg caggccgagg cctggcccag tgtcccaca gacctgctcc aactgctgct 480
gcccaggagc gacctggcgg tggccagcga gctggcccta ctgaaggccg tggacacctg 540
gagctggggg gagcgtgcct cccatgagga ggtggagggc ttggtggaga agatccgctt 600
ccccatgatg ctccctgagg agctctttga gctgcagttc aacctgtccc tgtactggag 660
ccacgaggcc ctgttccaga agaagactct gcaggccctg gaattccaca ctgtgccctt 720
ccagttgctg gcccggtaca aaggcctgaa cctcaccgag gatacctaca agccccggat 780
ttacacctcg cccacctgga gtgcctttgt gacagacagt tcctggagtg cacggaagtc 840
acaactggtc tatcagtcca gacggggggc tttggtcaaa tattcttctg attacttcca 900
agccccctct gactacagat actaccctta ccagtccttc cagactccac aacaccccag 960
cttcctcttc caggacaaga ggggtgtcctg gtccctggtc tacctcccca ccatccagag 1020
ctgctggaac tacggcttct cctgctcctc ggacgagctc cctgtcctgg gcctcaccaa 1080
gtctggcggc tcagatcgca ccattgccta cgaaaacaaa gccctgatgc tctgcgaagg 1140
gctcttcctg gcagacgtca ccgatttcga gggctggaag gctgcgattc ccagtgcctt 1200
ggacaccaac agctcgaaga gaacctctc cttcccctgc cccggcagag cttttcaaac 1260
gggctttccg caacgggtca atccgcgcct ttctaacttg acaaacttct tcag 1314

```

## (2) INFORMATION ON SEQ ID NO. 155:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 965 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

cctcccaaag gaactcccca atactagaac tcatcccaaa ccccttgac ttcaacaaat 60
taacgaaccc attccccaac ccacaatacc ccaccctcca acaacctaaa acaacgactt120
catgctcccg tgcccaaaac gcacagacct tcaacctgga cggctccctg arctatgaaa180
gactcccatc gtcttgacgt cggctcttcac cagcgtgcgg cagaaaatcg agaaggagga240
tgacagtga ggcgaggaga gtgaggagga ggaagagggc gaggaggaag gctccgaatc300
cgaatctcgg tccgtcaaag tgaagatcaa gcttgccgg aaggagaagg cacaggaccg360
gctgaagggc ggccggcggc ggccgagccg agggctccga gccaaagccg tcgtgagtga420
cgatgacagt gaggaggaac aagaggagga ccgctcagga agtggcagcg aagaagactg480
agccccgaca ttccagtcct gaccocgagc ccctcgttcc agagctgaga tggcataggc540
cttagcagta acgggtagca gcagatgtag ttccagactt ggagtaaaac tgtataaaca600
aaagaatott ccatatattat acagcagaga agctgtagga ctgtttgtga ctggccctgt660
cctggcatca gtagcatctg taacagcatt aactgtctta aagagagaga gagagaattc720
cgaattgggg aacacacgat acctgttttt cttttccggt gctggcagta ctgttgccgc780
gcagtttgga gtcactgtag ttaagtgtgg atgcatgtgc gtcaccgtcc actcctccta840
ctgtatttta ttggacaggt cagactcgcc gggggcccg cgagggtatg tcagtgtcac900
tggatgtcaa acagtaataa attaaaccaa caacaaaacg caaaaaaaaa aaaccaaggg960
cgaga                                         965

```

## (2) INFORMATION ON SEQ ID NO. 156:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3101 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ctcgcgccgg	acacagggag	cagcgagcac	gcgtttcccg	caacccgata	ccatcggaca	60
ggatttctcc	gcctcagccc	aacggggagg	gctagttgca	catagtgatt	tagatgaaag	120
agctattgaa	gctttaaaaag	aattcaatga	agacggtgca	ttggcagttc	ttcaacagtt	180
taaagacagt	gatctctctc	atgttcagaa	caaaagtgcc	tttttatgtg	gagtcatgaa	240
gacttacagg	cagagagaaa	aacaagggac	caaagtagca	gattctagta	aaggaccaga	300
tgaggcaaaa	attaaggcac	tcttgaaaag	aacaggctac	acacttgatg	tgaccactgg	360
acagaggaag	tatggaggac	cacctccaga	ttccgtttat	tcaggtcagc	agccttctgt	420
tggcactgag	atatttgttg	gaaagatccc	aagagatcta	tttgaggatg	aacttgttcc	480
attatttgag	aaagctggac	ctatatggga	tcttcgtcta	atgatggatc	cactcactgg	540
tctcaataga	ggttatgcgt	ttgtcacttt	ttgtacaaaa	gaagcagctc	aggaggctgt	600
taaactgtat	aataatcatg	aaattcgttc	tggaaaacat	attggtgtct	gcattctcagt	660
tgccaacaat	aggctttttg	tgggctctat	tcctaagagt	aaaaccaagg	aacagattct	720

tgaagaatTT agcaaagtaa cagagggTct tacagacgtc attttatacc accaaccgga 780  
 tgacaagaaa aaaaacagag gcttttgctt tcttgaatat gaagatcaca aaacagctgc 840  
 ccaggtaaaa gtgctgtttg tacgcaacct tgccaatact gtaacagaag agattttaga 900  
 aaaggcattt agtcagtttg ggaaactgga acgagtgaag aagttaaaag attatgcgtt 960  
 cattcatttt gatgagcgag atggtgctgt caaggctatg gaagaaatga atggcaaaga1020  
 cttggaggga gaaaatattg aaattgtttt tgccaagcca ccagatcaga aaaggaaaga1080  
 aagaaaagct cagaggcaag cagcaaaaaa tcaaatgtat gacgattact actattatgg1140  
 tccacctcat atgccccctc caacaagagg tcgagggcgt ggaggtagag gtggttatgg1200  
 atatcctcca gattattatg gatatgaaga ttattatgat tattatggtt atgattacca1260  
 taactatcgt ggtggatatg aagatccata ctatggttat gaagattttc aagttggagc1320  
 tagagcaagg ggtggtagag gagcaagggg tgctgtccca tccagaggtc gtggggctgc1380  
 tcctccccgc ggtagagccg gttattcaca gagaggaggt cctggatcag caagggcgt1440  
 tcgaggtgcg agaggaggtg cccaacaaca aagaggccgc gggcaggga aaggggtcga1500  
 ggcgggtcct gacctgttac aatgaagact gacttgctat gtgggattac accagaagct1560  
 tgcagtggag taatggtaag gaaatcaagc aaccttaaat atgtcggctg tataggagca1620  
 tattctattg cagaagacct tcctatgaag atcatggaat caaatacggg acattgaact1680  
 aatacttgga ctttgatatg aatttcttta acaattttct ctgcagtgc agttattaaa1740  
 ctaaaagctac tctattttca aaatgtgttc caacagaaat ccttcataac tcctagcatg1800  
 gtatcttaat aaagaataaa gttcttttaa aaatctgctc taagtagatt tttccccctt1860  
 tttaaattaa ggatcccaac agtgggtatt tgaaatattc tcttgaattt gtgcatttaa1920  
 attttattgc agtggtatag atgaatgcca ctgatggtat ccttaaattt tatttctgct1980  
 caccaagggt aatcatgatt gtctatatct tttttatagt gatcactttt gaattgtgtt2040  
 cagatatgca gtttcagggtg taatcatcag agctgggttag tcaggcattc cagatagtgg2100  
 ttcttttcag aaccttttta aaaggggttg ttaactacct cagtagcaga ggattgaact2160  
 atacctgtc tgtactgtac atagaaaatc tttgtagata aaagcaaggc ttgttaaata2220  
 tgatatgagg gtaagatttt aatataccaa atgtaacatt cttagtgtgc tttagtttca2280  
 gaggcttgta agacttcctc atgaccatca taacaggcct tgcttttgtc gtattttgtg2340  
 gctgaaaaag cagccttgct tcttcagata ttgtagttat ttggatgtat aatagttag2400  
 caagatgtta cttttgtaag acatcagatg ttcaaaaaag tgcattccga cttgtactaa2460  
 atactgcagt gtccctttat aaaaagtcag actaaaactg acaattgtac agcgaagcct2520  
 gacatttgga tattttgaag ttttttcata aatcatagaa attagtatat ggctgtagt2580  
 tagcttttta ggtaaaagggt atgtttcatt agtgcatttc ttctgctga tcaactgtaa2640  
 catgtgaatc agctttccat ttcttatgca ggtcatgata acttgtagag tagagtacaa2700  
 tcatttgtgc tatgttttta attttctaaa gcacctgat gacagtgagt gtccagtgg2760  
 gaagcatcct ctattgaacc accctcaaaa atttttttgc caagtcctaa gttgatagct2820  
 taaagtaaaa agtgaaaatt atagtttcat taggacttgg tgtaaagaaa tccccctccc2880  
 ccttccccaa agggatactg cagtttatat acatacccaa taggcaccac gatgaagatc2940  
 agagcttata cttaattaag gttttataca caccagttcc ccagtaaag caaatttaac3000  
 aagaaaatca gacatgtcat atgttcaaaa tgctcatggc aaacaatcat tttgcattcc3060  
 tgcaaaataaa attgttttat actgtaaaac aaaaaaaaaa a 3101

## (2) INFORMATION ON SEQ ID NO. 157:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 983 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

ggggcgggag cggcggtcca gactggggag ggacgcgcac cggccaggag gcttcaagag 60
gagggcacta gggccctgcg agcggcgtct taaccggcgg cgctaggact ccgcgggaaa120
cggcgggggc ggacgggcgg caccaggacc cagggggaacc gcgacgggcg ggcggcgagc180
aggcccggga gccgggaggt gcgggcggcg gcgctggacc cgacgcggcg agagaggccc240
cgagatgccg agcaagaaga agaagtacaa cgcgcggttc ccgcggcgcg ggatcaagaa300
gatcatgcag acggacgaag agattgggaa ggtggcggcg gcggtgcctg tcatcatctc360
ccgggcgctc gagctcttcc tagagtcgct gttgaagaag gcctgccagg tgacccagtc420
gcggaacgga aagaccatga ccacatccca cctgaagcag tgcacgagc tggagcagca480
gtttgacttc ttgaaggacc tgggtggcatc tgttcccgac atgcaggggg acggggaaga540
caaccacatg gatggggaca agggcgcccc caggggccgga agccaggcag cggcggcccg600
aagaacggtg ggatgggaac gaaaagcaag gacaagaagc tgtccgggac agactcggag660
caggaggatg aatctgagga cacagatact gatggggaag aggagacatc acaaccccca720
ccccaggcca gccacccctc tgcccacttt cagagccccc cgacaccctt cctgccttct780
gcctctactc tgccttttgc cccagcgccc ccgggcccct cagcacctga tgaagaggac840
gaagaagatt acgactccta gcgccttctg cccccagac catagcccct tttagttggt900
tttagttgct ctggggggag gagagaaggt agagctgttc ttaaatttat taaaaaaaaa960
aataaaaggg aaaaaaaaaa aaa

```

983

## (2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 293 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```
FIDSYRCFQP KQEGAFTCWS AVTGARHLNY GSRLDYTLGD RTLVIDTFQA SELLPEVMGS 60
DHCPVGAVLS VSSVPAKQCP PLCTRFLPEF AGTQKILRF LVPLEQSPVL EQSTLQHNNQ120
TRVQTCQNK A QVRSTRPQPS QVGSSRGQKN LKSYFQSPSP CPQASPDIEL PSLPLMSALM180
TPKTPEEKAV AKVVKGQAKT SEAKDEKELR TSFWKSVLAG PLRTPLCGGH REPCVMRTVK240
KPGPNLGRRF YMCARPRGPP TDPSSRCNSS SGAGPAEPME AWGHLAWSPL HMI 293
```

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 131 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```
ETLREKQEAA QGRGAGLRSC AGVTMPDVPR PPLVQLGLLQ RKNCTGRRGQ WEDPGAWHTC 60
RSGGPSWVLA SSQYASHMAP CGPHRGVCAR APPAQTSRMR SVTPSHLWLL KSWPAPSPLW120
PLPSLLESSG S 131
```

(2) INFORMATION ON SEQ ID NO. 160:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 94 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KRRPKLGPGE FTVRITHGSL WPPQRGVRKG PASTDFQNEV RNSFSSLASE VLACPFETTLA60  
TAFSSGVFGV MRALISGR LG SSMSG EAWGQ LG EG 94

## (2) INFORMATION ON SEQ ID NO. 161:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 136 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

LHQLAAQRLY LRPVRVGAWA LSLPGERRAE ISNQWSALVT WIPEGREGST VSSAADCCSK 60  
NVFSTSFESP SHGNPSTPTR DPTPAVSRIS STCTSRDPND SCTNEHYGSC SNCLSTHCYV120  
GWKAFGRRKG SSRLKG 136

## (2) INFORMATION ON SEQ ID NO. 162:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 281 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

PGSQKVAKAV PFPQRRTAAV RMSFPPHLNR PPMGIPALPP GIPPPQFPGF PPPVPPGTPM 60  
IPVPMSIMAP APTVLVPTVS MVGKHLGARK DHPGLKAKEN DENC GPTTTV FVGNISEKAS120  
DMLIRQLLAK CGLVLSWKRV QGASGKLQAF GFCEYKEPES TLRALRLLHD LQIGKKLLV180  
KVDAKTKAQL DEWKAKKKAS NGNARPETVT NDDEEALDEE TKRRDQMIKG AIEVLIREYS240  
SELNAPSQES DSHPQEEEEG KEGGHFPQIS SGPTDPLSTH H 281

## (2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

CSLVQESLGS LEVQVEEILE TAGVGS LVGV LGFPWEGDSN EVEKTFLLQQ SAAETVLP 60  
 RPSGIQVTSA LHWFEISARR SPGRLSAQAP TRTGRKYSRC AAS 103

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

NISLLDHPGL QSCLYFLFWI LFTNRERYIS AWKWPDPVWKL DIWHFGLHSH GYYSNNDGS 60  
 GNSFLDLQPF SRYLGIYYIL FCIFVLWRD SLAIFGLPEY VFCVYSAPVK WFCLVCHNPH120  
 GCYMSIS 127

## (2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 382 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```
HEVLCCRMALP LQKAKVIRLI KISPEKPITL AVGDGANDVS MIQEAHVIG IMGKEGRQAA 60
RNSDYAIARF KFLSKLLFVH GHFYIIRIAT LVQYFFYKNV CFITPQFLYQ FYCLFSQQTLL120
YDSVYLTLYN ICFTSLPILI YSLLEQHVDP HVLQNKPTLY RDISKNRLLS IKTFLYWTIL180
GFSHAFIFFF GSYLLIGKDT SLLGNGQMFG NWTFGTLVFT VMVITVTIKM ALETHEFTWI240
NHLVTWGSII FYFVFSLFYG GILWPFLGSQ NMYFVFIQLL SSGSAWFII LMVVTCLFLD300
IIKKVFDRHL HPTSTKAQM YSNTVALSDE FIALQPLSRA RNQLSKLSLL KQMQVSSAWT360
PCAVSRKEKQ RVHLLLECWN EL 382
```

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 85 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```
QELNKHKIHI LGAQKWPEPF SIKQGYKIK YNRSPGNEMV DPSPKMSFQS HLYCDCNNHD60
CEDQSAKCPV SKHLAISKQR CIPFY 85
```

(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 496 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

RLEKGPLPFQ MPGMRLPETQ VLPGEIDETP LSKPGHDLAS MEDKTEKWSS QPEGPLKLKA 60  
 SSTDMPSQIS VVNVDQLWED SVLTVKFPKL MVPRFSFPAP SSEDDVEIPT VREVQCPEAN120  
 IDTALCKESP GLWGASILKA GAGVPGEQPV DLNLPLEAPP ISKVRVHIQG AQVESQEVTI180  
 HSIVTPEFVD LSVPRTFSTQ IVRESEIPTS EIQTPSYGFS LLKVKIPEPH TOARVYTTMT240  
 QHSRTQEGTE EAPIQATPGV DSISGDLQPD TGEFFEMISS SVNVLGQOTL TFEVPSGSQL300  
 ADSCSDEEPA EILEFPDDDS QEATTPLADE GRAPKDKPES KKSGLLWFWL PNIGFSSSV360  
 ETGVDSKNDV QRSAPIQTQP EARPEAELPK KQEKAGWFRF PKLGFSSSPT KKSSTEDGA420  
 ELEEQLQEE TITFFDARES FSPEEKEEGE LIGPVGTGLD SRVMVTSAR TELILPEQDR480  
 KADDESKGSG LGPNEG 496

## (2) INFORMATION ON SEQ ID NO. 168:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 125 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

SLPASYWDS KHSHLKFLLA TSLQTAVQMR SQQKFLSFPL MIAKRQPHHW QMKAGLQKTN 60  
 QKVKNLVCSS FGFQTLGFPL LLMRQVLIPK MTSRDLLPFK HSLRHDQRQN CLKNRRRQAG120  
 SDFPN 125

## (2) INFORMATION ON SEQ ID NO. 169:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

MGADLWTSFL ESTPVSSTEE ENPMFGSQNQ SRPDFLLSGL SFGALPSSAS GVVASWLSSG 60  
 GNSRISAGSS SEQLSASWWP EGTSNVSVCC PSTLTLEEII SNGSPVSGWR SPEMESTPGV120  
 ACMGASSVPS 130

## (2) INFORMATION ON SEQ ID NO. 170:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

VVYRGVKCFI DKKKKTALEP TYSSSSSSSS SSSSSSSSSS SSSSSSSSSS SSFFFLFSA 60  
 LTTFFFAASG FPLARYAAIS FSYFSFQSQ SFHKAACHLQ QCYSTSLPVS SQHHQWTGQD120  
 VLL 123

## (2) INFORMATION ON SEQ ID NO. 171:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KKLYLLRSIQ NVNKTAAIFF LQLQSGIQLT EQQLSSYKLH QRQLMKKKIK PKKKTKRKKK 60  
 KKQKTKLPSP YITNLCCAPT RTCFKFPCQF TTPILYQARL VAIENTTRTG LSKDTFGSVL120  
 TIQKKTLYSL KTNLTQPYIS IFFFKRSELC TGGLNAL 157

## (2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 152 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

LNMGKGDPPK PRGMSSYAF FVQTCREEHK KKHPDASVNF SEFSKKCSER WKTMSAKEKG 60
KFEDMAKADK ARYEREMKTY IPPKGETKKK FKDPNAPKRP PSAFFLFCSE YRPKIKGEHP120
GLSIGDVAKK LGEMWNNTAA DDKQPYEKKA AK                                     152

```

## (2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 281 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

SGSAGPGPRG PRATESGKRM DCPALPPGWK KEEVIRKSGL SAGKSDVYYF SPSGKKFRSK 60
POLARYLGNT VDLSSFDERT GKMMPSKLQK NKQRLRNDPL NQNKGKPDN TTLPIRQTAS120
IFKQPVTKVT NHPSNKKVKS PORMNEQPRQ LFWKRLQGL SASDVTEQII KTMELPKGLQ180
GVGPGSNDT LLSAVASALH TSSAPITGQV SAAVEKNPAV WLNTSQPLCK AFIVTDEDIR240
KQEERVQQVR KKLLEALMAD ILSRAADTEE MDIEMDSGDE A                               281

```

## (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

IIDIYIKNTS KKALVSAIKK LYVLGYIFFL TGKSQWKHFC SISRNELLGK VGRKLPDHIL 60  
RLHLHCPFQY PSLLYQQLAT RCLPSVLLPI SCVLAVLALP VS 102

(2) INFORMATION ON SEQ ID NO. 175:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

IYTSKIHLKR HWLVLLKSSM CSGTFFFLQA KASGNIFVQF LGIFSWGKSV ESYLIIFLGF 60

ISTVHFNIHL FCISSSRQDV CHQCFQFLA YLLYSFLFP DVFICDNKSF AEGLRCVKPN120  
SRVLFHSSGD LPCDWRRACV QSTGNSR 147

(2) INFORMATION ON SEQ ID NO. 176:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ECPLGARGPW EPRHFFELGR GARSRHPCTH GRLAPPQSPP HSQQPFHSHC PSRSPQPSLR60  
PHPHPLRAQG CNPSLSTTHR WYSWG 85

(2) INFORMATION ON SEQ ID NO. 177:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 128 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

NALWGPGAPG SPATLSHLAG VPAAATPARM AGWHPPRALP TASSLSTVTA LPAVPSLPYG 60  
LTRTPSEPR A TPHYPPRTD GTAGAEQPHV EPERVPGARG QDAGGRMTAC PCLTSWGTTL120  
DRGIGQDP 128

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 106 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

MPFGGQGPLG APPPFPTWPG CPQPPPLHAW QAGTPPEPSP QPAAFPQSLP FPQSPAFPTA 60  
SPAPPQSPGL QPLIIHHAQM VOLGLNNHMMW NQRGSQAPED KTQEAE 106



## (2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60  
 LRHMKKLYIN PRQATNP 77

## (2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

PPTHTRQVGE EIQSCHGENS SVSILAPCGP LLHSGQRYHS QTWSQKGHKG LSTQTAPDPL60  
 QRLG 64

## (2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 206 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```
RLSCAGTLSG SGPHPSTRRLT QGRWVRKSRV AMEKIPVSAF LLLVALSYTL ARDTTVKPGA 60
KKDTKDSRPK LPQTLSRGWG DQLIWTQTYE EALYKSKTSN KPLMIIHLD ECPHSQALKK120
VFAENKEIQK LAEQFVLLNL VYETTDKHLs PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180
YAYEPADTAL LLDNMKKALK LLKTEL                                     206
```

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 206 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```
RVFQEEELVR RQRNGASGPR PGLRRLRGGR RAVRRKERLL HRQLPAVHKR GARVKLSSPE 60
RDVERDVFLY RAYLAQRKFG VVLDEIKPSS APELQAVRMF ADYLAHESRR DSIVAELDRE120
MSRSVDVTNT TFLMAASIY LHDQNPDAAL RALHQGDSLE CTAMTVQILL KLDRLDLARK180
ELKRMQDLDE DATLTQLKVL VSLQRV                                     206
```

(2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 111 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

LPRPRESEGO HRGRAGPRDE QERGRDQHHL PAHGRLHLSP RPEPGCRPAC AAPGGQPGVH 60  
 SHDSADPAEA GPPGPRPEGA EENAGPGRGC HPHPAQGLGK LATGVKAQGS F 111

## (2) INFORMATION ON SEQ ID NO. 184:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

GTILPIPEIR RILELLHPLQ AYQDLELGEG GILVQVLHSL QLLPGEVQAV QLQODLHCHG 60  
 CALQAVPLVQ RTQGGIRVLV VEIDGGGHEQ EGGVGHVHAP AHLVQLGHD AVPPTLVGEV120  
 VSKHAHGLEL RGRGGLDLIQ DHTELPLRQV RSIQEDVPLH VSLWA 165

## (2) INFORMATION ON SEQ ID NO. 185:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

LLSMRMILKP QSFMILMLR SSNRVTWKLL LIGLDYIRYQ MENQKTSLLL MENSKTRLLL60  
 LKLLNPLINV GKHCL 75

## (2) INFORMATION ON SEQ ID NO. 186:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 340 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
RTVIDAMSAL LRLRLTGAPA AACLRLGTSA GTGSRRAMAL YHTEERGQPC SQNYRLFFKN 60
VTGHIYISPFH DIPLKVNSKE ENGIPMKKAR NDEYENLFNM IVEIPRWTNA KMEIATKEPM120
NPIKQYVKDG KLRVANIFP YKGYIWNNGT LPQTWEDPHE KDKSTNCFGD NDPIDVCEIG180
SKILSCGEVI HVKILGILAL IDEGETDWKL IAINANDPEA SKFHDIDDKV KFKPGYLEAT240
LNWFRLYKVP DGKPNQFAP NGEFKNKAPA LEVIKSTHQC WKALLMKKCN GGAINCTNVQ300
ISDSPFRCTQ EEARSLVESV SSSPNKESNE EEQVWHFLGK 340
```

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 131 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
LSILYILFNG IHWLLGGNLH FSICPPRYFY NHIKQILIFI ISCFLHRNAI FLFRVHLQRN 60
IMKGGNVVTS YILKEEAVIL RAGLAALLSV VQGHSTARPG PCTGFPQPAR SGWGTRAQQP120
QORAHGVNDG P 131
```

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 436 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
GRGMGRVQLF EISLSHGRVV YSPGEPLAGT VRVRLGAPLP FRAIRVTCIG SCGVS NKAND 60
TAWVVEEGYF NSSLSLADKG SLPAGEHSFP FQFLLPATAP TSFEGPFGKI VHQVRAAIHT120
PRFSKDHKCS LVFYILSPLN LNSIPDIEQP NVASATKKFS YKLVK TGSVV LTASTDLRGY180
VVGQALQLHA DVENQSGKDT SPVVASLLQK VSYKAKRWH DVRTIAEVEG AGVKAWRRAQ240
WHEQILVPAL PQSALPGCSL IHIDYYLQVS LKAPEATVTL PVFIGNIAVN HAPVSPRPGL300
GLPPGAPPLV VPSAPPQEEA EAEEAAGGPH FLDPVFLSTK SHSQRQPLLA TLSSVPGAPE360
PCPQDGSPAS HPLHPPLCIS TGATVPYFAE GSGGVPVPTTS TLILPPEYSS WGYPYEAPPS420
YEQSCGGVEP SLTPES 436
```

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 127 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
SVLFTGVVSP GPSSLP PPPQ PQGEEGGCRG AGRGWAGPEW ARLGQERRHE ALGAPVPGQR 60
PGLPGEGSTG SALRGQAGFH AAAALLIRRW GLIGVAPRTV LWRKNQAGS GHWPPGALCK120
VGDSGTC 127
```

(2) INFORMATION ON SEQ ID NO. 190:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 213 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```
LVLNVGMQLQ CLPHHIAAEI SAGCEDHAAR LHQLVGELLG GRGHVGLLNW WDAVQVQGAQ 60
DIEHEAALVI LGKPWRVDGG PHLVHDLPER TLKGRGCSGR KQELEGEAVL SSGQAPLVCQ120
RQGTVEVTL HYPRCVISLV GDPAGTYAGH PDGSRQRCP QAHAGGPSQR LPGAVDDAAV180
AQADLEELHS PHAAASPASR AATPPPAARE SRL 213
```

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 635 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
GGVSPWRACV QORMEESPE RKRARTDEVP AGGSRSEAD EDDDYVPYV PLRQRRQLLL 60
QKLLQRRRKG AAEQQQDSG SEPRGDEDDI PLGPQSNVSL LDQHQLKEK AEARKESAKE120
KQLKEEEKIL ESVAEGRALM SVKEMAKGIT YDDPIKTSWT PPRYVLSMSE ERHERVRKKY180
HILVEGDGIP PPIKSFKEMK FPAAILRGLK KKGIIHPTPI QIQGIPTILS GRDMIGIAFT240
GSGKTLVFTL PVIMFCLEQE KRLPFSKREG PYGLIICPSR ELARQTHGIL EYYCRLLED300
SSPLLRCALC IGGMSVKEQM ETIRHGVHMM VATPGRLMDL LQKKMVSLDI CRYLALDEAD360
RMIDMGFEGD IRTIFSIFKG QRQTLLFSAT MPKKIQNFAK SALVKPVTIN VGRAGAASLD420
VIEVEYVKE EAKMVYLLEC LQKTPPPVLI FAEKKADVDA IHEYLLKGV EAVAIHGGKD480
QEERTKAIEA FREGKDVLV ATDVASKGLD FPAIQHVINY DMPEEENYV HRIGRTGRSG540
NTGIATTFIN KACDESVLMD LKALLLEAKQ KVPPVLQVLH CGDESMLDIG GERGCAFCGG600
LGHRITDCPK LEAMQTKQVS NIGRKDYLAH SSMDF 635
```

## (2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KPSRRRCRPCC RCCIAGMSPC WTLEESAAPV SAGAWVIGSL TAPNSRLCRP SRSATSVART 60  
 TWPTAPWTSE PTVFPSLQEA SVPKTATSLH IQQPPGQNH FSSAGLEWAR LVLAACSLCS120  
 SELLFLFPFT PAAIKAQTSS PKKKKKK 147

## (2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

DILLALPECL DGLSPFLLVF APMDGYGLNP LEQQVLVDGV HVCLLLCKDE YRGCLLQAL 60  
 EQVHHLGLLL HIFYLLDDIQ AGSPSAPHID GHRLYKGTLS KVLNLLRHGG TEEQGLSLAL120  
 EVGEDGTDVT LEAHVDHAVS LVQGQVATDV 150

## (2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 310 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```
EAPAAARTQS PAAAAQRGDN VYVVTEVLQT QKEVEVTRTH KREGSGRFSL PGATCLQEG 60
QGHLSQKKT V TIPSGSTLAF RVAQLVIDSD LDVLLFPDKK QRTFQPPATG HKRSTSEGAW120
PQLPSGLSMM RCLHNFLT DG VPAEGAFTED FQGLRAEVET ISKELELLDR ELCQLLLEGL180
EGVLRDQLAL RALEEAEQ QSLGPVEPLD GPAGAVLECL VLSSGMLVPE LAIPVVYLLG240
ALTMLSETQH KLLAEALESQ TLLGPLELVG SLLEQSAPWQ ERRPCPCPPG SWGTAGAKEH300
RPGSCWTSVA 310
```

(2) INFORMATION ON SEQ ID NO. 195:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 244 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
TTGIASSGTS IPEDNTRHSR TAPAGPSRGS TGPRLWPCSS ASSKARRASW SRSTPSRPSS 60
SSWHSSLSKS SSSLEMVSTS ARRPWKSSVN APSAGTPSVR KLWRHLIMER PEGSCGQAPS120
LVERLWPVAG GWKVLCLFLSG KRRTSKSESI TSWATRNARV LPEGMVTVFF WLRWPWPSPC180
KHAVAPGRENR PEPSRLWVRV TSTSFVCVST SVTTYTLSPR CAAAAGLCVL AAAGASHGAE240
SARC 244
```

(2) INFORMATION ON SEQ ID NO. 196:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 229 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```
TGHMATGLLA FLGLAAGGQT LCPAGELPGH ARAQASGAPG SVLIAVPGRR RVHTCGPGPA 60
APSTRGECPP PALGHTRPAR PRPVLLRPSC SPGARGAGTW SALLPRGTLL QEAAHQLERP120
QQGLRLQRLR QQLVLRFTQH GQCPQQVDNR DSEFRHQHSG GQHQALQDST CWTVQGLHRP180
KALALLQRL L QGSQGQLVPQ HPLQALQQQL AQLSVQKLQF LGDGLHLCF 229
```

(2) INFORMATION ON SEQ ID NO. 197:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```
TEILPVFVRL AGVPICSTGN ASAMLQPQKP GLSLQQQAEP CLWSGAVHSS VCLVLGLELD60
RGGVSSPSLN SEQTLCLAPV CPGNSPGPHW EPLVF 95
```

(2) INFORMATION ON SEQ ID NO. 198:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 101 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```
AVPRGSLRED GKVRCMSNLL MAGSPLCPLS LALVIAELCA QCCGLAVARL FLWGARAGCG 60
NQSSQTDVSQ AEDSFLAEVS PHLQVSGWGG ARRGRHTPCL T 101
```

## (2) INFORMATION ON SEQ ID NO. 199:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 155 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```
VRHTSHLAVL TQGAPGHCS AAWALLLRTP RAPNEGLGNC LGTLGPGTGS VLNSGKVKRP 60
HLYPAQAQEQ GRQSCGQHPT TDTVLPAGV RGLVSEAAAW HWHCLCYRWG LLRVSQIQGE120
FQFTQPKGPV CRAALTRAQ HSTELGKGRG ERVKD 155
```

## (2) INFORMATION ON SEQ ID NO. 200:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 138 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```
RMKCSQPPRC HFQSDFOKCA PCPRAQTHWL EPPGRVQTIS SMRNAQKGFA DSIRLWRLPA 60
SGVGWVVSPP IQTQEVAP EG MYLVGSSSGT LGGCRALTQV FLSLSSLGCV CACACACLCF120
SLWAHQDAPR RACARVPT 138
```

## (2) INFORMATION ON SEQ ID NO. 201:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 132 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

VHGREARLGT LAGTAALKPA LLSGYQTFKG QDVLRRVPVA ARRPAGACPR VTAWRCWGSG 60  
HLPCLECEQEG EAFEEASVLA ARSLSQPLPG SCTGQGLIPC HAGPLEQVGW GWYVLSPQPW120  
QPCPLGKVIS DL 132

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 131 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

RLFIGCSLQN KQRWDWGPSL GPCTPLSRAY NHVHRPGRGP ALCPTKSSLH QSSWSPFLRD 60  
PAQLPRSWG I GTRVPWRVQE MRRIPCTLR TPTPELWSRG HCERRQRERH VEDTLTDPVG120  
SGRAEDRHTK P 131

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 76 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

LAAIKDQLEG VQQALSQAAP IPEEDTDTEE GDDFELLDQS ELDQIESELG LTQDQEAQ60  
QNKKSSGFLS NLLGGH 76

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RVCSKHFLRL PPSQKRTQTL KKVMTLNYLT SQSWIKLRVN WDLHKTRKQK HSKIRSLQVS 60  
FQICWEAINL GISLQQSTKN TKKISNKKKK KKRKRKKLNC KL 102

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ICLHHNHCLC DTQLLAFYGL IPPTARLEMA VNGACFFTNK PKSTTAEITW KRFSLSRVLK60  
YTFKFFPKKL ILIVFPKSFN 80

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

GKPAALEAHQ GSRLQGRSRE QAAIPPLLSS RTQLCGLGFL FAGLAPCRTL VLELEGPILP60  
RGDSQGCRGI GWRRVL 76

## (2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

NLAVSQLPWK PTRAPDCREE AGSRQPYLHS CPQGLSCVAL DFFLRDLRPA GHWCWSWRVL60  
SCPGVTFRVA GG 72

## (2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

PGMSSLQDRH GRTIWFQVGP YCSHRQRPQE ADGWKRGVTI TGVVMLRVCL DPPRTTLFLR60  
 VTPLPSHASQ GCS 73

## (2) INFORMATION ON SEQ ID NO. 209:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 182 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

QRWLWTSSTS PCWIRAFLEPP AGQVWPCLSG RAPAPLTTLQ LTMQLMPKLW CPVCSSPGSH 60  
 CHLQRGSLLR PTLHLAPPW LLAWPNLAFC AMLELELLLF FRGGNRVESG KGLAPKCCCC120  
 GFFAFSKDAL PGPKLQTAVL SKQVRS LGFG AHLLSGSISI LLLATSGQRP PQPHIARCWQ180  
 KG 182

## (2) INFORMATION ON SEQ ID NO. 210:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

VGPGKQPWWG QVKQCGSQQG TPLKVAVAPR AAAHWTPQLW HQLHGELQSG QRGWGPAKRA 60  
 RPDLPGRQE GPDARRSRG SPQPPLLLIA TGTSGDRLCS WESRSPGFVG LPAGDRHVSH120  
 RERPGSRPQL 130

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VTGKGRDPGL SCSSSWKRWS RTVTIHADTE QQYETEQLRA VSSSAEAAWA ATPPFCNHMP 60  
 MSPPHLTSRW GWMAEQMKPA LWRGSLTEMH TFMGEVDGHL TSLMFHTVDC T 111

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 243 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

DVQVAGPEPD CRVHSHVLPQ QAHRLAPGPY SVGESLQPRE GCEDCDRQKA NLRIRFKPSL 60  
 FQHVGTSSSL AGKIQKLKDK DFGKQALRKE HVNPPAEVST SLKTYQHFTL EKAYLREDF120  
 WAFTPAAGDF IRFRFFQPLR LERFFFRSGN IEHPEDKLFN TSVEVLPFDN PQSDKEALQE180  
 GRTATLRYPR SPDGYLQIGS FYKGVAEGEV DPAFGPLEAL RLSIQTDSPV WVILSEIFLK240  
 KAD 243

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 244 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
GRIGVSVVMG IPSVRREVHS YLTDTLHSLI SELSPQEKED SVIVVLIAET DSQYTSVTE 60
NIKALFPTEI HSGLLEVISP SPHFYPDFSR LRESFGDPKE RVRWRTKQNL DYCFLMMYAQ120
SKGIYYVQLE DDIVAKPNYL STMKNFALQQ PSEDWMILEF SQLGFIGKMF KSLDLSLIVE180
FILMFYRDKP IDWLLDHILW VKVCNPEKDA KTVTGRKPTC GSASNRPSST TWALTPRWLA240
RSRN 244
```

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 210 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
PAESQPADPL QTVPLPARGH SLLAGWQDPE TEGQRLWKAG AAEGACEPAS RGEHEPEDIP 60
ALHPGESLPA RGLLLGLHPC RGGLHPLPLL PTSKTGAVLL PQWEHRAPEGG QALQHVCVCGGA120
ALRQPSVRQG GPAGGPHRHP PVPSEPRRLP PDRLLLQSGS RGRGGPSLRP SGSTAPLDPD180
GLPCVGDSE DLPEKGRSLC GLLRVPCGP 210
```

(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 128 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAGLVHGSA DWPC LAPWRV SSCFLPGTEL RGLGAPGAKS RLWCRGGGLS LNRHPEVLLR 60  
 CWVHPPEWHGE QLWPVLLPRP VLGKLSSGPS LQRPRMGWVW GTHGEWPEEL RVKRAPVCWL120  
 QRP GAPLS 128

(2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FPQDWPRKEH RPQLLPVPLR VDPASQEHLR VSVKROASTP APEPALSSRC PQTPQLCARQ 60  
 EAARHTPGRQ ARPVRGPMDB PSPASGKTGP FPTGHAPELW QIAGAIWGE ENKSPFENEK120  
 KKKK 124

(2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

VPHTHPILGL CKEGPELSFP RTGLGRSTGH SCSPCHSGWT QHLRSTSGCR LRDRPPPLHQ 60  
 SLLLAAPGAPR PRSSVPGKKQ LDTRQGAHKG QSADPWTSPA PPQKGQGLSL QDTPQSCGRL120  
 QEPSCGENLI KALLKMKKKK KK 142

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 379 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

RRGLEGFNGG WTEMPGILWM EPTQPPDFAL AYRPSFPEDR EPQIPYPEPT WPPPLSAPRV 60  
 PYHSSVLSVT RPVVVSATHP TLPSAHQPPV IPATHPALSR DHQIPVIAAN YPDLPAYQP120  
 GILSVSHSAQ PPAHQPPMIS TKYPELFPAH QSPMFPDTRV AGTQTTTHLP GIPPNHAPLV180  
 TTLGAQRPPQ APDALVLRTO ATQLPIIPTA QPSLTTSRS PVSPAQISV PAATQPAALP240  
 TLLPSQSPTN QTSPISPTH P HSKAPQIPRE DGSPKALW LPSPAPTAAP TALGEAGLAE300  
 HSQRDDRLL VALLVPTCVF LVVLLALGIV YCTRCGPHAP NKRTDCYRW VIHAGSKSPT360  
 EPMPPRGLT GVQTCRTSV 379

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

VDTDECQIAG VCQQMCVNYV GGFECYCSEG HELEADGISC SPAGAMGAQG SQDLGDELLD 60  
 DGEDEEDEDE AWKASTVAGR RCLGSCGWSL RSRLTLPWPI DRASQRTESH RYPTRSPPGH120  
 PRSVPPGSPT TPQCSPSPGL WWSLPRIPHC LLPTSLL 157

## (2) INFORMATION ON SEQ ID NO. 220:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 211 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

PPPPGPLCLL PIKSLCLLPP SPQSPPPSCP LRAPLTRPHP SALHIPIPKP PKSQGKMAPV 60  
 PSWPCGCPHQ LPQQPQQPWG RLVLPSTARG MTGGCWWHSW CQRVSFWWSC LHWASCTAPA120  
 VAPMHPTSAS LTAIAGSSML GARAQONPCP PGAASQGRCP AEPACDGVQT PLMEYGALDT180  
 WPGLHQGPMG AAQLDRWLPA PQAQPGSSLN H 211

## (2) INFORMATION ON SEQ ID NO. 221:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 117 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

LGEPOISGAQ PGRVWGQLCQ STSQAHPLPG MPWDHGQGR L WGSETPLLST PSQNTLRVSG 60  
 LWREWGRKN WHLPREGDER FALILREASE KCFKVCMRQ AVGSGLSSP LPPSFPA 117

## (2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 198 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

NKELSSLKSS DVMTHTESC ITVASRATHL FGLSDGHSFT TQQQTPHTGT RMSASTWEAV 60  
 AEPGRWPGPD HGLSGAGHQG VRVPMLPQGV GMTGRSLVTR QWTSLGEGWR ERAGQAPAAH120  
 RLAHANTLKA LLGGFSENQG EALVSFPRKV PILPPAPLSP EPRDPQGVLA GGAKQRCLRP180  
 PEPSLPMIPR HARQGVGL 198

## (2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

SHGMPGRGWA CEVDWHSCPH TLPGWAPFIW GSPSQHGVLG ACPGPFTRTE APHPLSHFSR60  
 WKTQRRKRPW GGVPSCQLQA PWVPLCGGSP DSISSASE 98

## (2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 298 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATRRRAAEAG MAAVLQERVER LSNRVVRVLG CNPGPMTLQG TNTYLVTGTF RRILIDTGEP 60  
 AIPEYISCLK QALTEFNTAI QEIVVTHWHR DHSGGIGDIC KSINNDTTYC IKKLPRNPQR120  
 EEIIGNGEQQ YVYLKDGdVI KTEGATLRVL YTPGHTDDHM ALLLEENAI FSGDCILGEG180  
 TTVFEDLYDY MNSLKELLKI KADIIYPGHG PVIHNAEAKI QQYISHRNIR EQQILTLFRE240  
 NFEKSFTVME LVKIIYKNTF ENLHEMAKHN LLLHLKKLEK EGKIFSNTDP DKKWKAHL 298

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 58 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GFSWGRSPLG RCWCLGGSWD PGYSPTHARL DWTAARRAAV QQPFPQPQA GVSPIWIL 58

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

SGSLSLNHIS IFQINILLIS ISYNFFSLRI PWEFFNAIGS VIIDAFTNIS YASRMISVPV60  
SHYNFLDCCV KFS 73

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 141 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AFLLRPSVTA STRLLPVCAS PRSSPGPSA QQQQAWQQAW SSARAPSROR ARPSSSERPC-60  
PAVGRLASLY CCCMVFASPP RRGRTWVHCT GWPRLATGLW PLTCQVWGTP RKQQPLPLL120  
SWPLAASWRL WMPWWSWAPR L 141

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 244 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

VPPPALGHRQ HAPASRLRES TQLPRPFTST AAAGMAASVE QREGTIQVQG QALFFREALP 60  
GSGQARFSVL LLHGIRFSSE TWQNLGTLHR LAQAGYRAVA IDLPGLGHSK EAAAPAPIGE120  
LAPGSFLAAV VDALELGPPV VISPSLSGMY SLPFLTAPGS QLPGEFVPVAP ICTDKINAAN180  
YASVKTPALI VYGDQDPMGQ TSFEHLKQLP NHRVLMKGA GHPCYLDKPE EWHTGLLDL240  
QGLQ 244

## (2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

WTDHNRGAQL QGIHHSRQEA ARGQLPNRGR GCCFLGVPQT WQVNGHSPVA SLGQPVQCTQ 60  
 VLPGLGGEAN TMQQYREAS LPTAGQLSE EEGLALHLDG ALALLHACCH ACCCCAGEGP120  
 GELRGLAQTG SRRVLAVTEG RRRN 144

## (2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60  
 EWDLRPRLGT TQAEKGRFHH SQCPPHSTTS ARAPPSLLPH PAIVRGATVG RRVPRRGLFL120  
 LPVPEKAFPL LKFKH 135

## (2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GGPVCWEPQV TPFSSYSVPG ASCPPLQILG KENVYVAGYC MVTSEGRPLG THLPTAAQAR60  
 AQAHLLVLRP QIKPSPHHMA SDRFLPSRKF CGCAVL 96

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CCGEGTVNDG NVPSQPGSCL TWVSNPTLPS PWSTLQRSRG PANAREVSTE KSLQNSHWKR60  
 RNKGHGKKPQ GRDRPRSQTL GRE 83

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 52 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

ASPASLAQAT SRQPAPSPRA RSHLATSTSW TSSARSDAGC GECRRDPGAP PR 52



## (2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

LGSAWQQLRR PEASETLRLV GTHRPRQAL PRQVASPPP RRLGLTSPP VRLGQVVPGL60  
 MPGVVSAAGT QVRLDEVPA SLRLQHHLQL REGL 94

## (2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

ARPSRSWRWC CSRSDAGTSS RRRTWVPAAL TTPGIRPGTT CPRRTGGEVR PSPRRGGGLA60  
 TRCLGKARWR GLCVPTSRRV SDASGRRSCC QAEPR 95

## (2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

APTNRSSSK FATSGSPGY IASSGASPEV RQRRTTFFRF RPPGESLCGDM KLLTHNLLSS 60  
 HVRGVGSRGF PLRLQATEVR ICPVEFNPVF VARMIPKVEW SAFLEAADNL RLIQVPKGPV120  
 EGYEENEEFL RTMHLLLEV EVIEGTLQCP ESGRMFPISR GIPNMLLSEE ETES 174

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

YRAQKHCVCW HWVKGWGYTR QNSETGYRST KIHSHNKKNW RLAQSTLSFL FTQQHVGDPA 60  
 ADGEHTSRFR ALQALYHFH LQQQVVHGPQ KLLILLISLN RPFRLDQTQ VIGRLQERRP120  
 LHFYHTRHE VGVEFHRADT DLGGLEAQGE ATGPHPPHMR AQQIVGKQFH VAAQTLARPE180  
 PEKGRPPLPH FRGCSTRCYW IARRTGSGEL AGTSRVCGSS FLYAN 225

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 209 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TFNEKKIYNT ELKNTVFGVI GSRVGDTHGR IRKQGIDQQK YTVITRKTGA WHNQLSVSSS 60  
 LSSMLGIPRL MGNIRPDSGH CRVPSITSTS SSRWCMVLRN SSFSSYPSTG PFGTWIRRL120  
 SAASRNADHS TLGIIRATKL GLNSTGQIRT SVAWRRRGKP RDPTPRTCEL SRLWVSSFMS180  
 PHKLSPGRNR KKVVLRLCLTS GDAPLDAIG 209

## (2) INFORMATION ON SEQ ID NO. 239:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 146 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIKVFSE SVGVSVNGCA LGGTVERCAK 60  
 SELQTIGQGH GVATRRRLSA GAPPRTHSQQ SSHWHEELKNK HLQGRGKRPR SRRSRARASA120  
 ARGAPTGSQR GGSPKRARSG RSRVLA 146

## (2) INFORMATION ON SEQ ID NO. 240:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 134 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

SRTFSFLSFL HCANILTLFV SFQEPHRHIQ VKRSLNKCLQ PSQCKNKYQS SRRSSSRAAP 60  
 KVPTATPNNY KSVQRECWRE CEWVCAGGHG GAVCKIGVAN HRTRAWSGYP PPTQGRGRASP120  
 HTLTAEFALG RVKK 134

## (2) INFORMATION ON SEQ ID NO. 241:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

PARTDRPRL ARFGLPPRCE PVGAPLAALA LARERRERGR FPRPCKCLFF NSSQCELCCE 60  
CVRGGAPALS RRRVATPCPC PMVCNSDFAH RSTVPPSAHP FTLTPTLSLN TFIIVRRGRW120  
DFGRSAAATA SGGILIFIFAL RWLKAFI 147

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 88 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PVLCRGNSGS LSRKFPPKPQ KPADKDHPT CVYLENRSPG KSDLSATPGR SGLESGYQNL60  
LRQHQPGRGRC PTWPGSRWKV PRRFPGYG 88

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 164 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

QDGCPSGDF AALQSLLKAS SKDVVRQLCQ ESFSSSALGL KKLLDVTCS LSVTQEEAEE 60  
LLQALHRLTR LVAFRDLSSA EAILALFPEN FHQNLKNLLT KIILEHVSTW RTEAQANQIS120  
LPRLVDLDWR VDIKTSSDSI SRMAVAPPGL VPDGRFQGGG QAMG 164

## (2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

FAWASVLQVD TCSRMIFVSR FLRFWWKFSG KRARIASAE RSRNATSLVR RCRAWSSSSA60  
SSWVTDKLEH VTSKSFFKPR AELEKLS 87

## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

DGPGGPTAHP HRCAPPGVC PGQAPAHLLL CAAAPGHFGQ GQQAAGGLV GDADRAGDLE 60  
CSPRRIFLHP RLHPPRHLGS CHLDRCGCA GWSCCLHLRE TGWYILGPAE DSASAGSFLH120  
SHRCPQTL 129

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 268 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
ASPSNSQPTS PASAPALPPP ARRSRGAQTV SLTMGTADSD EMAPEAPQHT HIDVHIHQES 60
ALAKLLLTCC SALRPRATQA RGSSRLLVAS WVMQIVLGIL SAVLGGFFYI RDYTLLVTSGI 120
AAIWTGAVAV LAGAAAFIYE KRGGTYWALL RTLLALAAFS TAIAALKLWN EDFRYGYSYY 180
NSACRISSSS DWNTFPAPTQS PEEVRRLLHC TSFMDMLKAL FRTLQAMLLG VWILLLLASL 240
APLWLYCWRM FPTKGKRDQK EMLEVSGI                                     268
```

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 103 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
DCTQDPQHDL HHPRGHQQPA AAPGLGGPGP QRRAGEQEL GQGRLLVDVH IDVGVLWGLR 60
GHLITVGCSH CQGHSLRSSG PASGRREGWG AGWRSGLRVG GGG                                     103
```

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 86 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

GSRRRDGGGA GAAPVAPRAL GRRARAGRCS EDEGGGGAQR VWGEQPVLAS GQSPPGQEGS60  
 FTRVWTRASL PTLGQVLQPG GVHVQV 86

## (2) INFORMATION ON SEQ ID NO. 249:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ARGGAMAAGL ARLLLLLGLS AGGPAPAGAA KMKVVEEPNA FGVNNPFLPQ ASRLQAKRDP 60  
 SPVSGPVHLF RLSGKCFSLV ESTYKYEFCP FHNVTQHEQT FRWNAYSGIL GIWHEWEIAN120  
 NTFTGMWMRD GDDCRSRSRQ SKVELACASP SNCV 154

## (2) INFORMATION ON SEQ ID NO. 250:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

PLDAVARART RQLHLALPAP GTAVVTVPHP HAREGVVGD L PLVPDAEDPT VGVPAEGLLV60  
 LGHVVERAEL ILVRGLHQAE ALARESEEMH GSRHG 95

## (2) INFORMATION ON SEQ ID NO. 251:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 240 amino acids
- (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

KVTDGHTTRTP RSGVPRQHEA GSPGLTASHA MSIHLAGSLT AMDSICASER SQGVWRAPTP 60  
 GCQGLSPGPR PGELPGGSSP EERLGRLAVA GPPRGAQNVN QAGPEAEAPP LRFGHAWGAQ120  
 TPRLGAPGPW TPLPTLPISH PPFWSQTEAQ RKEGFTEEGQ GRAWPQGGDE DISGPGSCRL180  
 LWEEEPVCVK LLGLAARPTA GPSLDPECTW SSCPLAAPGL GTGIEPRGLG WLGQGRDREG240

(2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 216 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSRQKARA EPGPREGMRT 60  
 FPVQVAAGCS GRKSHASVNC WGWPRAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120  
 WARAGTGRGS TSDPDVGWLC PPRREAQOTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180  
 GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP 216

(2) INFORMATION ON SEQ ID NO. 253:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```
VLRRLYIYIL YITNMKWFST QPLWLNTKQR SHRRGPGPPP APLSGVLGSR GLPHHPSQGW 60
GRAGPRAGAN VAWNSNCIVR WVGQWARGC SQPGFTTNL AMTCGGPWGS GCLLGSTLSE120
VSPWAPPSCP QGHPVLPTL WAWGLQDPLC RVRVGAGHGS RHQPDAPVGV ARSWDGVVRN180
TAPKTQNKNT TNGRRSPPT EVGFEPLLIF FVSFLQPW 218
```

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
RDGGGAGAAP VAPRALGRRR RAGRCSEDEG GGGAQRVWVS SLAGWRLER TARARSPLTL60
PLPVGGTTRS CLRFPVSRP 79
```

(2) INFORMATION ON SEQ ID NO. 255:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

LGLEATGLRQ ERVVPPTGSG KVSGERARAV PRSSRQPARL LTQTRWAPPP PSSSLHLPAR60  
ARRPRARGAT GAAPAPPPS 79

## (2) INFORMATION ON SEQ ID NO. 256:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

WPGGDWPEAR TGCSTYGKRO GQRGTGPRP PLEPPAREAA HPNALGSSTT FIFAAPAGAG60  
PPAESPRSNR SRASPAALA 79

## (2) INFORMATION ON SEQ ID NO. 257:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 51 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GHLGGPTGSV CSRILLASSP FYMNCCINKH RVPETTEVII LPTECWPGQA W 51

## (2) INFORMATION ON SEQ ID NO. 258:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

GGGFLGQIDK SKDNISLTV IQLHSYTV AL FGLSHEEVLV TNYVFGCF

49

(2) INFORMATION ON SEQ ID NO. 259:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AFTRNTTNKV SDMLANQARL RSLRRPNWLC LLKDSSGLVS ILHELLHK

48

(2) INFORMATION ON SEQ ID NO. 260:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 179 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

PGISVSVDKM ESSPFNRRQW TSLSLRV TAK ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60  
KKRSNTENLS QHFRKGT LTV LKKKWENPGL GAESHTDSL R NSSTEIRHRA DHPPAEVTSH120  
AASGAKADQE EQIHPRSLRL SPPEALVQGR YPHIKDGEDL KDHSTESKMM ENCLGESRH 179

## (2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

QATLLLEPKL TKKNKSTPDL DSGHLLKPSF RVDIPTSRV RILKTTQQKV KKWKIV 56

## (2) INFORMATION ON SEQ ID NO. 262:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DSAPSPGFESH FFENTVRVVF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60  
 RESSLAVTLN DSEVHCRLLN GDDSILSTDT EIPG 94

## (2) INFORMATION ON SEQ ID NO. 263:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

VMSDPADKAA RADSARAARG KRKKNVEENM AYSALMEVAG YCLIERMLWN PMLKIKSVWL60  
 CSYAVMVIPR QLAKV 75

(2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AMFSSTFFFL LPRAARAESA RAALSAGSLI TYAFYKRLPK KKLLTRNVDK PLKANKQQTV60  
 VFAFSYSWQA EVRA 74

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

DSKAFSLLSS NQPLPSKLSR PCFPPHFFFF YLEPLEPNRL EPPCLLDHSS PTHFIKGYPK60  
 RNC 63

## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

RRGSGSRSSM APVLASMLWM STRGTAMTST SLCTSRARSR PMPSSSSPTP TAWRCCCATR60  
 TRVSTSTRTG ASLRMWCCSG GRCLLLWPTS APTR 94

## (2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 254 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GDRKPLYHYG RGMNPAADKPA WAREVKERTR MNKQONSPLA KSKPGSTGPE PPSPQASPGP 60  
 PGLPWAPKPY HKFMAFKSFA DLPHRPLLVD LTVEEGQRLK VIYGSSAGFH AVDVDSGNSY120  
 DIYIPVHIQS QITPHAIIFL PNTDGMEMLL CYEDEGVYVN TYGRIIKDVV LQWGEMPTSV180  
 AYICSNQIMG WGEKAIEIRS VETGHLDGVF MHKRAQRLKF LCERNDKVFF ASVRSGGSSQ240  
 VYFMTLNRNC IMNW 254

## (2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 231 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
GKKHLVIPLT QELEPLSSFV HEDPVEVARL HRADLNGFLT PAHYLVGADV GHRSRHLPPL 60
QHHILNDAPV RVDVDTLVLV AQQHLHAVGV GEEDDGMGRD LALDVHRDVD VIAVPRVDIH120
SMEASTGAID DLEPLPLLYC QVDQORAVGE VGKGLEGHEF VVGFGGPGEA WGPWGGLGAG180
GLRPRAAWLA LGQGRVLLLV HPCSLEYLSG PGWFEVSGIHA PTIMVQGLPV P 231
```

(2) INFORMATION ON SEQ ID NO. 269:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 454 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
GAGCTSPGLW ARKAAARCLP TYPSTRAQPSN VGRRRRRRPG LGALAAGVPA MAESVERLQQ 60
RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS NPYSRLMALK RMGIVSDYEK120
IRTFAVAIVG VGGVGSVTAE MLTRCGIGKL LLFDYDKVEL ANMNRLFFQP HQAGLSKVQA180
AEHTLRNINP DVLFEVHNYN ITTVENFQHF MDRISNGGLE EGKPVDLVLS CVDNFEARMT240
INTACNELGQ TWMESEVSEN AVSGHIQLII PGESACFACA PPLVVAANID EKTLKREGVC300
AASLPTTMGV VAGILVQNVL KFLNFGTVS FYLGYNAMQD FFPTMSMKPN PQCDNRNCRK360
QQEYKKKVA ALPKQEVQEE EEEIHEDNE WGIELVSEVS EEELKNFSGP VPDLPPEGITV420
AYTIPKKQED SVTELTVEDS GESLEDLMAK MKNM 454
```

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 123 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

KLTVPKFNRN FNTFCTKIPA TPIVVGRLA AQTPSRFRVF SSIFAATTSG GAHAKQADSP 60  
 GIISCICPET AFSLTPDSIH VCPSSLQAVF IVIRASKLST QLRTRSTGFP SSNPPLLILS120  
 MKC 123

(2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CSSEYVLLLE LYLILLDEVG RKVYSYWLVP PCHNQRVATY QCHILSAFQQ SHYLLHQHLL 60  
 LLRQRYGFESH SRLQFFVSM PSSGCRDSP PPLSSSSRCG PGRPLRRRSS GPADSSPGQV120  
 PAPAPGPAAA GAPQTPPWLG LRPPTL PARA FAAAFAPRCS AGPARGTWGG TSPLPS 176

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN



(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

EARQAWTGAK GAGSLTFSSL QSGHLASGSQ SPESTKAPGT PPTPSYPGTP SRQLLWQWVQ 60  
PRPALPASSP CSRHQLYLPR QAMSWLLSPA PSVPLDFSGA SPVWATLCFP HPRLPHR 117

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

APALPPPAGN VLASQPSTIC SPRLLRGQPS LGHPLFPSSS APTQVTDPAD SFSLGKVGCC60  
LTSPSSPPPI HTHRHPTPG RLVSHM 86

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

EARTLPAGGG RAGAYCRERR LAVLAWAGPT AITVAYLGSL GRMEWVGCQG LWCFLVIGTL 60  
MPSAHFAKKK KLMTLLPWLL SMLAWPPRVG GTSPLLAEAG EQVLSYDPIH QAGVLSPSGH120  
HSSQHQPVG LGQGSEKGWQ EVPRSSQPGR GTNALNTSKL RDPKVSTPGS GLPPHRH 177

## (2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

QFPGPSVPEQ STSVSVTTSC LFPSLHLLQF IYMLLLLVHF CLPYQAVNEG RNLVCFIH60  
VPSAWHIVGL H 71

## (2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

FFFFFFFF FFFCLINMSI YLAPDGNTKS WQWEWKGSLS QILPYYVDPK AGLGSKAHKP 60  
PKQIFIEHLD YRPSILLGT MGDVKEVISH MICLQAKNA SG 102

## (2) INFORMATION ON SEQ ID NO. 277:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GVIESRRVLS RGVIRFIFKQ PNPGRGCPIL SALKKIPFPY LPASIMSVEE SNCGSFEGDG60  
PFFPV 65

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 65 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FFFFFFFFFF FFLFNKYEHL FGTRWQYKIL AVGVERFSLN NTSILCRPKG RTWQQGSQTT60  
QTNIIY 65

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 489 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LADSPFGSSP YEGYNYGSFE NVSGSTDGLV DSAGTGDLSG GYQGRSFEPV GTRPRVDSMS 60  
SVEEDDYDTL TDIDSDKNVI RTKQYLYVAD LARKDKRVLK KKYQIYFVNI ATIAVFYALP120  
VVQLVITYQT VVNVGTGNQDI CYYNFLCAHP LGNLSAFNNI LSNLGYILLG LLFLLIILQR180  
EINHNRRALLR NDLCALECGI PKHFGFLFYAM GTALMMEGLL SACDHVCPNY TNFQFDTSEFM240  
YMIAGLCMLK LYQKRHPDIN ASAYSAYACL AIVIFFSVLG VVEGKGNTAF WIVFSIIHII300  
ATLLLSTQLY YMGRWKLDSE IFRRLHVLV TDCIRQCSGP LYVDRMVLLV MGNVINWSLA360  
AYGLIMRPND FASYLLAIGI CNLLLYFAFY IIMKLRSEGR IKLIPLLCIV CTSVVWGFAL420  
FFFFQGLSTW QKTPAESREH NRDCILLDFD DDHDIWHFLS SIAMFGSFLV LLTDDDDLDLT480  
VQRDKIYVF 489

## (2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 182 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
APLCHRPVTL SCCGDESQLR CPALDGSRTA RSSLGAWDS HGVAWNLAAA LCRGAGLLPW 60
DPQMLAKLLL SSQCWGLPWA PVLWLSICPF ARGMEGTPS PFHALHFARP PPHNAPAWDL120
RPLFPILPL QGLVWGLNLC PVSQPQSLG CPWLPSLPPI VSQDGWGYEI LGVGQLVPDF180
WC 182
```

## (2) INFORMATION ON SEQ ID NO. 281:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 536 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
ARPGCPAAIQ CWAAYLGLIP TARQSDRSMT QRSSGFLEVK RRAQLLLEDI DLVPLHSIQV 60
VIQCQHQEG PEHGDGGEEV PDVVVVKEVE EDAVPVVLPR LCRGFLPGAEE SLEEEEREAL20
PDHGGANDAE QGDELDPPT PELHDDVEGE VKEQVADANG QQVGSEIIGA HDKPIGSQRP180
VDDVAHQH HAVHVERPAA LPDAVCVEHV EDAAEDPRVQ FPPAHVIELR AEEQGGDDVN240
DGEDDPERRV PFAKDHAQHR EEDDNGQAGV GTVGAGVDVR VPLLVELQHA ESGDHVHERC300
VKLEIGIVGA HMIASTEQPL HHQGCAGHVE KPKVFGDPTF QGTEVIAQQG PVVVDLPLQD360
DEQEKQPQD VPQVAEDVVE GAEIAQWVGA EEVVVADVLI PCDIHHRLVG DHQLHHRKGI420
EDSNGGNVPE VDLVLFQNT LVLPCQVSHI EVLLGANDIL VGIDVGQCVV VILLHRAHGV480
HSGPSTYRFK GAALVTVREV PSASAVNQTI GRSRNILKGA IVVTLIRGTA RKRISQ 536
```

## (2) INFORMATION ON SEQ ID NO. 282:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 551 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```
PLSSPSCCRY RRCRRRLRPP LRSVVQPGPR TMSLSRSEEM HRLTENVYKT IMEQFNPSLR 60
NFIAMGKNYE KALAGVTYAA KGYFDALVKM GELASESQGS KELGDVLFQM AEVHRQIQNQ120
LEEMLKSFHN ELLTQLEQKV ELDSRYLSAA LKKYQTEQRS KGDALDKCQA ELKKLRKKSQ180
GSKNPQKYSD KELQYIDAIK NKQGELENYV SDGYKTALTE ERRRFCFLVE KQCAVAKNSA240
AYHSGKGKELL AQKLPLWQQA CADPSKIPER AVQLMQQVAS NGATLPSALS ASKSNLVISD300
PIPGAKPLPV PPELAPFVGR MSAQESTPIM NGVTGPDGED YSPWADRKAA QPKSLSPQSQ360
QSKLSDSYSN TLPVRKSVTP KNSYATTENK TLPSSSSMAA GLERNRMRV KAIFSHAAGD420
NSTLLSFKEG DLITLLVPEA RDGWHYGESE KTKMRGWFPF SYTRVLDSGD SDR LHMSLQQ480
GKSSSTGNLL DKDDLAIPPP DYGAASRAFP AQTASGFKQR PYSVAVPAFS QGLDDYGARS540
MSSADVEVAR F 551
```

## (2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
AGEAAGQPGS PPSHQLAKCP PLTQGYPR LH GHVTRGVYPQ EAAQPPWAAQ PLGLALQGPA 60
PHSARPCLEQ LGSSPGQTQV GQDQAAGAWM FSTQERTDDD RTGYMGRAGE ATRWAALQMW120
PSAEEGGRPV VGHCRQLQDV GKGLITLVRR LRIWPLPHRR CSWTALHSHP GPGRRRRARPH180
CRASA 185
```

## (2) INFORMATION ON SEQ ID NO. 284:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 518 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

SGGSESGHFH IGAAGHPRSI VIQALGEGGH GHTVGELLEA AGRLGGEGPG GGAVIGGWDG 60
QVVLVQEVAR AAALPLLQAH VQPVTAIAVQ DPGVGEKPA PHLGLLTLSV VPAIAGLRHQ120
QGNEVTLLA QEGAVVPSSV GEDGLHPHTA IALQAGCHGA RARQSLVLGG GIAVFWGHAL180
AHGECVGVGV AELALRLRRR QGFGLSLAV SPRAVVLAIR ACDVHDGCA LLGRHPPHER240
CQLGGHRQGL GPRNGVGNDQ VGLGGROGAG EGGAVAGHLL HELHRALRDL AGVGTGLLPQ300
RQLLRQQLLA LGVVGGRVLG HGALLLHQEA EAPALLCQCG LVAVGHVILQ LALLVADGVD360
VLQLLVRLVLL RILAALALLP KLLQLSLTLV QGVAFAPLLS LVFLQRSTQI PGVQLHLLLQ420
LRKQLVVKRL QHFFQLILD L PVD FSHLEEN VSEFFGALAL AGQLPHLHQG VKVAFGCIRH480
TCQCLLVILP HGDEVPEARV ELLHDGLIDI FREPVHLL 518

```

## (2) INFORMATION ON SEQ ID NO. 285:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 217 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

VREAAARREQR YQEQQGEASP QRTWEQQQEV VSRNRNEQES AVHPREIFKQ KERAMSTTSI 60
SSPQPGKLRS PFLQKQLTQP ETHFGREPAA AISRPRADLP AEEPAPSTPP CLVQAEAAV120
YEEPPEQETF YEQPPLVQQQ GAGSEHIDHH IQGQGLSGQG LCARALYDYQ AADDTEISFD180
PENLITGIEV IDEGWWRGYG PDGHFGMFPA NYVELIE 217

```

## (2) INFORMATION ON SEQ ID NO. 286:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 162 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

AGASGRLWLP SAFICLFSFS LASKGWPPPL FRMTLGNSE RELFLAEFVT KVRVDHGGLA 60  
 AGNLSWSLL CAPHSISLSL CLGYGKWGCR WPSSHPGYSK TADTTCSSTR LTRCLQAPVC120  
 ASTDSDFRKS NTEWPWPVVF PYFLSQLIRV SEEQICFWTK KK 162

## (2) INFORMATION ON SEQ ID NO. 287:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 173 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LLACRGWPGR RWHEELNSGK VMYAFCRVKD PNSGLPKFVL INWTGEGVND VRKGACASHV 60  
 STMASFLKGA HVTINARAE DVEPECIMEK VAKASGANYS FHKESGRFQD VGPQAPVGSV120  
 YQKTNAVSEI KRVGKDSFWA KAEKEEENRR LEEKRRAEEA QRQWSRSAGS VSA 173

## (2) INFORMATION ON SEQ ID NO. 288:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 597 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```
EKCGQYIQKG YSKLKIYNCE LENVAEFGEL TDFSDFKLY RGKSDENEDF SVVGEFKGSF 60
RIYPLPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120
KVIEDRDHYI PNTLNPVFGR MYELSCYLPQ EKDLKISVYD YDTFTRDEKV GETIIDLENR180
FLSRFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFFQPILSED GSRIRYGGRD240
YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGLQMWV300
DVFPKSLGPP GPPFNITPRK AKKYYLRVII WNTKDVLDE KSITGEEMSD IYVKGWIPGN360
EENKQKTDVH YRSLDGEENF NWRVFVFPDY LPAEQLCIVA KKEHFWSIDQ TEFRIIPRLI420
IQIWDNDKFS LDDYLGFELE DLRHTIIPAK SPEKCRDMI POLKAMNPLK AKTASLFEQK480
SMKGGWPCYA EKDGARVMAG KVENTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540
SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLFVAVL LYSLPNYLSM KIVKPNV 597
```

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 120 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
DQHSCFKMSP DSKASHNPFS PKMGVESDME DETTAWMNLK PTKSCTSTSG PLKSGLLETS 60
SGLRGWSLST WKQGLCTAPS SPTFPRENER CGWMFSPRVW GHQALLSTSH PGKPRNTTCV120
```

(2) INFORMATION ON SEQ ID NO. 290:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 289 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

ETQVVIQRKL VIVPYLNDQP GWDSKFRVLN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60  
FTIQRVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120  
CDVERRAWWP QTLGENIHPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180  
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240  
NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIID RNFQVFFLR 289

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 201 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GTGDGSKEIN IVWGIQVPIF HNGPWVSTNH EVARFFRITS LASEGIIVPS TSTIRGMGVW 60  
RASCDCRAD STSSIAQDRG PGLTIGHQAL GSLVWVGESW GQTWGEYLG G PRWLGWLDLR120  
QSWALSISEE VVKKRDFLFH FLNFLCMLVE DMFAHKLRTL EFLATERTQP LILAQFLRVG180  
GDELLHFLW VFAPHLGLF L 201

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 171 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SVIFFKIGFC EGRLVGRGGV PGSEAQSCVL SSSVWISLAA SLMSLRITICL CWVMPLMLRT 60  
RRVRSLETPG LSSHRRRMF CRFQQISLML TLRSKVTQPR RKNLLSGWGS ESATRIKPGY120  
LLQREMISAR EMLGAMLRMK REQVLCSGRG LHSSPAASLG FSHSSSLGFS F 171

## (2) INFORMATION ON SEQ ID NO. 293:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 485 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

EKEKPKEE EW EKPKDAAGLE CKPRPLHKTC SLFMRNIAPN ISRAEIIISLC KRYPGFMRVA 60  
 LSEPQPERRF FRRGWVTFDR SVNKEICWN LQIRLRECE LSPGVNRDLT RRVNRNINGIT120  
 QHKQIVRNDI KLAAKLIHTL DDRTQLWASE PGTPPLPTSL PSQNPILKNI TDYLIEEVSA180  
 EEEELLGSSG GAPPEEPPKE GNPAEINVER DEKLIKVLDK LLLYLRIVHS LDYYNTCEYP240  
 NEDEMPNRCG IIHVRGPMPP NRISHGEVLE WQTFEEKLT PLLSVRESLS EEEAQKMGRK300  
 DPEQEVEKFV TSNTQELGKD KWLCPPLSGKK FKGPEFVRKH IFNKHAEKIE EVKKEVAFFN360  
 NFLTDAKRPA LPEIKPAQPP GPAQILPPGL TPGLPYPHQT PQGLMPYQGP RPPILGYGAG420  
 AVRPAVPTGG PPYPHAPYGA GRGNYDAFRG QGGYPGKPRN RMVRGDPRAI VEYRDLDAPD480  
 DVDF 485

## (2) INFORMATION ON SEQ ID NO. 294:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 368 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ESSGFQAIGR AEDDARSCWV KTSESTRPYQ LLRRRRPTLI TYRIFRHHRRH KDTSSGDHLT 60  
 CRLDPQAKDL KDGTOEEATK RQEAQVDPRP EGDQRTVIS WRGAVIEPEQ GTELPSRAAE120  
 VPTKPPLPPA RTQGTVPVHLN YRQKGVIDVF LHAWKGYRKF AWGHDELKPV SRSFSEWFGL180  
 GLTLIDALDT MWILGLRKEF EEARKWVSKK LHFEDVDVN LFESTIRILG GLLSAYHLSG240  
 DSLFLRKAED FGNRLMPAFR TPSKIPYSKV NIGTGVAHPP RWTSDSTVAE VTSIQLEFRE300  
 LSRLTGDKKF QEAVEKVTH IHGLSGKKDG LVPMFINTHS GPVSPTWGVF HGGAPGADSL360  
 LLSYLFER 368

## (2) INFORMATION ON SEQ ID NO. 295:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 94 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ALRSPPRMRI VLSNRLTSTS FSKCNFFDTH FLASSNSFLR PKIHMVSSAS ISVRPRPNHS60  
LKDLDTGFSS SWPHANLRYP FHACRKTSIT PFWR 94

(2) INFORMATION ON SEQ ID NO. 296:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 94 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

LLRHPLPGFL KFFPQTQDPH GVQRVDQCET EAKPLTEGPG HRLQLVMAFC KLAVSEPCM60  
EDVNHALLAI VQHWALCP GRWQGRLGGH FCSS 94

(2) INFORMATION ON SEQ ID NO. 297:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 146 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

SGPLLGPAT LTGRMSEVRL PPLRALDDFV LGSARLAAPD PCDFQRWCHR VINNLLYYQT 60

NYLLCFGIGL ALAGYVRPLH TLLSALVVAV ALGVLVWAAE TRALCAAAAA ATLPAPWPQC120  
LPSASWCSGS RAALAPSCSA SPGRCF 146

## (2) INFORMATION ON SEQ ID NO. 298:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 152 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TQRHSHPPFS MLIPKLGPGA RHSQILNPGP KLFQTPPYLP TQVKTLPNLE LRTQVFHAPV 60  
 WMESGILTVG PLVQVIPTLT SPICLPPALL RHFAHPNVF HHRQPRGEVG TGLSREWGVY120  
 VSVAATIKPV ASLMPKKKKK STGRKYSSSS RP 152

## (2) INFORMATION ON SEQ ID NO. 299:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 172 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RTTTTIFAA GRLEFFFWHE RCNRLYCCSN TNIYAPFFAE ACPHLTPWLS MVWNIGVRGK 60  
 MPKQSWREAN GTGEGRDHLD QGSNSQDTRL HPHRGMEHLG SEFKIWQCLD LGWKVWGGL120  
 KLWSRVQDLR VPCSRPQFGD EHGEWGMGVS LGSQFEIGHG CSHGLKPQFWG WM 172

## (2) INFORMATION ON SEQ ID NO. 300:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 178 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

WFWRESYWQT IKVDLQVEHP YQFLLKYAKQ LKGDKNKIQK LVQMAWTFVN DSLCTTSLIQ 60  
WEPEIIAVAV MYLAGRLCKF EIQEWSKPM YRRWWEQFVQ DVPVDVLEDI CHQILDLYSQ120  
GKQQMPHHTP HQLQQPPSPE PPTPLPGPCG CWASHLKEGK VVQPEPVEQC PVWPPKPK 178

(2) INFORMATION ON SEQ ID NO. 301:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 113 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CISQDVCANL KYKNGPPNPC IGDGGSSLFK MSRSTFWKTS ATKSWIFTHK ENNRCLITPP 60  
ISCNSPHLLS LPPRCLGPVV AGPPTSRRGR LYSPNPWSNA LSGLQONQKT GSL 113

(2) INFORMATION ON SEQ ID NO. 302:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 90 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GGRPSNHRAQ AAGWEAQEMG AVAADGGCDE ASVVFLVSKD PGFGGRCLPK RRPGLHLEQTA60  
PTISYTWVWR SILVFQICTN VLRDTSLLLL 90

## (2) INFORMATION ON SEQ ID NO. 303:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 158 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRCVFEL PAENDKPHDV EINKIISTTA 60  
 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LRMKRTVQSN120  
 SPISALAPTG KEEGLSTRLL ALVVLFFIVG VIIGKIAL 158

## (2) INFORMATION ON SEQ ID NO. 304:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 112 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDTESSL 60  
 GREWATWGLL CGADRTPOHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

## (2) INFORMATION ON SEQ ID NO. 305:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

FKGKTCEMSS YINFFLHMVM INLNPMIWWI HQSNLPSCAC YLYKAIFPII TPTIKNKTTR 60  
AKSRVLRPSS FPGVANAEMG LLLCTVFLIR SPSSSLNCLF SSRSL 105

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 126 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

RPPQRTLRLHS AQLGAAPAAL PQPLWELPRA HGSQRQPGPG EAADHAEQER EEAAERPGSS 60  
PEEGQEGSGA FGGHTGHRAC ARCLGRGALG GRIPCGLLCQ LFRRDGC PAD SEVQH HHHQH120  
WQQLLP 126

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 240 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

NVGRCEAQA RAGAASLNAS LDGLHNALFA TORSLEQHQR LFHSLFGNEQ GLMEANVSLD 60  
 LGKLQTMLSR KGKKQQKDLE APRKRDKKEA EPLVDIRVTG PVPGALGAAL WEAGSPVAFY120  
 ASFSEGTAAL QTVKFNTTYI NIGSSYFPEH GYFRAPERGV YLFAVSVEFG PGPGTGQLVF180  
 GGHHRTPVCT TGQSGSGSTAT VFAMAELOKG ERVWFELTQG SITKRSLSGT AFGGFLMFKT240

## (2) INFORMATION ON SEQ ID NO. 308:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

KAGIEGHRGS CLPERRAQT WHRPCDEYVH QRLRFLLVPL PGSEFQVFLLL LPFPAQHGLQ 60  
 LPQVQADVGF HEPLEVPKEA VEEPLVLLQA ALSGEECVVE AVKGGVEGGG PGPGLGLAAP120  
 PDI 123

## (2) INFORMATION ON SEQ ID NO. 309:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

PTTTLVIPLF FLSSRKRKQK DSFQTALCSL HCSFPKQAAS TGKAHVVTYPY FSEVLLFHGV60  
 TLLSESKFRK QVLPLADKNH TSFL 84



## (2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CDRVPLFLSY WCAVADSWLT ASSVSHVKG I LSPQPTCAP PGPANCFNF FFFFFFFLVET 60  
 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQPEQD DLNLINSTPK QQLSLSQGCQ120  
 GGLCEGKD 128

## (2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRYLYKKLV WFLSAKGKTC FLNLLSDNKV60  
 TPWKRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

## (2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

ISTSIAALWL PGGQDAGGGA LWPLCGSRGL CVSDRFPGNF RARLTSWKFK YSIALEF 57

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 52 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

SAHQLQHCY QGVRMAVEP SGLCVVAEDS VSATVFRETS GRDSHLGNSN TQ 52

(2) INFORMATION ON SEQ ID NO. 314:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 43 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

NSRAIEYLNQ QDVSLARKFP GKRSLTQSPR LPHKGQRAPP PAS 43

## (2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 247 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60  
 HNWTGTVKDEL TESPKEYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120  
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EAAHEDSVMD180  
 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240  
 EAFPALA 247

## (2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

FMKNKSLPL PISTFIWFSO IKFYFCPVLI LNSLPLIQSH LEWTLLFYLF NFILLIFSVC60  
 HWMFFTFRC FLSHI 75

## (2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

SFGILKHAKA LNR RVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60  
VHLVLPCHV LGGQGLQN 78

(2) INFORMATION ON SEQ ID NO. 318:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 235 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

LHLGAQRALA PGLFRLQGM L RALLGRQLFR ARGPPVVREP LPRTRRLAVR HVWPECDRPL 60  
RVGPGSFLPP GPLHMHLLPA PAHQGVLPGA RRQALLPALL PEALRLTARS ARPLPRRPRP120  
PGKAGSSRPR GLALRAGGPT HWRAPPLRY Y ESSGVKFRNG PARPKPTRPQ SGLHTDKNSR180  
AGLHSIPTLE GAPLLGEGPC NSSSESEARPG RPCSLPHPCS VHFFYLHKHT HSTSK 235

(2) INFORMATION ON SEQ ID NO. 319:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 478 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GSRPPPCSPR ATGPRPAMED LDALLSDLET TTSHMPRSGA PKERPAEPLT PPPSYGHQPQ 60  
 TSGGESSGAS GDKDHLSTV CKPRSPKPAA PAAPPFSSSS GVLGTGLCEL DRLLQELNAT120  
 QFNITDEIMS QFPSSKVASG EQKEDQSEDK KRPSLPSSPS PGLPKASATS ATLELDRLMA180  
 SLSDFRVQNH LPASGPTQPP VVSSTNEGSP SPPEPTGKGS LDTMLGLLQS DLSRRGVPTQ240  
 AKGLCGSCNK PIAGQVVTAL GRAWHPEHFV CGGCSTALGG SSFFEKDGAP FCPECYFERF300  
 SPRCGFCNQF IRHKMVTALG THWHPEHFCC VSCGEFFGDE GFHEREGRPY CRRDFLQLFA360  
 PRCQGCQGPI LDNYISALSA LWHFDCFVCR ECFAPFSGGS FFEHEGRPLC ENHFHARRGS420  
 LCATCGLEPVT GRCVSALGRR FHPDHFTCTF CLRPLTKGSF QERAGKPYCQ PCFLKLFG 478

## (2) INFORMATION ON SEQ ID NO. 320:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 285 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

EQGLGVWRTR LFREGAASGG EGEPSGLSAE ELQEAGLAVG LAGALLEGPL GERAQAEAGAC 60  
 EVVRVEAATQ GRHAAAGHRE ATRGAQRAAS CVEVVLAQRA ALVLEKAASR EGREAFFADE120  
 TVRVPERAER RDVVIQDGLA AALARGEQL QEVPAAVGAA LALVETLISE GLPATDAAEM180  
 LWVPVSAQGG HHLVSDGLVA EATSWREALK VALGAEGGSI LLEEAAASQG GGTASANEVL240  
 GVPGAAQSRH HLPSNRFIAG ATEAFGLGNN TPAAEVGLQQ PQHGV 285

## (2) INFORMATION ON SEQ ID NO. 321:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 99 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GLHLQPLLWR QSTEEEVREE GQALTEPKSC GAQGGAQHRG LTPCPTGNGL GLAQP KIPAL60  
 SNSWRVDSVL ACLVSSDIFH TVEQNHQPCT DVTLCRKRP 99

## (2) INFORMATION ON SEQ ID NO. 322:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 99 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

ETQSSQRLTC PRSLGLDLSL RLRLQNPHSI CYISQGWGQG SCEQKEKYQL LKGLGFVGRA60  
 RQGQRGIQNK GASTSAWDGP IHSGRGCGVS FVLNRHLAS 99

## (2) INFORMATION ON SEQ ID NO. 323:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 83 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

SNPKAPVSMW VKGPTMGTYT QEDESSLASE SDCLPQTTPQ NRLLSHLPLH SDKTQAHIPG60  
 PGVFACICID GNAGPAKAFF YIK 83

## (2) INFORMATION ON SEQ ID NO. 324:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 111 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

VFPTVLRGVL VPSSVTSKPG LIVPIGDEGG MRRSHLQLLS VERTSGTEKN RGPHGSLEGR 60  
GTRVGELIAE RRDVQRPSAP LSWDVNRIFP STPSLPPVLP LFFFPSIKRC I 111

(2) INFORMATION ON SEQ ID NO. 325:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 272 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

SSRASGITRA ARPCPAKNEG PSKAFVNCDE NSRLVSLTLN LVTRADEGWY WCGVKQGHFY 60  
GETAAVYVAV EERKAAGSRD VSLAKADAAP DEKVLDSGFR EIENKAIQDP RLFAEEKAVA120  
DTRDQADGSR ASVDSGSSEE QGGSSRALVS TLVPLGLVLA VGAVAVGVAR ARHRKNVDRV180  
SIRSYRTDIS MSDFENSREF GANDNMGASS ITQETSLGGK EEFVATTEST TETKEPKKAK240  
RSSKEEAEMA YKDFLLQSST VAAEAQDGPQ EA 272

(2) INFORMATION ON SEQ ID NO. 326:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 241 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TLVFGRLRTK PFRIPGFLQR KRRWQIQEIK PMGAHLWIP AALRNKVEAP ERWSPPWCPW 60  
 AWCWQWEPWL WGWPEPGTGR TSTEFQSEAT GQTLACQTSR TPGNLEPMTT WEPLRSLRRH120  
 PSEKKSLLP PLRAPQRPKN PRRQKGHPRR KPRWPTKTSC SSPAPWPPRP RTAPRKPRRC180  
 RLLLPAPMTI TFRIMSILGP SAPGDPTPCS NTCLGFSYCP QRRAGPLLSG IKAWPNCSYW240  
 G 241

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 121 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

AVVRVTWYKG EGITLPPVLT PALVRGESIP IRLFLAGYEL TPTMRDINKK FSVRYYNLV 60  
 LIDEEERRYF KQQEVVLWRK GDIVRKSMH QAALASQRF E GTTSLGEVRT PSQSDNNCR120  
 Q 121

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRRLPC 60  
 THLPWWAGFS LLGSTLPSPV HDTDFRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120  
 GQKEVACGNL RSPHPRFPKR 140

## (2) INFORMATION ON SEQ ID NO. 329:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 127 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60  
 SPSSKTQGSF PRKGAHVPQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120  
 DLFSGCK 127

## (2) INFORMATION ON SEQ ID NO. 330:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 418 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GSTSTKNTKI SQACGVIVEL IKSKKMAGGA VLLAGPPGTG KTALALAIQA ELGSKVPFCF 60  
 MVGSEVYSTE IKKTEVLMEN FRAIGLRIK ETKEVYEDEV TELTPCETEN PMGGYGKTIS120  
 HVIIGLKTAH GTKQLKLDPS IFESLQKERV EAGDVIYIEA NSGAVKRQGR CDTYATEFDL180  
 EAEYVPLPK GDVHKKKEII QDVTLDLDV ANARPOGGQD ILSMMGQLMK PKKTEITDKL240  
 RGEINKVVNK YIDQGIAELV PGVLFVDEVH MLDIECFTYL HRALESSIAP IVIFASNRGN300  
 CVIRGTEDIT SPHGIPDLL DRVMIIRTML YTPQEMKQII KIRAQTEGIN ISEEALNHLG360  
 EIGTKTTLRY SVQLLTPANL LAKINGKDSI EKEHVEEISE LFYDAKSSAK ILGLTRQG 418

## (2) INFORMATION ON SEQ ID NO. 331:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 142 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VPQCGLGANL PQVVOCLLTD VDSFRLGTDF NDLFHFLWSI QHGPDYHHSV QKVKRDAVRG 60  
 CDVLSASDDT VASVGCKDDD GSDRRLQGA VQGEALNVQH VDLINKQHTR DQLSNALVDV120  
 LVHHLINLPS KFCDFCLLW LH 142

## (2) INFORMATION ON SEQ ID NO. 332:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 124 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LAHHGQDILS PLGPRISHIQ VMQGHILDDF FLFVHIPFWQ GDILFSFKVE FCGIGITPAL 60  
 PLHGPTVGFN VNHISSEFYS FLQTFKNAGV QFQLFGSFGC FESYDHMANG FAISSHGILC120  
 LTRS 124

## (2) INFORMATION ON SEQ ID NO. 333:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 176 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

QAMGKKQKNK SEDSTKDDID LDALAAEIEG AGAAKEQEPQ KSKGKKKKKEK KKQDFDEDDI 60  
 LKELEELSLE AQGIKADRET VAVKP TENNE EEFTSKDKKK KGQKGKKQSF DDNDSEELED120  
 KDSKSKKTAK PKVEMYSGSL TNFLKLLKGG LKNQIRSGMG QRRMRITVKK LKSVQE 176

## (2) INFORMATION ON SEQ ID NO. 334:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 193 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

RFKIKKDCKT ESGNVLWEFN KLPKKAKGKA QKSNKKWDGS EEDEDNSKKI KERSRINSSG 60  
 ESGDESDEFL QSRKGQKKNQ KNKPGPNIES GNEDDDASF KKTVAQKKAE KKERERKKRD120  
 EEKAKLRKLK EKEELETGKK DQSKQKESQR KFEZEETVSK VTVDTGVI PA SEEKAETPTA180  
 AEDDNEGDKK NER 193

## (2) INFORMATION ON SEQ ID NO. 335:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ETVAFARPF F PSLSFPPLS SFLFLIFRS FCLLHCHLLQ LWESLLSLQR QELLQYQQSL 60  
 WILQFLLQIS FEIPFVYSDP FYLFLTLLFL SASAVSLFLH LAFFSRAPSF LPSFGPLS 118

## (2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 230 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

LQRLPPGAE RPAHLCTGPG GEDGAGGRVP GTRPQRPPAL QRAEDGROGG LRVAGTAGFP 60  
 PGVPLRPGQG GSGHQEQGAS HPGSLDQGLT GAKRPQGCPA CGRRPPCVGG VPGSAHRPQP120  
 EGAALRRGRS RLQQAGPCCC RVLWLRRCHP AGLPRRPPAA DPGARAAAGG RHVLCRSPLH180  
 PGLRPPLPQW GLLRPEGGCL CVPVSRGILR TALREGAGGE VSGGRGYLGL 230

## (2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 416 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

QDGGSPFLAD FNGFSHLELR GLHTFARDLG EKMALEVVEL ARGPSGLLLY NGQKTDGKGD 60  
FVSLALRRDR LEFRYDLGKG AAVIRSREPV TLGAWTRVSL ERNGRKGALR VGDGPRVLGE120  
SPVPHTVLNL KEPLYVGGAP DFSKLARAAA VSSGFDGAIQ LVSLGGRQLL TPEHVLQVD180  
VTSFAGHPCT RASGHPCNLG ASCVPREAY VCLCPGGFSG PHCEKGLVEK SAGDVDTLAF240  
DGRTFVEYLN AVTESEKALQ SNHFELSLRT EATQGLVLWS GKATERADYV ALAIVDGHLO300  
LSYNLGSQPV VLRSTVPVNT NRWLRVVAHR EQREGSLQVG NEAPVTGSSP LGATQLDLDG360  
ALWLGGLPEL PVGPALPKAY GTGFVGCLRD VVGRHPLHL LEDAVTKPEL RPCPTP 416

(2) INFORMATION ON SEQ ID NO. 338:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 241 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

NQHMKNNTAMA RPRYPGRRQR STPSHSELLS IAPRRWGVV EGYGHVQGGW AGPAEQDQTQ 60  
IGPGLASAPQ QPGLAQARE QRRVPSSNI VWKSQYWRRR PRQGPETHQE GAAQIGAWKG120  
PVGSPGGRAP SDLSSPFLSG TRVPPDGAHV IQEPGLLPQG DTVGQAQCKA GAQHLEAGVC180  
VLRFPSTPSP PRCHLACPSL STRSVCSTAA WTEGRPGQOS LRPTLRQENH IKKRQVYKNR240  
K 241

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

LLQPQGEMPP GNPPMSTRGQ EATVLRTPEN LAGELFLVHP SLQLYLCPAD NVKDWSKVVL60  
AYEPVWAIGT GKTATPQQG 79

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

FPVGVQLQSCQ YQWPTQAHRP GRPCSSPSRY LQGRDTAGGK GEQERALQPG SPEYEERWPP60  
AP 62

(2) INFORMATION ON SEQ ID NO. 341:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 80 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

SLLGCCSLAS TNGPHRLIGQ DDLAPVLHVI CRAEIQLEGR VNKKELSSQV LRSTKNGGLL60  
PPSGHWGISR WHLPLGLEKS 80

## (2) INFORMATION ON SEQ ID NO. 345:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 257 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
KNLSQLEPRE NAKKEVRKER GMGWVAAGAA QLLSLLSTST ASDSSVISSS ACTSGLLP RR 60
RSPASPRSAH LHHLGGLLEHF HLALADLLDV EGEGLVDR GLGARVHHV GREGFAQLVP120
RRLQFLAPLG GHQARAQLVH ALLQGVPRLL QVFLGLEARL LQVLAGTHLG LLHLLGEG180
LEVVAHQAL RLIRSARDSS ITSSTSTASS DESSSAAASS SGRSPSPSS PSFSGSASDS240
FSDLLMLSLA GSFTSSW 257
```

## (2) INFORMATION ON SEQ ID NO. 346:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 237 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```
KSRRCQRRR ARSWARASGP RRTQRRWSFR RTRRWLRRL LRSPAQSVSS AGPAARGRLQ 60
EGLQGEDGE DQGAYPREPG EDAPQDQKP GEDAAHPGEA HEQAGHAPGA RRAARETEDV120
AGQVAQILHA RPRGVRLQD RGLQGATLHL PRQEDPRGPG GSAQGHDRGG GGRSGGRPAT180
CGAGAAPTCT RCWRSRPSRT PCWWTRATAT ERPLPPTPF LAPSELPLSH SLSARAG 237
```

## (2) INFORMATION ON SEQ ID NO. 347:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60
TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSLER120
QAGQIKKLEV NEAELLRRRN FKVMYQDEV KLPKLSISK SLKESEALPE KEGEELGE180
RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240
TWRRRASRPR KTWRRRGTPW RSA                                     263

```

(2) INFORMATION ON SEQ ID NO. 348:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

SSGSSRFGSS GSRRRYASLY FCCAIEDQDN ELITLEIHR YVELLDKYFG SVCELDIIFN 60
FEKAYFILDE FLLGGEVQET SKKNVLKAIE QADLLQEEAE TPRS GS                106

```

(2) INFORMATION ON SEQ ID NO. 349:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 78 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

LELMPQNKVR MVICQEFFIT VSYKKRVALF TVLCVKSLFK ARMFPLGYLL KLNLFCEPPL60  
 RSAAHFTAAS FLSMALPS 78

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 65 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TCLHGLYFHL YMLGWIKLCC DCDQHS GHVS TVLSHRQLVV INVQRTKKKK GAASLGGITG60  
 SGVKR 65

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 196 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

LPGLPLRQLG GVCHGHRPGL LLHQQHGGGA GAVQQPQREE EALHDPGQGS APAELCQFQQ 60  
 HVPRFPLQQF QAVQEGGGAG AGQGLVLWQP GAGLQGVQPG DDGAPDLQHG DAAGDSHHDD120  
 PAQELPAAEH RAQGPGGPRP ALRGGARSNC RVCLVQMCPE APEGSHQLMP ASDPQQGWFA180  
 AAAQGEFVSD PGHHHH 196

## (2) INFORMATION ON SEQ ID NO. 352:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 361 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

SLASLSDSLG VSVMATDQDS YSTSSTEEEL EQFSSPSVKK KPSMILGKAR HRLSFASFSS 60  
 MFHAFLSNNR KLYKKVVELA QDKGSYFGSL VQDYKVYSLE MMARQTSSTE MLQEIRTMMT120  
 QLKSYYLQST ELKALVDPAL HSEEELEAIV ESALYKCVLK PLKEAINSCL HQIHSKDGSL180  
 QQLKENQLVI LATTITDLGV TTSVPEVPM EKILQKFTSM HKAYSPEKKI SILLKTCKLI240  
 YDSMALGNPG KPYGADDFLF VLMYVLARSN LTEMLLNVEY MMELMDPALQ LGEGSYYLTT300  
 TYGALEHIKS YDKITVTRQL SVEVQDSIHR WERRRTLKA RASRSSVQPL HLRVVGARA360  
 A 361

## (2) INFORMATION ON SEQ ID NO. 353:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

VDGFLQGLQD TFVQGRLYNC FELLGVOGG VHQGLELQAL QQVALELGHH GANLLQHLRA 60  
 GGLARHHLQA VHLVVLHQAA KVRALVLRQL HHLVQLAVV GEESVEHAAE TGKAQPVPSL120  
 AQDHGGLLLH AGAAELLQLL LRAAGGVGV VGGHDRHPQA V 161

## (2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

```

SGRGPKYVID VEQPFSC TSL DAVVNYFVSH TKKALVPFLL DEDYEKVLGY VEADKENG 60
VWVAPSAPGP GPAPCTGGPK PLSPASSQDK LPPLPPLPNQ EENYVTPIGD GPAVDYENQD120
VASSSWPVIL KP KKLPPKPPA KLPKPPVGP K PEPKVFNGGL GREAAASSVSA QPLLSPQAGL180
GRHGRQSYRR SWEKRRGTGS MVSDTPGTSG LVPGRARW                               218

```

## (2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 253 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

AGEGVDGLTQ ETPLKPVSQL PGPAGAPTGR RGQAEDPGSV MASALRPPRV PKPKGVLPSH 60
YYESFLEKKG PCDRDYKKFW AGLOGLTIYF YNSNRDFQHV EKLNLGAF EK LTDEIPWGSS120
RDPGTHFSLI LRNQEIKFKV ETLECREMWK GFILTVVELR VPTDLTLLPG HLYMMSEVLA180
KEEARRALET PSCFLKVSRL EAQLLLERYP ECGNLLLRPS GDGADGVGHH AADAQRDARG240
PALQGEAGGA PST                               253

```

## (2) INFORMATION ON SEQ ID NO. 356:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

LTTASREVQE NGCSTSITYL GPLPLHLVMP DHVRPVVHLP RGDRHRRRRP RWAAAAGSRT 60  
RGSAPGAVVP PAGSPSGSTR VSPVHGAPPL WPRLOTSCIG AQEAGSSRSR HGAPPPLR 118

(2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 223 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

DHTCGCAGNL QEAIMLRSGV TSQGIHPGSP WCCTPTQAEI IVGDQSGAIH IWDLKT DHNE 60  
QLIPEPEVSI TSAHIDPDAS YMAAVNSTGN CYVWNLTGGI GDEVTQLIPK TKIPAHTRYA120  
LQCRFSPDST LLATCSADQT CKIWRTSNFS LMTELSIKSG NPGESSRGWM WGCAFSGDSQ180  
YIVTASSDNL ARLWCVETGE IKREYGGHOK AVVCLAFNDS VLG 223

(2) INFORMATION ON SEQ ID NO. 358:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 193 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

FFFFFFFFFP EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHGGGQ LLAGTNKPFH 60
LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLRPLSSFPG SADFPQCRL AQSRSVQPG120
GRALSHLDKQ LGAESPRAAW PSRSRRHRGP SGPVAQAGRG GSALTWVLHG SLQLPPPAPG180
SPEGSQASPA HCH
193

```

## (2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 251 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

PGCCMGPPSSC HHLHQAVPRG HRLAQHTVIE GQADNSLLVA AILSLDLSSL HTPEPGQVVR 60
GSSDDVLGVP REGAAPHPA A GGLPGVAALD AQLRHQGEVG RPPDLARLIS RAGGEERG120
AEATLQGVAR VGRDLSLGDE LGHLVTNAPR QIPDIAVSGA IDSCHVAGVG IDVGGRDGD180
GLRDQLLVVV CFQVPDWDSP ALVTHDELCL GWGAAPGTPR VNALGGHTGP QHDCFLQVTS240
TSACMILTSS C
251

```

## (2) INFORMATION ON SEQ ID NO. 360:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:  
 GNIPHSNLTD ASSPKRIKIV ACTDQENILG RMKYVCLFFF KNKGFWNSGE

50

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

KGNQLYQGET RALGTMTRT AFILHSDCF QSSNDCQATS QMTDNFCCSF LYKMLRQQA 59

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

DKILLSPRME CSGMIMAHCS LDLPGSHLSL PSSWDHRHVP PCPANFYFGR DKVSPCCLGR60  
 FQTPGLK

67

(2) INFORMATION ON SEQ ID NO. 363:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 84 amino acids

- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

MRRCIHPSHS LSGSRQTQSP LSHSASNGST TKVAQQMRRA AAVVGESTEE TRLGRALGAA60  
GFTNKQLSEN TAQGEKRVN CLQN 84

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 127 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

CAYRTEKWKS HTVPCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60  
RGSTGQPTAN TAASLVASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120  
HHCIPNR 127

(2) INFORMATION ON SEQ ID NO. 365:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

PYVHSPAWSP WGLVGRLVSV HTDIPATFRT LIVSAEVALG SQLQTQQPPW FQLLSFYIL 60  
ETTPGLIFLR TQHSLSCHFSV RKP KMAPCHL EADQVITVSP TASTVCIWYI VQAP 114

(2) INFORMATION ON SEQ ID NO. 366:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

NLHSNIKVFF YNVEKISGPQ QAVFVPEFFN

30

(2) INFORMATION ON SEQ ID NO. 367:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 44 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

KECMSEAQFL ATTLTKGNNC RGILQLIHTQ HLLHTVFTDS NLVG

44

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:



- (A) LENGTH: 34 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

NVDFRCKNML EIRFSAIKPN TKKIKKNVCQ KPNS

34

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

QPSSLLHHCP YPYPPRHLLA TPLLKPQLLA GSPAHLIS FLASPQRASR QHGGPSQRAG 60  
 TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPA GDRRLPEWG RVSLAESPGA120  
 EFRCPGSLGE WGEIPEKESS AHPKTEE 147

(2) INFORMATION ON SEQ ID NO. 370:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 244 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

NHSCWQGPQL MPASSPFLLA PKGPPGNMGG PVREPALSVL LWLSWGAALG AVACAMALLT 60  
 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRRAVLTK120  
 QKNDSDVTEV MWQPALRRGR GLQAQGYGVR IQDAGVYLLY SQVLFQDVTF TMGQVVSREG180  
 QGRQETLFRG IRSMPSHPDR AYNSCYSAGV FHLHQGDILS VIIPRARAKL NLSPHGTFLG240  
 FVKL 244

(2) INFORMATION ON SEQ ID NO. 371:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 185 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESFFCFWVS TALLFRDLSP LSQASRASEL 60  
 CSGRLCQGYF SPFWEGPPVP CSRLTSLRL CSSVCWVSRA MAQATAPRAA POLNQRATES120  
 AGSLTGPPML PGGPLGASKK GDEAGMSWGF CQQLWFQEWG SKEVAGRVRV RAVVQKGRRL180  
 LRKEK 185

(2) INFORMATION ON SEQ ID NO. 372:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 148 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

VLYHCASRYR RRARQTCAPS YTRSADLPSR TPPVEDLLEL SRAFWVGADG GGRVRVLGGT 60  
 EAHEDGIPPE SMDHYADGHR PQHCHLGYRC HGRPQREGLP RCLKVPPVNL SSVSVFPFVT120  
 HRAGMEFNGC SGQTLVHGQT SLLWILQD 148

## (2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 135 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CLPVRRLRQF EPKTPKVEAE FQSMGSRLSQ PFESYITAPP GTAAAPAKPA PFATPGAPTS 60  
 PAEHRLLKTC WSCRVLGSLG LMGAGGYVYW VARKPMKMGY PPSPWTITQM VIGLSIATWG120  
 IVVMADPKGK AYRVV 135

## (2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 152 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPCLLCVSRG KGQRQKTDLS VVLSNNAVGL PFGVCHDNDT PGGNAEADDH LKNGPWTRGV 60  
 SHLHGLPCHP VHVPARPHQP QPRKHATAPA GLQAVFCWG GRRSGCSWGR REGGRGGGTG120  
 RRSDIGLKRL GQPRPHALEL GLNLGRLWFK LA 152

## (2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GAEQLRSCA MAVSQEGLDG EVKAPDARIF IPCANTAFTP DLQVLQQVLS SFTVSSPLFH 60  
SGFICYTPNL FSQSTPQSLP CWGQHRKRQN LRKEKGNLQP AMDLMIP 107

## (2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

IPKNFYHNIH RSLYQLYLEV KQAWESIDCS ACPRVEALNK ATKTPFITDL TFQWPTGPGS 60  
GOVGHQANHL FPCASLCKSW SVPLARPSLV QDLGPQTKES RGLGFDPDRM VSL 113

## (2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

FGGPQAQPHS AVGSSLSSQI QVNLSEKNG EPQTCSTTRD NNTPWQEDHV LDCLRTATVR 60  
QEACCDPLCS MPDQAASSIP YHLPPLFFG TTTLAKREYG KQRPRALLQY RHFEVGRQHM120  
LHSL 124

(2) INFORMATION ON SEQ ID NO. 378:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 66 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HKILISRYR RNSVVTQAI LYTPMILQRK HPSLLPLW QKICCSSTL KRRKRNNLSL60  
IPKLPH 66

(2) INFORMATION ON SEQ ID NO. 379:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 67 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

PEKSPGAGPL LGGSPFFFFF YVSKSTEFIL KHSIKFESHE TKASLHYMLI LAKSKDQHTI60  
DIHDNVV 67

## (2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

FCIHFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNQDS FFRMLKAQCL RFMLAALLAL60  
 LLPKMTKQN R 71

## (2) INFORMATION ON SEQ ID NO. 381:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

MDGAQGRLLP VSSRHSNLAL LKPTSROLTA PPEGASLMTV GGITAPRDVQ VWNPRTWESV 60  
 TLRGKRDPAF VLQFRISWWG DDRGWLRWAL SNHGGPYKGR GVTRVCA 107

## (2) INFORMATION ON SEQ ID NO. 382:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 143 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

EVENHTNLLS YSSRGQESKM VFTRLKSCQC GFVSPRRLWG RIQCLFQLLQ GPPHRLAPGL 60  
 LAIFTARSFL ASCADPRDSP SLIRAPMITQ GPPQPSTVIS PPRNPCLKHR RRVPFATQGN120  
 TFPRPGVPNL DISGGCYSTH RHQ 143

(2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

SHTHAQLSNH GGVQEPPLPL GVPKPWGS DS GALS RPGCKL KTPGGFQNAQ CLGHNLDQLN60  
 LNLQRDITAP QETPRGSQSA KPEETI 86

(2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

LEPIRFQQKV MEKETEKRI S EIEDAAFLAR EKAKQDAEY AAKKYATSNK HKLTPEYLEL 60  
 KKYQAIASNS KIYFGSNIPN MFVDSSCAL K YSDIR TGRES SLPSKEALEP SGENVIQNKE120  
 STG 123

## (2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

DNSCVRYVEA QQKSHGTTSR NLSAVRPVSL MTVCWLCQTL YLGKESPDLN GSFPWALSYR60  
GICNMEKIIF HFCSFNSINS LYK 83

## (2) INFORMATION ON SEQ ID NO. 386:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 88 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CLTFQCRQYL SIRLSSFMS SLEARN TYRIL DKTVAEKTIC VSDSWLYPPI SGAPRTIAGE60  
VEQMKCKFSV NLKSPYND CS HLTPWATS 88

## (2) INFORMATION ON SEQ ID NO. 387:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes



- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 173 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AQESPWQLCR GARTSKRKLP KLGMEQHCNE MCPSSSLFLP GAYKAQMYSD VWTNTKKKKK 60  
 KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRPISLVLQ TSSQAIFYQK120  
 GENSCLSFLK NAFLYLSIRH YTSELYKRPG GTMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60  
 RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPS 105

## (2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 262 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RCPRRGREMD SGCWLFGEF EDSVFEERPE RRSPPASYC AKLCEPQWY EETESSDDVE 60  
 VLTLLKFKGD LAYRRQEQYK ALQEYSSISE KLSSTNFAMK RDVQEQQARC LAHLGRHMEA120  
 LEIAANLENK ATNTDHLTV LYLQLAICSS LQNLKTIFF LQKLISLHPF NPWNWGKLA180  
 AYLNLPALS AALASSQKH SFTSSDKTIK SFFPHSGKDC LLCFPETLPE SSLIFCGRDT240  
 RNGRKIGKFC KCANLVGERG TG 262

## (2) INFORMATION ON SEQ ID NO. 391:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

KPVPLSPTRL AHLQNFPIFL PFLVSLPQKI KELSGKVS GK HKRQSFPECG KKDILIVLSLE60  
 VKLCCF 66

## (2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 78 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

QAGGRVPWLN GLCWLLYFPS LQQSPAPFYA YPGEPDTEPD LPGHPFSWQN WLMTIFQRYW60  
NTPAVLSDTL VVCRPGLL 78

(2) INFORMATION ON SEQ ID NO. 393:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

TSLEGIDLQP SHLTIYTAAL KEKTPDFRRL SPRVSETADS RKVARGPRFV MRDNPGRGGD60  
HRGLQAPGWM KEGRGWGV 79

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

VTPPPPSQIS SFLPPSTAFF TKPPIPDPPS STPAPGDPYD HPRARGCPAL QIGAHGRPYG60  
SPRSPRREER DV 72

## (2) INFORMATION ON SEQ ID NO. 395:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

PPPPPPKFHP SFRLLQPPLQ NPPSPDLLHP PRRLETPMIT PAPGVVPHYK SGPTGDLTG60  
 RGLRDARRET SEVWRLFLQG CCVDCEVGGG KINSLEGG 98

## (2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

NWRQTVWQRV REGACQESS RPASGCRFLR CAIGASAFSG DRGSAVATNT QPHTNHHTK60  
 WGQPHFVQAF TNVISVLFF 80

## (2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

YDNSSTCKKG KVFPKGISVT VSETFDPEEK HSMAYQDLHS EITSLFKDVF GTSVYGQTVI 60  
 LTVSTSLSPR SEMRADDKVF NVTIVTILAE TTSDNEKTVT EKINKAIRSS SSNFLNYDLT120  
 LRCDYYGCNQ TADDCLNGLA CDCKSDLQRP NPQSPFCVAS SLKCPDACNA QHKQCLIKKS180  
 GGAPECACVP GYQEDANGNC QKCAFGYSGL DCKDKFQLIL TIVGTIAGIV ILSMIIALIV240  
 TARSNNKTKH IEEENLIDED FQNLKLRSTG FTNLGAEGSV FPKVRITASR DSQMNPYSR300  
 HSSMPRPDY 309

(2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

QALIASTTFN VIDSYLASEL DSLQTFTTSI QRGWQMSDGR KTFEARSLLV LTSPSVFELNT 60  
 LNNSLYIGWG PWRVPHSYDS NSQGGACCCV LNRDFASGCL WRPLS 105

(2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

CFSCFVICSV SLCTLNIYPL CDKKKKKKKK SRTSTFDFSQ PQPRKNGSWD KQLVFVSKTQ60  
 IGHINATAFR SFDFFD 75

## (2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

RKKAVCFMND LICFLDNTFK NNVLSQAWWC VHLVPTIWEA EAGGSLEPRS LKLQCPVVAP60  
 VNNCTPAWAT 70

## (2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

LVPQGSLLQT HPEVFFSFLE MRSRYVAQAG YQLFTGATTG MCSFKLLGSS DPPASASQIV60  
 GTRCTHHHA 69

## (2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

PPLWVATVRN GCCHVFWTLP ANRSLPGFGN TSITSLLLFC RDKTFEVARP RTSKDSCYSA60  
TVYTAHLSYS HVLSSLVRLF 80

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLP RCYFSAGIKL LRWPDPEHPR60  
IPVTVLQYTL LIYPILMCFL L 81

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

VSHYPHSVSK PPKHQTKQMV VALTHSRLTS EFKWENTPYT TVIIPLWTLN ITYFLKIILL60  
KKKAHENRIN EQCIL 75

(2) INFORMATION ON SEQ ID NO. 405:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 328 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

RYLNMGNLLK VLTCTDLEQG PNFFLDFENA QPTESEKEIY NQVNVVLKDA EGILEDLQSY 60
RGAGHEIREA IQHPADEKLQ EKAWGAVVPL VGKLLKKEYEF SQRLEAALRG LLGALTSTPY120
SPTQHLEREQ ALAKQFAEIL HFTLRFDLQ MTNPAIQNDF SYRRTL SRM RINNVPAEGE180
NEVNNELANR MSLFYAEATP MLKTLSDATT KEVSENKNLP IENTTDCLST MASVCRVMLE240
TPEYRSRFTN EETVSECLRV MGVVILYDH VHPVGAFKAT SKIDMKGCIK VLKDQPPNSV300
EGLLNALRYT TKHLNDETTT KQIKSMLQ                                     328

```

## (2) INFORMATION ON SEQ ID NO. 406:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 115 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

YYIHLIINFL LRLCRLGIFK IKEKIWPLLK VCACQNFKKI PHVKVPSASA GDSVLVLLSS 60
ARASRRSQSR SCALLDRRGG SSAALGGAPG PERGSGGSRT GSPSTPAPVA EPPQA      115

```

## (2) INFORMATION ON SEQ ID NO. 407:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 100 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

QEPALALDAG WENMGYLLRL PEDLLMLLLT SEKIRKISLI CLLVEQLHPM PSLATSHLLD 60  
AGLPLVFRGQ LLCMTASPPR CLLHLLILHS PDYKFPSQTL 100

(2) INFORMATION ON SEQ ID NO. 408:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

TVLHSHLPSS CLPCLSTHSV KEPRGATSPR LCFPTACGMG VSSATAGLRC FHQPCRHLVL 60  
HEEQTLRGWS GMGRSPLGGQ ALVPSRFPSL APGVHTAQSA PGGWKPPCFR SLGSPP 116

(2) INFORMATION ON SEQ ID NO. 409:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

SPDERCSIRT SPPRACPASP RTVLRSEQEP LRPDFVSPPP AAWVCPVPPL ASAASISLVA 60  
TWSFMKSRHL EAGREWGRP WEGRRWFQAG SRPWRLECTQ PSRHLVAGSH PALDHSGPHL120  
RRVPALDQSR GH 132

## (2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

WKQRRPAVAL DTPMPQAVGK QSLGEVAPLG SLTLCVERQG RHEEGRCEWS TVHPGISQPE 60  
 SPPSLAAPEH SLWPTATEMS ACQDTWRRKK TRHQKKLPQ EQIELLDQGH TRSGRHPAPC120  
 AOGKETQFNV WLLCSRETAT LP 142

## (2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 244 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

KRRGVRQFRW LVCTRRASPG AARSAPIAPA TGSGRRPNMD SAGQDINLNS PNKGLLSDSM 60  
 TDVPVDTGVA ARTPAVEGLT EAEELRAE LTKVEEIVT LRQVLAAKER HCGELKRRLG120  
 LSTLGELKQN LRSWHDVQV SSAYVKTSEK LGWNEKVTQ SDLYKKTQET LSQAGQKTS180  
 ALSTVGSALS RKLGDMRNSA TFKSFEDRVG TIKSKVVGDR ENGSDNLPSS AGSGDKPLSD240  
 PAPF 244

## (2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 149 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

```

LGHFLLPLSK FLRSFHIGAR DLHVMPAPGQ VLFQLPQGGE AQPPELSTV PLLGCQDLAQ 60
SDNFLFHLGK LSPDLLLSL CQTLSRSPG SHTCVDNRIR HGVRQQTFR RIQVDILAGG120
VHVRAASGPC RGRYGRAGG AGRSSPRTH                                     149

```

(2) INFORMATION ON SEQ ID NO. 413:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```

ALETCTSCQL LDRFCFSSPR VERPSLLLS PQCLSLAART WRRVTISSST LVSSALSSSS 60
SASVRPSTAG VRAATPVSTG TSMESDSRP LLGEFRLISW PAESMFGRRP DPVAGAMGAE120
RAAPGEARRV HTSQRNCLTP RRF                                     143

```

(2) INFORMATION ON SEQ ID NO. 414:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RGRGALWAA KELRRTKKLS DYVGKNEKTK IIAKIQQRGQ GAPAREPIIS SEEQQLMLY 60  
YHRRQEELKR LEENDDDAYL NSPWADNTAL KRHFHGVKDI KWRPR 105

(2) INFORMATION ON SEQ ID NO. 415:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 386 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

AAELRDCGSR RISRSPSSNS HLSPRISLSG NLGPQTSRLG GPPSPSATWS VFWQLPRQQS 60  
LPGRGSANLL PSVRSESAVL SDCVGGFPGR SSVRAWIAGP RCTPASPTRV LSLSWRLFNS120  
ASLLLLLATST SGSECRFP RS PRARERGIPD CERLLVRRSC WRS GDPRPAG PAGHAAGAFS180  
TPQYLGGTAM VLLHVKRGDE SQFLLQAPGS TELEELTVQV ARVYNGRLKV QRLCSEMEEL240  
AEHGIFLPPN MQGLTDDQIE ELKLKDEWGE KCVPSGGAVF KKDDIGRRNG QAPNEKMKQV300  
LKKTIEEAKA IISKKQVEAG VCVTMMEMVKD ALDQLRGAVM IVYPMGLPPY DPIRMEFENK360  
EDLSGTQAGL NVIKEAEAHC GGQPRS 386

(2) INFORMATION ON SEQ ID NO. 416:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 182 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GVEKAPAAWP AGPAGRGSPD RQQLRRTNSR SQSGIPRSLA RGERGKRHSL PEVDVAKSNS 60  
 EAELKSRQLK LRTRVGEAGV HRGPAIQART ELRPGKPPTQ SERTADSERT DGRRFADPLP120  
 GSDCCRGNCQ NTDQVAEGEG GPPNRLVWGP RFPLREIRGL RWELLDGERE IRREPQSRSS180  
 AA 182

## (2) INFORMATION ON SEQ ID NO. 417:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 467 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

HTLSRWTKHS IPRWNDARTD DTWHESEDMR KIGQARNTLM DMRLSQVSDS VSGQTVVDPK 60  
 GYLTDLNSMI PTHGGDINDI KKARLLLKSV RETNPHHPPA WIASARLEEV TGKLQVARNL120  
 IMKGTEMCPK SEDVWLEAAR LQPGDTAKAV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR180  
 VLRKALEHVP NSVRLWKAAV ELEEPEDARI MLSSRAVECCP TSVELWLALA RLETYENARK240  
 VLNKARENIP TDRHIWITAA KLEEANGNTQ MVEKIIDRAI TSLRANGVEI NREQWIQDAE300  
 ECDRAGSVAT CQAVMRAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP360  
 SKKSVWLRAA YFEKNHGTRE SLEALLQRAV AHCPKAENVLW LMGAKSKWLA GDVPAARSIL420  
 ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLAKARTV PPPPGCS 467

## (2) INFORMATION ON SEQ ID NO. 418:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 352 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TPGRWGHCPR LGQQPPGPLV LIILGLQLHG CQPDLLTVGV GLEGQGDAP CCRHIPCQPL 60  
 GLGAHEPQHL CFGAVGHSP L QECFQGLPSA MVLLEVRGAQ PHTLLAGEHL QGVGVDSCT120  
 LQGVIGYTTV SILHPGMLPI FLLNPNNPHG THDGLAGGHT PSPVTFLGIL DPLLTVDLHT180  
 VGPQRGDGSV DLLLHHLRVP IGFLQLSSRD PDMSVCNRNL PRLVQDLAGI FIGLQPCQSK240  
 PELHAGGAAL HSSAQHDSSI FRFFQLNGCF PQANRVWNML EGFPKNPLLC TNVRFQLCGS300  
 DVNPDRLWEM TDSLGYHGLG CVPRLQPGCF QPDIFTLGAI LRPLHDKVPS YL 352

## (2) INFORMATION ON SEQ ID NO. 419:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 424 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

PPGAPFFLFF FFLTRDIKTF NEGGSSEPF HMRPNPAPRR PAMATAQSEG VLDAAGHQP 60  
 DVPDLLLLPVG DVLGHGAPQL PMPRLCTLTA LPHLLLLLLS AMLQLKLVVE GPGIPQVRVN120  
 LHSAVEPLPG LGDLPLTPKQ LGHGQEHMGV MLTLLQGIHA LGPPLGPCLE EDGLRPQDTG180  
 VGALLQRLGH ECICDVLQPR TVLQPHGLQP QPRVLWVLQT RLFQNGPCSS KLPNLLLQPR240  
 EQKPQCGCVG TLLQPLVIGF PRLHHLLLL LDPLLHHPQL GEVLIVPQGL LAQILGCPDV300  
 VLHPLQLHRL HEHPGGGGTV RALASSLRAR SYSSFSOSS TAASQISSLI GLAWKARARM360  
 LLAAGTSPAS HLDLAPMSHS TSALGQWATA LCRSASRDSR VPWFFSKYAA RSHTLFLLGN420  
 TCRA 424

## (2) INFORMATION ON SEQ ID NO. 420:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 109 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GRTLPRGGGT VWVQGHGLEG WWAALSGSGF PAVGFLFWLL RLVYFLSLLP VTPGAPEYRL 60  
 FSPWAVSLSC FLTLLPGLLC VHLRLAWSKQ VRPLLLYSLV LFWHLVKLA 109

## (2) INFORMATION ON SEQ ID NO. 421:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

VSVPSSSAAG TLFQGLCGAP DAPHPLSKIP GGRGGGRDPS LSALIYKDEK LTVTQDLPVN 60  
 DGKPHIVHFQ YEVTEVKVSS WDAVLSSQSL FVEIPDGLLA DGSKEGLLAL LEFAEEKMKV120  
 NYVFICFRKG REDRAPLLKT FSFLGFEIVR PGHPCVPSRP DVMFMVYPLD QNLSDED 177

(2) INFORMATION ON SEQ ID NO. 422:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

ASRPYILELR EKDPCRPLAH RGSSTVGEGH QEHRGPGTM CLQHWSWGHL LNGKILLSWV 60  
 FIILGGSAAQ GRRRRGEWVG GRVGGCGVAR AGRSLWAKSL SGRGRVPSSC LSER 114

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 50 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

PFCSSLAKLQ GIWGMWDLQF PAPASALSQV LTPAPASAPA PGRAPAPAAA

50

(2) INFORMATION ON SEQ ID NO. 427:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 114 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EDKMRPGLSF LLALLFFLGQ AAGDLGDVGP PIPSPGFSSF PGVDSSSSFS SSSRSGSSSS 60  
RSLGSGGSVS QLFSNFTGSV DDRGTCQCSV SLPDNNFPVD RVERWNSQLI VISQ 114

(2) INFORMATION ON SEQ ID NO. 428:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 113 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

EITMSCEFQR STLSTGKLLS GRETEHWQVP RSSTEPVKLE NNWDTEPPLP KLRLELEPDL 60  
ELELKLELES TPGKELKPGL GIGGPTSPKS PAAWPRKNRR ARRNERPGLI LSS 113



## (2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAAGAGARPG AGAEAGAGVN TWERAEGAG NWRSHIPQIP CSLAKEEQKG

50

## (2) INFORMATION ON SEQ ID NO. 430:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 224 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

QTQKVVTSP RITLHWLLPC AAHPPDLHKK QENSGCAPA TAHSAPPGRS PPELRAGLQR 60  
 LARAVLPVSR FSAPQPPAAS FSGPRVAPSE ESGPGTSSNS GRLALPRLRS LCPLGVARPR120  
 CCRALARCCC SSSPRTAAWA RRAGSSSLAS PTSPTSDELQ AHPGQPAAPV RHRIPEHAAA180  
 QPAGPRDHEG GAGAGRRLDP AGHEAVPPGH QEVPVLALRP RLPR 224

## (2) INFORMATION ON SEQ ID NO. 431:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 408 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
PALLGLPFIG SSLAPPTLQI CIKKAKKTLA VPQORLILLP RVGAPRSCAR ACSASPALSS 60
RCPASPRPSR RLPAPFRGPES HPAKRAGPGQ ARTPAASFPF GSAPSAPSGS RAHDAAGPWL120
AAAALPRLAL LPGLGARALP LWPARLLLQA QNCKPIPANL QLCHGIEYQN MRLPNLLGHE180
TMKEVLEQAG AWIPLVMKQC HPDTHKFLCS LFAPVCLDDL DETIQPCHSL CVQVKDRCAP240
VMSAFGFPWP DMLECDRFPQ DNDLCIPLAS SDHLLPATEE APKVCEACKN KNDDDDNDIME300
TLCKNDFALK IKVKEITYIN RDTKIILETK SKTIYKLNGV SERDLKKSVL WLKDSLQCTC360
EEMNDINAPY LVMGQKQGGG LVITSVKRWQ KGQREFKRIS RSIRKLQC 408
```

(2) INFORMATION ON SEQ ID NO. 432:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 323 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

```
VISFTFIFSA KSFLQSVSIM SLSSSFLFLQ ASHTFGASSV AGRRWSLLAR GMQRSLSWGK 60
RSHSSMSGQG KPKADMTGAQ RSFTCTQSEW HGWMVSSRSS RQTGAKSEHR NFLVSGWHCF120
MTSGIQAPAC SSTSFVSWP SRLGSRMFY SMPWHSCRLA GMGLQFCACR RSRAGQGRA180
RAPSPGSSAR RGRAAASQG PAASWARDPE GAEGAEPPGKG EAAGVRACPG PALFAGCDG240
PRKAGSRRLG RGEAGHREDS AGEALQARAQ LRGAPTRGSR MSRCWGTARV FLAFFMQIWR300
VGGAREEPMK GNPRRAGHYF LGL 323
```

(2) INFORMATION ON SEQ ID NO. 433:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 333 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```
RGRTWELFLA GRRVLVTGAG KGIGRGTVQA LHATGARVVA VSRTQADLDS LVRECPGIEP 60
VCVDLGDWEA TERALGSVGP VDLRGDCADM ELFLAGRRVL VTGAGKGIGR GTVQALHATG120
ARVVAVSRTQ ADLDSLVRER PGIEPVCVDL GDWEATERAL GSVGPVDLLV NNAVALLOP180
FLEVTKEAFD RSFEVNLRAV IQVSQIVARG LIARGVPGAI VNVSSQCSQR AVTNHVSVC240
TKGALDMLTK VMALELGPHK IRVNAVNPVT VMTSMGQATW SDPHKAKTML NRIPLGKFAE300
VEHVVNAILF LLSDRSGMTT GSTLEVEGGF WAC 333
```

(2) INFORMATION ON SEQ ID NO. 434:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 210 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
APGHNLRLHD DRTQVHLKGS VKGLLGDLQE GLQQGDSGVV HQQVHGAHAA QRPLGGLPVT 60
QVHAHGFYPR ALADKAVKIR LSPAHSHPHRR ARRVRQLDRA APYTFACPGD QHPAAREEQ120
HVGAVSAQVH GAHAAQRPLG GLPVTQVHAH GFYPRALADK AVKIRLSPAH SHHPRARRVQ180
RLDRAAPYTF ACPGDQHPAA REEQLPSCPT 210
```

(2) INFORMATION ON SEQ ID NO. 435:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 132 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```
FFFFFFFFFL GSRIRFIGGI GGRMSTAWGL RCVEGAQQAQ KPPSTGKVEP VVMPLRSLSR 60
KRMAFTTCST SANLP SGIRF SIVLALWGSL QVAWPMDVIT TVGFTAFTRI LWGPSSRAIT120
LVMSRAPLV EQ 132
```

## (2) INFORMATION ON SEQ ID NO. 436:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

KAKSWVPSDF RFQELPENTR SQRVIFWSLF CRDSWEYGHF APRCGNESSR SGEAALADVQ60  
 LAAPVSNQLH PDGVEDRGVG GLLPELHAE PYLV 94

## (2) INFORMATION ON SEQ ID NO. 437:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

FSGVCFAGIA GSMATLLHDA VMNPAEVVKQ RLQMYNSQHR SAISCIRTVW RTEGLGAFYR60  
 SYTTPSPISC 70

## (2) INFORMATION ON SEQ ID NO. 438:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60  
LRSGVLRKFL EPKIRRNPGI SFLRSKMYIQ SAQVSTDS 98

(2) INFORMATION ON SEQ ID NO. 439:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 270 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

RSVVRRLKLM AAEPQQQKQ EPLGSDSEGV NCLAYDEAIM AQDRIQQEI AVQNPLVSR 60  
LELSVLYKEY AEDDNIIYQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSL EALLDDSKEL120  
QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180  
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVPEM CKESDHIHII ALAQALSVSI240  
QVEYMDRGE GGTNPHIFPE GFRAQGLTLF 270

(2) INFORMATION ON SEQ ID NO. 440:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 145 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

RWRRRLSSR SRSRWAATPK VLTWVPMMP SWLSRTEFSK RLLCRTLWCQ SGWSSRSYTR 60  
SMLKMTTSIN RRSRTSTKST RTSARPGLTA TVSIGLSDSP TWRHCWMTAR SCGSRRLCLP120  
RARKTWCPR SLNSQLRIST TRSWT 145

## (2) INFORMATION ON SEQ ID NO. 441:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 210 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

IAPSRLKQ GK TLGSEALRED VRIGGAALAA VHVHLHDGHA EGLGQRNDVD VVALLAHGLH 60  
 LLLAELLDSP STLDEVLEEL ALALQVARGE QPQVDHKVVG GALVIEGGQQ VGDRGLLLHL120  
 LNQVHERVVE ILNCFSEAL GHQVFLALGR HSLEPLQLLA VIQQCLQVGE SESPIETVAV180  
 RPGLADVRL FVEVLDLLLI DVVIFSILLV 210

## (2) INFORMATION ON SEQ ID NO. 442:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 322 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

NSERGLQAM MTHLHVKSTE PKAAPQPLNL VSSVTLKS SA SEASQSLPH TPTTPTAPLT 60  
 PVTQGSPVIT TSMHTVGPI RRRYS DKYNV PISSADIAQN QEFYKNAEVR PPFTYASLIR120  
 QAILSPKQ LTLNEIYNWF TRMFAYFR RN AATWKNAVRH NLSLHKCFVR VENVKGAVWT180  
 VDEVEFQRR POKISGNPSL IKMQSSHAY CTPLNAALQA SMAENSIPLY TTASMGNP TL240  
 GNLASAIREE LNGAMEHTNS NESDSSPGRS PMQAVHPVHV KEEPLDPEEA EGPLSLVTTA300  
 NHSPDFDHDR DYEDEPVNED ME 322

## (2) INFORMATION ON SEQ ID NO. 443:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

FGTRAPASHD DPPACEVYRT QSCPSAPESG IKCHPLQVRI GGFSTELTSY SNDPNRPPDS 60  
 RHPRPLCHHN HQHAHGTHP QAVLRQIQRA HFVSRYCAEP RIL 103

## (2) INFORMATION ON SEQ ID NO. 444:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

SLSWSKSGLW LAVVTKDRGP SASSGSRGSS LTCTGCTACI GDLPGLLSLS LLLVCSIAPF 60  
 SSSRIALAKL PRVGFPMEAV VYRGILFSAI EACKAALRGV Q 101

## (2) INFORMATION ON SEQ ID NO. 445:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 539 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

```
LDVQVKDDSR ALTGLALTLP LARLLTAPEL ILDQWFQLSS SGPNSRLYMK LVMRILYLD 60
SEICFPTVPG CPGAWDVDSE NPQRGSSVDA PPRPCHTTPD SQFGTEHVLR IHVLEAQDLI120
AKDRFLGGLV KGKSDPYVKL KLAGRSFRSH VVREDLNPRW NEVFEVIVTS VPGQELEVEV180
FDKDLDKDDF LGRCKVRLTT VLNSGFLDEW LTLEDVPSGR LHLRLERLTP RPTAAELEEV240
LQVNSLIQTQ KSAELAAALL SIYMERAE DL PLRKGTKHLS PYATLTVGDS SHKTKTISQT300
SAPVWDESAS FLIRKPHTES LELQVRGEGT VVLGSLSLPL SELLVADQLC LDRWFTLSSG360
QGQVLLRAQL GILVSQHSKV EAHSHSYSHS SSSLSEEP EL SGGPPHITSS APRLRQLTH420
VDSPLEAPAG PLGQVKLT LW YYSEERKLVS IVHGCRSLRQ NGRDPPDPYV SLLLLPDKNR480
GTKRRTSQKK RTLSPEFNER FEWELPLDEA QRRKLDVSVK SNSSFMSRER DCWGRCSWT 539
```

(2) INFORMATION ON SEQ ID NO. 446:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 99 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```
LLCLPAFVSL HHRLNVMSLK LGSKGRACAL QPFHLTG PYS GLCLTKEKNR MFPLLHGLYP60
SGPLGRGP EL AVSCFACTLF SLPPNSSGPS VSVPGWQH 99
```

(2) INFORMATION ON SEQ ID NO. 447:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

VWIKLFTCST SSNSAAVGRG VRSRRKCRP PDGTSSRVSH SSRKPLFKTV VRRTLHLPRK 60  
 SSLSKSLSKT STSSSWPGTD VTITSKTSFQ RGLRSSRTTW LRKLRPANFS LT 112

## (2) INFORMATION ON SEQ ID NO. 451:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

FFFFFFVETGF RHVDETGLEL LASSDLPPQL LKVLGLYRHE PLSLALKRFS QRPSVR 56

## (2) INFORMATION ON SEQ ID NO. 452:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

IRFGISCPGP GISLQEPLPL CWRHSFRIRR RREKRKCKGG RSFPGRITISV THMDPR 56

## (2) INFORMATION ON SEQ ID NO. 453:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 57 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

VTEMVRPGKD LPPLHFLFSL LLLILKLCLO QRGRGSCREI PGPGQEMPNI IYLTEGL 57

(2) INFORMATION ON SEQ ID NO. 454:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

ILAFWRAAPL WHHQTLLCFP STWNSSNIRG CEGLAILLSW VHVSDRNGAA WERSPSFTFS60  
LLPPPPYSKT VPPTEGQGLL 80

(2) INFORMATION ON SEQ ID NO. 455:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 182 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

ARLPLLAAED RGQPGSVKDP KMAGRKLALK TIDWVAF AEI IPQNQKAIAS SLKSWNETLT 60  
SRLAALPENP PAIDWAYYKA NVAKAGLVDD FEKKFNALKV PVPEDKYTAQ VDAEEKEDVK120  
SCAEWVSLSK ARIVEYEKEM EKMKNLIPFD QMTIEDLNEA FPETKLDKKK YPYWPHQPIE180  
NL 182

## (2) INFORMATION ON SEQ ID NO. 456:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

AQSIAGGFSG KAALEVRVS FQDFRELAMA FFWGMMISAK ATQSMVERAS FRPAILGSFT60  
 DPGCPRSSAA SNGSRA 76

## (2) INFORMATION ON SEQ ID NO. 457:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

CPECVIQGPE LPPGLNFINS QLVGEANRDT FSCLIWFLGK LHSSPQWSSD QMELSSSSSP 60  
 SLSHILQSWP LRETPTQHKI SHLLFLRHPP GQYIYPLARE PSAH 104

## (2) INFORMATION ON SEQ ID NO. 458:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 223 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

RGAGGHQGES GRPEGWPPPF LHPRGRFQVP WLESVLIVVS NNIDEEALAR LAQEGSEVNV 60  
IGIGTSVVTG PQQPSLGGVY KLVAVGGQPR MKLTEDPEKQ TLPGSKAAFR LLGSDGSPLM120  
DMLQLAEEPV PQAGQELRVW PPGAQEPCTV RPAQVEPLL R LCLQQGQLCE PLPSLAESRA180  
LAQLSLSRSL PEHRRLRSPA QYQVLSERL QALVNSLCAG QSP 223

(2) INFORMATION ON SEQ ID NO. 459:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 157 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

VIRVSSQPR SESQGDCAH RLFTRACSLS DSTTWYCAGL RSRLCSGLSR LRDSWAKALD 60  
SARDGSGSHS CPCWRQSRSS GSTWAGLTVQ GSWAPGGHTL SSCPACGTGS SANCSMSMSG120  
DPSEPRSRKA ALLPGNVCFS GSSVSFIRGW PPTATSL 157

(2) INFORMATION ON SEQ ID NO. 460:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 93 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

PPLFPHLLFL WGVSDSCCF QSAPLRVSGG LPRTQTVHQG LQPLGQHHLV LCRAPQPPVL60  
RAESAQQQLG QGSRLCQWE RLTQLSLLEA EPQ 93

## (2) INFORMATION ON SEQ ID NO. 461:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 328 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

```

FSLILCKHSI GDRKNYASAK LSELLPEEVE AEVKAAAEIS MGTEVSEEDI CNILHLCTQV 60
IEISEYRTQL YEYLQNRMMMA IAPNVTVMVG ELVGARLIAH AGSLLNLAKH AASTVQILGA120
EKALFRALKS RRDTPKYGLI YHASLVGQTS PKHKGKISRM LAAKTVLAIR YDAFGEDSSS180
AMGVENRAKL EARLRTLEDR GIRKISGTGK ALAKTEKYEYH KSEVKTYDPS GDSTLPTCSK240
KRKIEQVDKE DEITEKKAKK AKIKVKVEEE EEEKVAEEEE TSVKKKKKRG KKKHIKEEPL300
SEEEPCSTTA IASPEKKKKK KKKRENEE                                     328

```

## (2) INFORMATION ON SEQ ID NO. 462:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 124 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

```

YNRNSFLLIL VLSLFFLELL FLWTSNCCAG TWFFLAKWFF LNVFLFTPFL LLLHRCFFFF 60
CHFFFTLFFN FNFNLGFFGF LFSNFILFIY LFYFAFFRTG WKCGVTRRIV SLHFTFVFIF120
FCFC                                                                 124

```

## (2) INFORMATION ON SEQ ID NO. 463:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
SSFSLFFFFFF FFFSGLAIAV LVHGSSSESG SSLMCFFLPL FFFFFFFDVSS SSATFSSSSS 60
STLTLILAFL AFFSVISSSL STCSILRFLE QVGSVESPEG S                               101
```

(2) INFORMATION ON SEQ ID NO. 464:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 427 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```
GGSSRRHGGG YAAVALLVLL LLGPGGWCLA EPPRDSLREE LVITPLPSGD VAATFQFRTR 60
WDSELQREGV SHYRLFPAKAL GQLISKYSLR ELHLSFTQGF WRTRYWGPPF LQAPSGAELW120
VWFQDVTVDV DKSWEKLSNV LSGIFCASLN FIDSTNTVTP TASFKPLGLA NDTDHYFLRY180
AVLPREVVCT ENLTPWKKLL PCSSKAGLSV LLKADRLFHT SYHSQAVHIR PVCARNARCTS240
ISWELRQTLS VVFDAFITGQ GKWDWSLFRM FSRTLTEPCP LASESRVYVD ITTYNQDNET300
LEVHPPPTTT YQDVILGTRK TYAIYDLLDT AMINNSRNLN IQLKWKRPPE NEAPPVPFLH360
AQRVSGYGL QKGELSTLLY NTHPYRAFPV LLLDTVPWYL RLLHPLPACP GPAATPPPGD420
ADSAAGQ                                         427
```

(2) INFORMATION ON SEQ ID NO. 465:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

SPSILYGSCT CHSHKAFGGP DTGGHPSCR P HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60  
SSAPLSTST PPTQSLPLPP SNPWVWPM TL TTF CAMLCC RGRWSAPKTS PPGRSSCPVV120  
PRQASLCC 128

(2) INFORMATION ON SEQ ID NO. 466:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 124 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

PQAWRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60  
ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLLEDP ILGATLPAGP IRCRAVGLVP120  
RHCH 124

(2) INFORMATION ON SEQ ID NO. 467:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 106 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

FLHKTHNRAV EEAKEPFLCL CSRTERGELA SVSLLVLPGL YQALRRGMET PHSGAWLGEG 60  
EAAGVLWASR GYNLSSSLGNV CPFVGSSEPTR RGTQLYTG TI CVWSVL 106

## (2) INFORMATION ON SEQ ID NO. 468:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
ISTKQTTTHRL SQCKVESPDV SDYCLQMDTR SPSSDYTLTLE KPKEPLPPPL PQARQSGAF 60
PYPASRPGTV REEPAGSRWP EGLSQSYRG IKRAPLLPPQ PCCESCAGIN LRNSPEAETG120
LMPWERSECE PMAPSL LGTN LPKYVKAEGD RDLAEGRKSF SSRN 164
```

## (2) INFORMATION ON SEQ ID NO. 469:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```
EIRGRPPLEFM PPLSCVDEFL QNRPHDTCPS VKLSPPTCRT TAYKWTHVPQ RAQIIPSRSP 60
KNPCRLPFPK PGPRVGRFHT PPQGLVQSGK NQQAHAQRA SLSPTEA 108
```

## (2) INFORMATION ON SEQ ID NO. 470:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 317 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```
NMVDDYYEVLG VQRHASPEDI KKAYRKLALK WHPDKNPENK EEAERKFKQV AEAYEVLSDA 60
KKRDIYDKYG KEGLNGGGGG GSHFDSPF EF GFTFRNPDDV FREFFGGRDP FSFDFFEDPF120
EDFFGNRRGP RGSRSRGTS FFSAFSGFPS FGSGFSSFD T GFTSFGSLGH GGLTSFSSTS180
EGGSGMGNFK SISTSTKMVN GRKITTKRIV ENGQERVEVE EDGQLKSLTI NGVADDDALA240
EERMRRGQNA LPAQPAGLRP PKPPRPASLL RHAPHCLSEE EGEQDRPGAP GPWDPLGVRS300
RIERRWQEEE AEAERGV                                     317
```

(2) INFORMATION ON SEQ ID NO. 471:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 123 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

```
SMPLVQLPSS FKLLSLLLLL PLATFFQSCC GRRGGPRARV PQVGPARPPP QRDSEARVSA 60
ARQAGAASAG GGRQAGLAGR SGLSACAPQR GHRRRPHLL LRTLGHLLQ LLLFLDRSRQ120
FSL                                     123
```

(2) INFORMATION ON SEQ ID NO. 472:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 105 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

KIRSNQCLWS NFLPPSNSSL CFCFFLLPES FNPAADAEGV PGPGCPERSVL LALLLRETVR 60  
RVSQQRGRPG RLRRAEAGRL GWQGVLASPH ALLSEGIVVG HTIYC 105

(2) INFORMATION ON SEQ ID NO. 473:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 159 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

IVSERSLRSL WTAHWALPEM DSRIPYDDYP VVFLPAYENP PAWIPPHERV HHPDYNNELT 60  
QFLPRITLTK KPPGAQLGFN IRGGKASQLG IFISKVIPDS DAHRAGLQEG DQVLAVNDVD120  
FQDIEHSKAV EILKTAREIS MRVRFFPYNV HRQKERTVH 159

(2) INFORMATION ON SEQ ID NO. 474:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

PPTGRPPPPFF FFFFFFFFSIV FYFLGERLGG GRGENSVSLE SQKCMNLLVQ QGWDKMAREV60  
RWKIPKILFA TDFYN 75

## (2) INFORMATION ON SEQ ID NO. 475:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

LGGLSSSDVK SQLSSRLLQ CDGSGQKLGQ LIVVVRVVYP LMRRNPCWRI LIGRQENHRV60  
 VIIRNPAVHL GQGPVGSFQR PQTPLTDNSV WEPEADA 97

## (2) INFORMATION ON SEQ ID NO. 476:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 274 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

GHLWRPAGGR LPRHHDQVCR AAEPHRGGGL CGHQRRLP HR PRVQEGWGLC PHESLHQVPA 60  
 DRPWHEPGAG CAADCEDPHR RPGACEPGAP PAARAAGLGR GTRHGNGDIL SFEDANRAMQ120  
 TGVGTGIMIAR GALLKPWLFT EIKEQRHWDI SSSERLDILR DFTNYGLEHW GSDTQGV EKT180  
 RRFLLEWLSF LCRYDPVGLL ERLPQRINER PPYYLGRDYL ETLMASQKAA DWIRISEMLL240  
 GPVPPTSPSC RSTRPRTTSS LRLSQGHPGA RRVQ 274

## (2) INFORMATION ON SEQ ID NO. 477:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 256 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```
AGPAPVQPGP HTRCRCPRGH GSRGRSQAGK LWCPAGPRRP GTSTPPSSPV RTCGPLTDED 60
VVRLRPCEKK RLDIRGKLYL APLTTCGNLP FRRICKRFGA DVTCGEMAVC TNLLQGQMSE120
WALLKRHOCE DIFGVQLEGA FEDTMTKCAE LLSRTVEVDF VDINVGCPID LVYKKGGGCA180
LMNRSTKFQQ IVRGMNQVLD VPLTVKIRTG VQERVNLAHR LLPELRDWGV ALVTEMGTS240
HLRMPTAPCR LVSPGS                                     256
```

(2) INFORMATION ON SEQ ID NO. 478:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 165 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```
NLLYSPRPRV PLGKPEATCT RWPCASARRR GGGHWPKEHL ADADPVGCLL AGHQRLQVVA 60
AQVVGRLVD PLWEPLQQPH GIVPAQEGQP LEQKAPGLLH ALRVRAVLQ AVVGEVPQDV120
QALGRDVPV PLLLDLREEP RLEQGATGNH DPGDTSLHGA VGILK                               165
```

(2) INFORMATION ON SEQ ID NO. 479:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 262 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

GSPMSPARAM QTLFVPEHGD HGAGVCSDDH HRGGHVPAEP LQAVCTVLHQ PAQPGAEERR 60  
 CPVLRMPVA SETQCQATES QSRSLTPRLG PPTAWPCALR PAERFPPLPA QCLLVQLQT120  
 LFVPEHGDHG AGVCSDDHHR GGHVPAEPLQ AVCTVLHQPA QPGAEERRCP VLRMPVALG180  
 EHSVRQRNPR AAGLRPASAH RPPGRAALRP AGALPPLPAH LSVPAARDRP AAHHLAVRRG240  
 GAPTLPGPLD LQSGPRGGV GN 262

(2) INFORMATION ON SEQ ID NO. 480:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 270 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

AAQCLLVQC KRSLFQSMET TELEFVQIII IVVVTCLLSH YKLSARSFIS RHSQGRRED 60  
 ALSSEGCLWP RRHSVRQRNP RAAVLRPASA HRPPGRAPFA QRSVFHRCQP NVSCTCNCKR120  
 SLFQSMETITE LEFVQIIIIIV VVTCLLSHYK LSARSFISRH SQGRREDAL SSEGCLWPSE180  
 STVSGNGIPE PQVYAPPRPT DRLAVPPFAQ RERFHRFQPT YPYLQHEIDL PPTISLSDGE240  
 EPPPYQGPWT FKVRDPEEEL EIERGLGAET 270

(2) INFORMATION ON SEQ ID NO. 481:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 124 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

ATTSC LHGPS SAGTARGGGE KMPCPKDAC GPRRAQCQAT ESQSRSTPR LGPPTAWPCR 60  
 PSPSGSASTA SSPPIRTCT RSTCRPPSRC QTGRSPHPTR APGPSRFGTP RRSWKLNWDW120  
 VRRP 124

## (2) INFORMATION ON SEQ ID NO. 482:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

RVLVSPLSLS MWRWKVEKDT VSILKLLRFS ERGRHLNRQV GFSVLSALGI WREMGLLSLC60  
 TQEGHALKT VFDQRRLYST GGIQMSLRGR EETWQADYI 99

## (2) INFORMATION ON SEQ ID NO. 483:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

VLEEEKKHGK QITSEPFELC FSFFPCLFSK IYLNLETQDI FLGNLLPMSE VASAASRQIP 60  
 GNPEPQNVIP PGSAPDPVL SAGFTYQSHS SFSINTPKSS PNHH 104

## (2) INFORMATION ON SEQ ID NO. 484:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

KLDSTQCRPS LHTNMYVLLS ECHLLCTQCH DSKIKISVSN QNINQARNSW AQRGVRGLSY 60  
TAVKQPTCSA HSQAESDWSC RQRGGGRVLC CPLLCMVSWV FQGGQLLSPN KTVNSLRGTGP120  
LPH 123

(2) INFORMATION ON SEQ ID NO. 485:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 303 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

LGRKPSWVGG AGLEPSQSGS LSHHPAPQSD SAPTSPPPIG EPGPQREVDK WGGSLGRPES 60  
SGHPGRTPAT CCHCAAVMAR SGSATPEARA PGAPERSPPQ RLVQDVSGPL RELRPRLCHL120  
RKGPQGYGFN LHSDKSRPGQ YIRSVDPGSP AARSGLRAQD RLIEVNGQNV EGLRHAEVVA180  
SIKAREDEAR LLVVDPETDE HFKRLRVTP T EEHVEGPLES PVTNGTSPAQ LNGGSACSSR240  
SDLPGSDKDT EDGSAWKQDP FQESGLHLSP TAAEAKEKAR AMRVNKRAPO MDWNRKREIF300  
SNF 303

(2) INFORMATION ON SEQ ID NO. 486:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 149 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

APRRPRPRRR LEPCESTSAR HRWTGTGSVK SSATSEPLPA CLGTLGPLPH GPWASACPEL 60  
PQPQWTGGWS CHCPEISPSP GEPPSCPCPP GTGGLWQQR GRETQRCERE SETETERERE120  
RHRERQRESE RARGSRGARA FAALPGPAD 149

## (2) INFORMATION ON SEQ ID NO. 487:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 217 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

FLNGNRTTLQ STEAGGARGR LRPKVRAGGV PGSRDRQEGA QKLLKISRFL FQSICGARLL 60
TRMARAFSLA SAAVGLRWRP LSWKGSCFQA LPSSVSLSEP GRSLRDEHAE PPLSWAGLVP120
LVTGDGRGPS TCSSVGVTRS RLKCSSVSGS TTSSRASSSR ALMLATTS AW RSPSTFCPFT180
SMSRSWARRP ERAAGEPGST ERMYPWGRDL SLCRLNP 217

```

## (2) INFORMATION ON SEQ ID NO. 488:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 298 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

EIRAVGGGVC VDGMGTPGEG LGRCSHALIR GVPESLASGE GAGAGLPALD LAKAQREHGV 60
LGGKLRQRLG LQLELPPEE SLPLGPLLGD TAVIQGDTAL ITRPWSPARR PEVDGVRKAL120
QDLGLRIVEI GDENATLDGT DVLFTGREFF VGLSKWTNHR GAEIVADTFR DFAVSTVPVS180
GPSHLRGLCG MGGPRTVVAG SSDAAQKAVR AMAVLTDHPY ASLTLPDDAA ADCFLRPLGL240
PGVPPFLLHR GGGDLPNSQE ALQKLSDVTL VPVSCSELEK AGAGLSSLCL VLSTRPHS 298

```



## (2) INFORMATION ON SEQ ID NO. 489:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 175 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

AGHRYQGDIR ELLQCLLAVG QIPTSTVQEE RGHTRQPRTK KETVSSCVIW EGQGGIWVIC 60  
 QHCHCPDSSL GSVAAACHNS ARSPHAAETA QVGGTRDWHS GDGEVPERVR HDLSSSVIGP120  
 FGEAYEKLPA GEENVSAIQ RVLVSFHN S EPQVLQGFAD SIDLWPTSGA PGPRD 175

## (2) INFORMATION ON SEQ ID NO. 490:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

LGPCPLGSRP CRQAAVPAAM TPQVAVLAAV APVVASVYLP APRAPFELWP DPEREGQPPH 60  
 LPPTPGSLGL PGSGHGSSGP APPPASPSHP HRLPLQPLGF LSFLVSSPVS SGHPHSCRAV120  
 ISAGAPPPED RVGGEGSPRL QASGTGSSGF 150

## (2) INFORMATION ON SEQ ID NO. 491:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

FVKRTKQPRQ TLDAPCSALR LWGRCLLGEA VAQGVHCEAG PVDSAGGIHL ASGCLVSVYS60  
DIAFCCHLSC GQRGVSWHEN IFFFKCGSF 89

(2) INFORMATION ON SEQ ID NO. 492:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 63 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

LTHLLFEKCL LPSLGLITKF DHDHIVVSQS ALEIVSGLHE VAMGVWSTLK LYQSCTYFQT60  
FLK 63

(2) INFORMATION ON SEQ ID NO. 493:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 73 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

DGSRMLCHYI QKQDNKLNG CPLQSQQVQP HSARPELQPL PKGIFPTAST PSKEHQGFVS60  
VVLFFLQTID IYS 73

## (2) INFORMATION ON SEQ ID NO. 494:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 318 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

```
KCATFWSFPR RQGGLGIAIS EEDTLSGVII KSLTEHGVA T DGR LKVG DQ ILAVDDEIVV 60
GYPIEKFISL LKTAKMTVKL TIHAENPDSQ AVPSAAGAAS GEKKNSSQSL MVPQSGSPEP120
ESIRNTSRSS TPAIFASDPA TCPIIPGCET TIEISKGR TG LGLSIVGGSD TLLGAI IHE180
VYEEGAACKD GRLWAGDQIL EVNGIDL RKA THDEAINVLR QTPQVRVRLTL YRDEAPYKEE240
EVCDTLTIEL QKKPGKGLGL SIVGKRNDTG VEVSDIVKGG IADADGR LMQ GDQILMVNGE300
DVRNATQEAV AVWIKVFP                                     318
```

## (2) INFORMATION ON SEQ ID NO. 495:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```
SAFAEMGSDH TQSSASKISQ DVDKEDEFGY SWKNIRERYG TLTGELHMIE LEKGHSG LGL 60
SLAGNKDRSR MSVFIVGIDP NGAAGKDGRL QIADELLEIN GQILYGRSHQ NASSIIKCAP120
SKVKIIFIRN KDAVNQMAVC PGNAVEPLPS NSEN LQNKET EPTVTTSDAA VDLSSFKNVQ180
HSGASQGGRG VWVLLSAKKI HSVESS                                     206
```

## (2) INFORMATION ON SEQ ID NO. 496:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TSWIIMAPSS VSEPPTMLRP SPVRPLEISM VVSQPGIMGQ VAGSEAKIAG VDDLLVFRMD 60  
SGSGEPDCGT IRDWELFFFS PLAAPAAEGT AWESGFSAWM VSFTVIFAVF RRLINFSIG 119

## (2) INFORMATION ON SEQ ID NO. 497:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SAPSLTKCRS THVYPLSLIM FMSGGSSRST LRRMVPTPST TSLSPRSSSS TSKLLTQSGP60  
SLPQPPASRP F 71

## (2) INFORMATION ON SEQ ID NO. 498:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 139 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

SRSPACGASE HGDGAMSLIC SISNEVPEHP CVSPVSNHVV ERRLLIEKYIA ENGTDPINNQ 60  
 PLSEEQILIDI KVAHPIRPKP PSATSIPAIL KALQDEWDAV MLHSFTLRQS CRQPAKSCHT120  
 LCTSTMPPAV SLPVSPRKL 139

(2) INFORMATION ON SEQ ID NO. 499:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

TTGRERGCRC CAGLFYCFLE LMKLDHCLQN PAQALLPIPF TVSLVRRAMT RQAASCWYRA60

CDSSWRVVCS SGAE

74

(2) INFORMATION ON SEQ ID NO. 500:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

FSFFNETRSL LTKPCTSPPA HPLHSSLGSA SPVSQELQQN GCGTATTTSI ERQEGRGAVG60  
 LVQGFIVFF F

71

## (2) INFORMATION ON SEQ ID NO. 501:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 284 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```

EARGLATRTR SGAAAHAGDR FTDADDVAIL TYVKENARSP SSVTGNALWK AMEKSSLTQH 60
SWQSLKDRYL KHLRGQEHKY LLGDAPVSPS SQKLKRKAE DPEAADSGEP QNKRTPOLPE120
EEYVKEEIQE NEEAVKKMLV EATREFEEVV VDESPPDFEI HITMCDDPP TPEEDSETQP180
DEEEEEEEK VSQPEVGAAI KIIRQLMEKF NLDLSTVTQA FLKNSGELEA TSAFLASGQR240
ADGYPIWSRQ DDIDLQKDE DTREALVKKE GAQNVARRIE FRKK 284

```

## (2) INFORMATION ON SEQ ID NO. 502:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

```

ETFSSSSSSS SSGCVSESSS GVGGSSSHIV ICISKSGGLS STTSSNSRV ASTSIFLTAS 60
SFSWISSFTY SSSGKSGVLL FCGSPLSAAS GSSSAFRLSF WEEGLTGASP SRYLCSWPRR120
CLR 123

```

## (2) INFORMATION ON SEQ ID NO. 503:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 175 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

VFLRCGWIII THSYMYFKIR RALIHNNLLK LPGGFHKHLF DCFILLDFF LHILFFRQIW 60  
SSLILWFFPAI RGLRVLLRLP LELLGGGAHR RVPQQVLMML APQVLEVAVL QGLPRVLRER120  
ALLHRFPQGV TGDGAGRAGI FLHVGKDGIV VRIREAIARV RCRSAPRARR QAPGF 175

(2) INFORMATION ON SEQ ID NO. 504:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 78 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

CPPEKSLQMF QPLSSPDSHR KGTGFGLGIV FSLTFFKRRM WPLAFGSGMG LGMAYSNCQH60  
DFQAPYLLHG KYVKEQEQ 78

(2) INFORMATION ON SEQ ID NO. 505:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 95 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

SKTSTLPVAI WTRQRLEHLQ GFLGWTSITR ILSSRPHPD TGPTSCRAFT QTCSPPPAPPA60  
 FLSAGPRAPT PESLARAGNK SQVRKAGADA PDIAR 95

## (2) INFORMATION ON SEQ ID NO. 506:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 156 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

AIPNPMPEPK ANGHILLKK VSEKTIPNPK PVPFLWLSGL DRGWNICRDF SGGHQLPGFY 60  
 LHDRIHQTPV PLPAELRLH VPHRLQLSS RPAPALRPLK VSRELETSFR SGRQAQTLQI120  
 SRDDPLPSL PVFSVGRQGD AVVWRLEVTL TLGCAY 156

## (2) INFORMATION ON SEQ ID NO. 507:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 169 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

AASGMLGSWP ARTFHGACV SRRPSAPWKH TASGKDSPDL RFSEHGVSQE FWAGGLVAVL 60  
 EMTSPSPWG TQEGPAGMCS LWVVGWCPGR GAGVRDLVLV HAGVWCKHVC AVQRDACGES120  
 RTPAPPRKGG AVTSVLCFL IKTFPLFSYK FASCKQVHKD BPLVKSGFE 169



## (2) INFORMATION ON SEQ ID NO. 508:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 155 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TQNTGNRSFAF PGWRWCAALS TRVSLYSTYM FTPHTCVDEH QITHPSSTTG TPADYPQAAH 60  
 SGRALLGAPR GGARGHLQHC HQAASPEFLG NTVLGKPKVR AVLPRGRVLP GCGGPAADTG120  
 PRVEGPGRPA SKHARRSLGE PGSVASSLLS LRSPI 155

## (2) INFORMATION ON SEQ ID NO. 509:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 148 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

ENRGNVLIKN KHKTLVTAPP FLGGAGVRLS PHASLCTAHT CLHHTPAWTS TRSRTPAPRQ 60  
 GHQPTTHRLH IPAGPSWVPH GEGLGVISST ATRPPAQNSW ETPCSENRRS GLSFPEAVCF120  
 QGAEGRRLTQ APGWKVLQAGQ LPSMPDAA 148

## (2) INFORMATION ON SEQ ID NO. 510:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

NAYISGYERD FMTIQSNITL ADRETEVFHD LPSLPASLRQ NWIPTLVFFL PFTSFSLLYN60  
VLRDQNSHQN RLFLR 75

(2) INFORMATION ON SEQ ID NO. 511:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

FRDTEGLLAL MTFWMGLQLM TILILEERTL LIFSPIALLR RSTSYSESLH IPLVFLQAPE60  
PLVQMLY 67

(2) INFORMATION ON SEQ ID NO. 512:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

IEFFFFFFFFFF PLRHLFNNCR NPKELASNLE VVSEAAGWLD WAQPLSCLNR PRNGIMMTMR 60  
TSILSSSHCV YYVFSFNKAF VPMALGLGGR LKECVVILSK M 101

## (2) INFORMATION ON SEQ ID NO. 513:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

FGTMGGISDP DTLHIWKTNS LPLRFVWNIL KNPQFVFDID KTDHIDACLS VIAQAFIDAC 60  
 SISDLQLGKD SPTNKLLYAK EIPEYRKIVQ RYYKQIQDMT PLSEQEMNAH LAESRKYQN120  
 EFNTNVMAAE IYKYAKRYRP QIMAALANP TARRTQLQHK FEQVVALMED NIYECYSEA 179

## (2) INFORMATION ON SEQ ID NO. 514:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

DRGAPALTPG HLHPLPPVPR SVSGMEAREL VRLPHLPSTA CTVPTHLLHN VQLVLLPRAP 60  
 CIQAAKHKLK ERRPPARRLQ PRNSTSSTLV QGALLELTFD WFLQLPKCY LHFPLTRGS120  
 WPQTVSSSVR FLLGLRLLE WAVPAPWGAL WASPGAGRVE GRDGGHRSWE PRLQEKERG 179

## (2) INFORMATION ON SEQ ID NO. 515:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 200 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```
SGDRWEGMEV PRGQGGGAPV SESSPSSCPR PSRLCSVFPS LSHRHGVEDQ VEAQWASISP 60
SSSLTNPCV SGLTVALVDV VLHQSHLLK LVLQLCPPGR GVGLQRGHD L RPIPLGVLIN120
LCHGHIGVEL ILVFPRLGQ MGIHLLLAER RHVLDLLVVA LHDLPVLRNL LGVEELVGWR180
ILAQLQVRDG AGVDEGLRDD                                     200
```

(2) INFORMATION ON SEQ ID NO. 516:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

```
TSMEALLFRL FKLPAATLRC IGLRRPLVTH TLARKCEHKA SRLCHGGCCC TLEPCVGRHR 60
DWDLERGKSS AKTGGEHGR RTAAARGGSE RPYLGHRRRD PDAGGLRGQD GEALQHRGWH120
IPGSETLPGR GGHVPWPRPG RRHPHMC GF WDSQSLA                               157
```

(2) INFORMATION ON SEQ ID NO. 517:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 401 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

RTRCAGSVNT KPPGFVMAAA AARWNHVVWG TETGILKGVN LQRKQANFT AGGQPRREEA 60  
 VSALCWGTGG ETQMLVGCAD RTVKHFSTED GIFQGQRHCP GGEGMFRGLA QADGTLITCV120  
 DSGILRVVHD KDKDTSSDPL LELRVGPGVC RMRQDPAHPH VVATGGKENA LKIWDLQGSE180  
 EPVFRANKVR NDWLDLRVPI WDQDIQFLPG SQKLVTCTGY HQVRVYDPAS PQRREPVELETT240  
 YGEYPLTAMT LTPGGNSVIV GNTHGQLAEI DLQGRLLGC LKGLAGSVRG LQCHPSKPLL300  
 ASCGLDRVLR IHRIQNPRGL EHKVYLKSQL NCLLLSGRDN WEDEPQEPQE PNKVPLEDTE360  
 TDELWASLEA AAKRKLSGLE QPQALQTRR RKKKRPGSTS P 401

## (2) INFORMATION ON SEQ ID NO. 518:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 222 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

SWEKLYVLVP DGNPQVQPI PHVLGPEHRF LRALQVPYLO SILFPTCGNH MGVCWVLAHP 60  
 THPRAHSQFQ EWVRGCVLVL VMPDSENPRI HTCDEGAVGL GEATEHALPA RAVSLTLEYA120  
 ILGAEVLRHP VRAAHQHLGL AAGAPTQGAH CLLAPRLSSG REVRRLFSLK IYPFQDPSLG180  
 ADPHMVPACS SSRHDKAWRL CVHTSGAACA SPAGVEVRCT AV 222

## (2) INFORMATION ON SEQ ID NO. 519:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

DPRPVSLTL ALLPRCHFSL SSVKYRLHIL SLNASTICVT PKDFWDFDET CEGEDTEKPV60  
 ICKHLLLFPH HLWDISAVVS KWQIIN 86

## (2) INFORMATION ON SEQ ID NO. 520:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 77 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ISSVNYHMTI QAQYKLGHCI LCGWISVAVF LTSPKKTSCR AELLVQAPDN DAPDFAFWGL80  
SLLLSHFLKL FAWPWHH 77

## (2) INFORMATION ON SEQ ID NO. 521:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 71 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
    (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CGNKSCKLQI TGFSVSSPSQ VSSKSQKSLG VTQIVLALSD KMCSLYLTEE ERKWHLGSSA60  
RVSKETGLGS Q 71

## (2) INFORMATION ON SEQ ID NO. 528:

- (i) SEQUENCE CHARACTERISTIC:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: Protein  
    (C) STRAND: individual  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

LTYLFFFFFF FFLGRSLGFI PSVGTLPSE APPSHGVGDS GPGNPSEHR GGWWSMYTA 50  
 LPHLFHGVPC QGQALICGEG SKQRRRPFRG GERAAPRTF SPAHDIPEKE TKIKPRGLST120

(2) INFORMATION ON SEQ ID NO. 529:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 90 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

PLLKGKKLSA ALTNLSFFFF FFFFGKKPW LYSLCGDTVP FRGPSQPWGG GQWWAWESQR60  
 ASWRVRLHV FCSSPSFPWG PLPGSSTNMW 90

(2) INFORMATION ON SEQ ID NO. 530:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 96 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

NKAPGPFYVG APLKYGMVVG REAVAQQSLs PDYQLWGGFQ GARSRLGSSS HRHVGGGRKY60  
 LQGGTVSEEQ DGRGFSACYG ILFKEMGVKP GTVAHA 96

## (2) INFORMATION ON SEQ ID NO. 531:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 497 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

```
TPALVQRFRE GSGAPEQAE CVELLLALGE PAEELCEEFL AHARGRLEKE LRNLEAELGP 60
SPPAPDVLEF TDHGGSGFVG GLCQVAAAYQ ELFAAQGPAG AEKLAAAFARQ LGSRYFALVE120
RRLAQEQGGG DNSLLVRALD REHRLRAPG ALLAAAGLAD AATEIVERVA RERLGHHLQG180
LRAAFLGCLT DVRQALAAPR VAGKEGPGLA ELLANVASSI LSHIKASLAA VHLFTAKEVS240
FSNKPYFERGE FCSQGVREGL IVGFVHSMCQ TAQSFCDSPG EKGATPPAL LLLLSRLCLD300
YETATISYIL TLTDEQFLVQ DQFPVTPVST LCAEARETAR RLLTHYVKVQ GLVISQMLRK360
SVETRDWLST LEPRNVRAVM KRVVEDTTAI DVQVGLLYEE GVRKAQSSDS SKRTFSVYSS420
SRQQGRIAPS YTPSAPMDTN LLSNIQKLF S ERIDVFSPVE FNKVSVLGTI IKISLKTLAG480
SVCGLRTFLA LCGLQQG                                     497
```

## (2) INFORMATION ON SEQ ID NO. 532:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 153 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```
CGSGWSWPHW PATRPGQGPP SQPREVLPA P GGRLSGSPGR PPGDPAGGGP GARGPLVPRS 60
PWQRLRARQR PAGPREPASA GGSGPAPAPA VSCHHHHPAPA PAAAPPAQNS GCPAAGRPP120
ASRHLLGPGP QTAPGRPPPP GRGRPRSHCL HGR                                     153
```



## (2) INFORMATION ON SEQ ID NO. 533:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 221 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

YDQALHLHV V GQPPRRFP G LCTQRAHGRH WELILHQKLF ISESEDVGDG GRLVVQAEAG 60  
 EQQEQRWCG TPLLPRVAE ALSRLAHRVD EAHDEALTD T LTAELTPEVG LVGEGHLFGG120  
 EKVHCCQRGL NVAQDGAGHI GQQLGQARAL LPSHARCCQR LADVCQAAQE GRPETLQVVA180  
 QALAGHSFHD LRGSVCEPGS GQQGPGSPQA PVEAVQRPHQ Q 221

## (2) INFORMATION ON SEQ ID NO. 534:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

PSILIPMTPG GFFSVMVRK TGSTHRCSPA VYPLMRRI PC WRILIGRQET TG

52

## (2) INFORMATION ON SEQ ID NO. 535:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

AGKKPPASHH KESGCPSRPS PTGHSTPPSD PLTDNSVW

38

(2) INFORMATION ON SEQ ID NO. 536:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

SGCVPSHEED SMLEDHRQA RNHRLVIIRN PVVHLGQAPL ATPHRPQIRS LTIQS

55

(2) INFORMATION ON SEQ ID NO. 537:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

TRGPRKRLRR SGRRGGLRSW AGRERVLGTA LLGIYIVFPR IPGSGSEEAV TPYDRRLDLS 60  
 RNSPQAPAGQ STTSSSFCFC DGLSRGLKH TVSIDCIRFV QKPGQLTESH FLA 113

## (2) INFORMATION ON SEQ ID NO. 538:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

EPADSQARGR QCLLLHQQVQ GIWLKACIFP GHKLPEPLKW EARQFQTNLF STHHSTFKVC 60  
 LLLLPVHPPS LQFFHSLTSE RVPGGSMVNK LTCMLQKKKK K 101

## (2) INFORMATION ON SEQ ID NO. 539:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 198 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

YSLCSQCVSA PLTLNRHRSR RKRKWWIAQL EPGDCYDCLD LCGHRASQPP QTLSLECGGT 60  
 QCRFPGGLSP RPSPCPPSSS GLLFYRFFLV SFLGLLFTEG TAALGFLVTS ALLGSDGSAS120  
 ASWDLGGMGT MASTQMSWK APRKSPYRSR FSRKVGSGTS GGEKSRSEAM AQVACCLTSL180  
 LTHHSLEPTP APPRRSPR 198

## (2) INFORMATION ON SEQ ID NO. 540:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```
KKNSSALIFL EEAADEFGCQI SLRNGHFLRC FFLTESVDKL IKRLSHFKIT PKSSSTVFFF 60
FSFCFKITNQ VRSPTSSSMN SFVTELLSVC SPHCALNTVS AAPVCPLFRK ESIFNTFTIC120
TPWNLHMLTS YYKPTHPLQLS SGTGHPL 147
```

(2) INFORMATION ON SEQ ID NO. 541:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 138 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```
KNDREFPWTSL PGLKGALIKL FTEHVAEKHI YGLMPLLLEA QSTPFQVTPS TMANIVKGLY 60
TLRPEWVQMA PTLFSKFIPN ILPPAVESEL SEYAAQDQKF QRELIQNGFT RGDQSRKRAG120
DELAYNSSSA CASSRGYR 138
```

(2) INFORMATION ON SEQ ID NO. 542:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 179 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

KACIPSDQSG FRWLQLYFLN LEQTSLRRW NLNFLNMLLK IRNFKENLYR MVLQGVTSFG 60  
 RELGMSWLII ARQHVQVPGG TDSECIYAF LPEKRTWWSG RDCIQSTVGA AHTQELCHKA120  
 VHGRCGWTG LVCNEKTKTA KAKNSAARDG GDFEMGQSFN EPIRFOZER ASQAVTISA 170

## (2) INFORMATION ON SEQ ID NO. 543:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 92 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

IQFLEAAFAV FLHCMRFGNE CRNLLWAFTF LCQFGFYCLN LMLTWRGDGG QCCCGASSES60  
 VCGELCCADV AVGGQVRGSA PSWKKSLRV YV 92

## (2) INFORMATION ON SEQ ID NO. 544:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 99 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

KPNWHRKVNA HSKFLHSFPN RIQCKKTAKA ASRNCIYWPL PEQQAAMPAP WPELDACCA60  
 DVLTLMRMLG YGSDSEIHL SYSSLERSSC VFNMKHFIW 99

## (2) INFORMATION ON SEQ ID NO. 545:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

QSQNTKVFVP IRIYTDPLTK VLLIMQFASS PSSWLGSSPI WHDHIKRTPS DMISSKKVPS60  
 LLPDHQRPHQ HNTTLRIQIH CWPHNSTVPH LLSRSA 96

## (2) INFORMATION ON SEQ ID NO. 546:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GRDAGQSEPW LSTSGCCAWG GCAPGARGCW GPGPPSLGVG RKPGRVVSAS SVPERWIAWS 60  
 PRPSEASATF RGAPKSILTA RLWASAWRPQ HRGSQNERPW SSSMKTSG 108

## (2) INFORMATION ON SEQ ID NO. 547:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

PGRRAKRAMA VYVGMLRLGR LCAGSSGVLG ARAALRSWQ EARLQGVRL SSREVDMMVS 60  
TPIGGLSYVQ GCTKKHLNSK TVGQCLETTA QRVPEREALV VLHEDVRLTF AQLKEEW 117

(2) INFORMATION ON SEQ ID NO. 548:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 117 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

PLLLELGKGQ PDVFEMDDQG LSFWDPLCCG LQALAHSLAV KMLFGAPLNV AEASDGRGDH 60  
AIHLSGTEEA DTLQPGFLPT PREGGPGPQH PRAPGAQPPQ AQHPOVDSHG SLCPASR 117

(2) INFORMATION ON SEQ ID NO. 549:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 68 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

RLSGPAANPR GAAGWRAAGA QELGMSYKPM RPWLPSSTPW SARHPLGPGA PRFPDREACA60  
CAVRGCSV 68

## (2) INFORMATION ON SEQ ID NO. 550:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GHCSPPARRTR TPQCQGTGVP RAPGGAWQTR GCCWAARGAW VCRTSPTPGR QRHASRPLLG60  
 GWLRGRSA 68

## (2) INFORMATION ON SEQ ID NO. 551:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

DTAAPHGARA RLPVREPGCP GPQGVPRPG GAAGQPGAHG FVGHPQLLGA SGTPAGRSSG60  
 VGCGAAQP 68

## (2) INFORMATION ON SEQ ID NO. 552:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

SPISITETQQ FSNLIHTIT CLLRMALYLF SL

32

(2) INFORMATION ON SEQ ID NO. 553:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 33 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

ITLQPISQNM FLLLNTQLF YLCVLFMPDH QYQ

33

(2) INFORMATION ON SEQ ID NO. 554:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 43 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

SFYFGWSHYN ENKYNAILNR QVMVCIKLLL NCCVSVIDIG DQA

43

## (2) INFORMATION ON SEQ ID NO. 555:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CFTHWNVFPR LWMTSFLMER VQEGWKTPGF KLSIPHMGFS IIFRPEAARP EVRLHLSALF60  
 VLLLATLGFL LGTMCGCGMC EQKGG 85

## (2) INFORMATION ON SEQ ID NO. 556:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

FNDGKTWQLK KTLVTNGGFL LFFPHPPFCS HMPQPHMVPS RNPKVARSSST KRADKCRRTS 60  
 GRAASGLKMI EKPMWGMLSL NPGVFHPSWT LSIRKEVIHN RGKTFQ 106

## (2) INFORMATION ON SEQ ID NO. 557:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

NINYIEIIFL FLLISPLGP HRLSPAQLAQ LAQLAHSPQV SRRHRALTMV GWHGVSNNAN 60  
SSHHPHPHSP SQRPLVVGPA VFQKGLTCTN LRQTYAPFSV SLASPSWED 109

(2) INFORMATION ON SEQ ID NO. 558:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

LGIFVAYRNQ LGVPSLMRCS WKAIYARGGF TFVAPPFIDP SAFKKLECEN

50

(2) INFORMATION ON SEQ ID NO. 559:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 44 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

FRLPFLTWHF CSLQEPAWCT FSYEMQLESH LCKRWFHFCR SSIH

44

## (2) INFORMATION ON SEQ ID NO. 560:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

RVNEWRSDKS ETTSCINGFP AASHKRRTYK LVPVSYKNAK LRMGV

45

## (2) INFORMATION ON SEQ ID NO. 561:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

MRSRLPCEGL VARHPRELRV PSVREWIDWP WVLT

34

## (2) INFORMATION ON SEQ ID NO. 562:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

VSTHGQSIQK RTEGTRSSRG CRATSPSHGN RLLIQESFPQ NPPRARFQGH PLGRQSRQQP60  
FTEAMSQ 67

(2) INFORMATION ON SEQ ID NO. 563:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

APMASQSRSA LRARVAHAGA VPPALHTAID SSFRNHFLKT HQGLGSKGTR 50

(2) INFORMATION ON SEQ ID NO. 564:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 54 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

YSIIFEQFFK CKSVSYSECV SEVIKDISQR YWPISLCNQR NSVSRLLLCV ICGS 54

## (2) INFORMATION ON SEQ ID NO. 565:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

CTMVNV DNTV SFLSSFLNVN LYLTQSVCLK LLRTFPNVTG PFPFVIRGIL FQDYCCV . 57

## (2) INFORMATION ON SEQ ID NO. 566:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

EKCQPHSLIL LWPENFILIK SHRSHTTIL KQNSSDYKKGK WASNVGKCP

49

## (2) INFORMATION ON SEQ ID NO. 567:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

GEGRVWNPEG SKSRHWPDHP APWAPSPRQE QLFSIPSQTS SIFITMTFRE VSQASSRCPT60  
IPSGGKRQEN SPRVPVLLS PSQFRLSRTS YLQP 94

(2) INFORMATION ON SEQ ID NO. 568:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

GLTLKKGTFP RGPEIQADPN LTPCSRTQAH RPLNSNPTSP PPPPTPDFLI SWNAFQDWKS60  
PQGSSEPILS PARISSMHPG HAFHISRNK 89

(2) INFORMATION ON SEQ ID NO. 569:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

DVLDSLNNWDG ESSMTGTRGE FSCLFPPEGI VGHLELAWET SLKVIVIKIE LVWEGMENS60  
SCLGLGAQGA GWSGQCLDLL PSGFHTRPS 89

## (2) INFORMATION ON SEQ ID NO. 570:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

KSIAHSVIGY FHDFKWFYEE TESSDDVEVL TLKKFKGDLA YRRQEYQVEF NIWCLKWALV60  
LSVMAYVNNS VPS 73

## (2) INFORMATION ON SEQ ID NO. 571:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

SADSQEIQRR PGLQTTTRVSG RIQHMVLEVG SCFISYGICK

40

## (2) INFORMATION ON SEQ ID NO. 572:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

NKSPLQAPYV EFYLILLSSV GQVSFEFLES QHFNIIATFC FFIKPLEIMK IAYYRVSYAF60

(2) INFORMATION ON SEQ ID NO. 573:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 318 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GNLSLES LCN LYNWRYKNLG NLPHVQLLPE FSTANAGLLY DFQLINVEDF QGVGESEPNP 60  
YFYQNLGEAE YVVALFM YMC LLGYPADKIS ILTTYNGQKH LIRDIINRRC GNNPLIGRPN120  
KVTIVDRFQG QQNDYILLSL VRTRAVGHLR DRRRLVVAMS RARLGLYIFA RVSLFQNCFE180  
LTPAFSQLTA RPLHLHIPT EPFPTRKNG ERPSHEVQII KNMPQMANFV YNMYMHLIQT240  
THHYHOTLLQ LPPAMVEEGE EVQNETELE TEEEA MTVQA DIIPSPTDTS CRQETPAFER300  
ESRPGGEGAI ALGGLGCF 318

(2) INFORMATION ON SEQ ID NO. 574:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

KTPKPPQRNC PFPTGAALTL KGWSFLTAAG VCWTGYDVSL NSHGLEFCFQ LCFLILNFLT60  
LFYHSRW 67

## (2) INFORMATION ON SEQ ID NO. 575:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 155 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

SLMIMMCSLY QMHVHVYK CHLGHIFYL YFMRWSLSIL SSSWERFCWN YMQMKGASCE 60  
LTESWSQFKT VLEEGYSGED IKSKSGSRHG HYQATDIPQM AHCPGSYQRK KNIVILLTLK120  
SINSCHLVWS SNQWIVSTSS IDDVANKMLL AIICC 155

## (2) INFORMATION ON SEQ ID NO. 576:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 57 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

DHLGFISTKM RTNHGVRKGS LEEHKNLKL GGYHYISYF HRSDLAKLCI LSLTTFI 57

## (2) INFORMATION ON SEQ ID NO. 577:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

CSF CCILCKKTAN RGRRTLQIKT ILVSFPQR

48

(2) INFORMATION ON SEQ ID NO. 578:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

LYFFKTLKEK CVLFAASFVR RLPTEEGLY KLRPSWFHFH KDENKSWC

48

(2) INFORMATION ON SEQ ID NO. 579:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

GSFPNTMICS HLCGNETKMV LICKVLFPLL AVFLQRMQQK EHIFLSKF

48

## (2) INFORMATION ON SEQ ID NO. 580:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

HCRIQLGLSP LVGREKTTQV MRNFYSFQEL EEQLLIKFAH LVTKYFYS

48

## (2) INFORMATION ON SEQ ID NO. 581:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 59 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

IMPRAPLYRI PLNCNYVLLK SQLVKEELMV SVFVGNTCNT AEFYKGFLW WAGKKPLKS 59

## (2) INFORMATION ON SEQ ID NO. 582:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

GTLRPRSSDV LPIYLCFTTC LLSLTPNIPT YFSNSACHKF AASP

44

(2) INFORMATION ON SEQ ID NO. 583:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 46 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

NVDSCQTHSL ALIPPLLSSS DIVNNDKQLL CTECFMCCS HFIHMY

46

(2) INFORMATION ON SEQ ID NO. 584:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 41 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

LYMCIKCEQH IKKHSVHSSC LSLTISLLE RGGIRARLC V

41

## (2) INFORMATION ON SEQ ID NO. 588:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

GKPLVLHATP LSRCPLPLHP TRSLILRPSL HLDPSFHYY LQRCYYAPV YRGCPMTVP 60  
 SQSNYSSGPK VWLSRAPLPR RGRPFQALPG WNWCRSLGC IVRPGVGVA LL 112

## (2) INFORMATION ON SEQ ID NO. 589:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

GRSREAPAGW PKSTKPPSAR ENPWFSMPHL SPGALCLFTP QEALSYVLLS IYRTPVSITI60  
 SRDVAIMRPS TGGARR 76

## (2) INFORMATION ON SEQ ID NO. 590:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AGLDQKEELR GVRQHQHQGV RYTRGSSDTS SSPEGLGMAC HAGAMERVKA KPWDPKSNLT60  
AKAPSSSGTP CRRAHNSYIS GDSDGNWGP I DGEKDVG 97

(2) INFORMATION ON SEQ ID NO. 591:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 63 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

NGARLTSQPQ LYQRNHFIQI SQHFQRNTNV YGRVNIRSEN PLEESVSMF IISAFRGLPV60  
WAK 63

(2) INFORMATION ON SEQ ID NO. 592:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

NGSFGTVGAV MSTWLHKNP YEFTVKFNY TCVTADFGGR QGLGLPFYLS

## (2) INFORMATION ON SEQ ID NO. 593:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

AYLFIFLKGK NTFTFSSSPE AQTLLYLTTT QLTPLCDHQC GVVRLKDDSG HMTSL

55

## (2) INFORMATION ON SEQ ID NO. 594:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

SGDVCTESHG GLSRVKEKEQ QELSLGRWRR GGIDQARPPW W

41

## (2) INFORMATION ON SEQ ID NO. 595:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

FKVGLWKGGDI VEGERAFLYT YKWYTPFIHG GQRSSDQVTY VQKVTVA

47

(2) INFORMATION ON SEQ ID NO. 596:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 44 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

SVLTTSQRLS SHFKSQIPTR AKVLLDLFHP FSTSLSTLA APSP

44

(2) INFORMATION ON SEQ ID NO. 597:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 1651 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

```

GAGCTGCCAA GCAGCCCACC TCCTGGGCTT CCCGAAGTGG CCCCAGATGC AACCTCCACT 60
GGCCTCCCTG ATACCCCCGC AGCTCCAGAA ACCAGCACCA ACTACCCAGT GGAGTGCACC 120
GAGGGGTCTG CAGGCCCCCA GTCTCTCCCC TTGCCTATTG TGGAGCCGGT CAAAAACCCC 180
TGCTCTGTCA AAGACCAGAC GCCACTCCAA CTTTCTGTAG AAGATACCAC CTCTCCAAAT 240
ACCAAGCCGT GCCCACCTAC TCCCACCACC CCAGAAACAT GGGGGGGGGG GGGGGGGGGG 300
GCGCCGTCAT CTACTCCTTG TTCAGCTCAC CTGACCCCTT CCTCCCTGTT CCCTTCCTCC 360
CTGGAATCAT CATCGGAACA GAAATTCTAT AACTTTGTGA TCCTCCACGC CAGGGCAGAC 420
GAACACATCG CCCTGCGGGT TCGGGAGAAG CTGGAGGCC CTGGCGTGCC CGACGGGGCC 480
ACCTTCTGCG AGGATTTCCT GGTGCCGGGG CGCGGGGAGC TGAGCTGCCT GCAGGACGCC 540
ATAGACCACT CAGCTTTCAT CATCCTACTT CTCACCTCCA ACTTCGACTG TCGCCTGAGC 600
CTGCAACAGG TGAACCAAGC CATGATGAGC AACCTCACGC GACAGGGGTC GCCAGACTGT 660
GTCATCCCTT TCCTGCCCCC GGAGAGCTCC CCGGCCCAGC TCAGCTCCGA CACGGCCAGC 720
CTGCTCTCCG GGCTGGTGCG GCTGGACGAA CACTCCCAGA TCTTCGCCAG GAAGGTGGCC 780
AACACCTTCA AGCCCCACAG GCTTCAGGCC CGAAAGGCCA TGTGGAGGAA GGAACAGGAC 840
ACCCGAGCCC TCGGGGAACA GAGCCAACAC CTGGACGGTG AGCGGATGCA GGCGGCGGCA 900
CTGAACGCAG CCTACTCAGC CTACCTCCAG AGTACTTGT CCTACCAGGC ACAGATGGAG 960
CAGCTCCAGG TGGCTTTTGG GAGCCACATG TCATTGGA CTGGGGCGCC CTATGGGGTC1020
AGAATGCCCT TTGGGGGCCA GGGGCCCCTG GGAGCCCCGC CACCCTTTCC CACTTGCCCG1080
GGGTGCCCCG AGCCGCCACC CCTGCACGCA TGGCAGGCTG GCACCCCCCC ACCGCCCTCC1140
CCACAGCCAG CAGCCTTTCC ACAGTCACTG CCCTTCCCGC AGTCCCCAGC CTTCCTACG1200
GCCTCACCCG CACCCCTCA GAGCCCAGGG CTGCAACCCC TCATTATCCA CCACGCACAG1260
ATGGTACAGC TGGGGCTGAA CAACCACATG TGAACCCAGA GAGGGTCCCA GGCGCCGAG1320
GACAAGACGC AGGAGGCAGA ATGACCGCGT GTCCTTGCC TACCACCTGG GGAACACCCC1380
TGGACCCAGG CATCGGCCAG GACCCCATAG AGCACCCCGG TCTGCCCTGT GCCCTGTGGA1440
CAGTGAAGA TGAGGTCATC TGCCACTTTC AGGACATTGT CCGGGAGCCC TTCATTTAGG1500
ACAAAACGGG CGCGATGATG CCTGGCTTT CAGGGTGGTC AGAACTGGAT ACGGTGTTTA1560
CAATTCCAAT CTCTCTATTT CTGGGTGAAG GGTCTTGGTG GTGGGGGTAT TGCTACGGTC1620
TTTTAATTAT AATAAATATT TATTGAATGC T

```

## (2) INFORMATION ON SEQ ID NO. 598:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AAACCCTCTT GGCTGTCTGC TGTCCAGGGA GTCGCCACTC CCTTCATTAT AGCCTTGCTC 60  
 AGAGTGCAGC GGCAGGCCCTG GGGATGGCCT CGGGAGAGGG ACCACAGAGC ACCAGCCTGC 120  
 ATGGAACCTC CTTCTCACT CAGCTTCCCA CGTTGCCAGC TGGGACAGGG GAGATGGAGT 180

AATTTTGCTG TGGAAAGACT TCACGTCTTG CCGAATGAAA GTCCCGCCTG TCTGTCACGC 240  
 TGATGCCCCT GCAGCTGTCT GAGCACCCTG AATGGAATGA GTCTATGCAC TCCCTCCGGA 300  
 TCAGTGTGGG GGGCCTTCCT GTGCTGGCGT CCATGACCAA GGCCGCGGAC CCCCCTTCC 360  
 GCCCCGCTG GAAGGTGATC CTGACGTTCT TTGTGGGTGC TGCCATCCTC TGGCTGCTCT 420  
 GCTCCCACCG CCGGCCCCC GGCAGGCCCC CCACCCACAA TGCACACAAC TGGAGGCTCG 480  
 GCCAGGCGCC CGCCAACCTG TACAATGACA CCTACCCCT GTCTCCCCCA CAAAGGACAC 540  
 CGGCTGGGAT TCGGTATCGA ATCGCAGTTA TCGCAGACCT GGACACAGAG CCAACCGCCC 600  
 AAGACGAAAA CACCTGGCGC AGCGACCTGA AAAAGGGCTA CCTGACCCTG TCAGACAGTG 660  
 GGGACAAGGT GGCCGTGGAA TGGGACAAAG ACCATGGGGT CCTGGAGTCC CACCTGGCGG 720  
 AGAAGGGGAG AGGCATGGAG CTATCCGACC TGATTGTTTT CAATGGGAAA CTCTACTCCG 780  
 TGGATGACCG GACGGGGGTC GTCTACCAGA TCGAAGGCAG CAAAGCCGTG CCCTGGGTGA 840  
 TTCTGTCCGA CGGCGACGGC ACCGTGGAGA AAGGCTTCAA GGCCGAATGG CTGGCAGTGA 900  
 AGGACGAGCG TCTGTACGTG GCGCGCCTGG GCAAGGAGTG GACGACCACT ACGGGTGATG 960  
 TGGTGAACGA GAACCCGGAG TGGGTGAAGG TGGTGGGCTA CAAGGGCAGC GTGGACCACG1020  
 AGAACTGGGT GTCCAACCTAC AACGCCCTGC GGGCTGCTGC CGGCATCCAG CCGCCAGCTA1080  
 ACCTCATCCA TGAGTCTGCC TGCTGGAGTG ACACGCTGCA GCGCTGGTTC TTCCTGCCGC1140  
 GCCGCGCCAG CCAGGAGCGC TACAGCGAGA AGGACGACGA GCGCAAGGGC GCCAACCTGC1200  
 TGCTGAGCGC CTCCCCTGAC TTCGGCGACA TCGCTGTGAG CCACGTCGGG GCGGTGGTCC1260  
 CCATCCACCG CTTCTCGTCC TTCAAGTTCA TCCCCAACAC CGACGACCAG ATCATTGTGG1320  
 CCTCAAATC CGAGGAGGAC AGCGGCAGAG TCGCCTCCTA CATCATGGCC TTCACGCTGG1380  
 ACGGGCGCTT CCTGTTGCCG GAGACCAAGA TCGGAAGCGT GAAATACGAA GGCATCGAGT1440  
 TCATTTAACT CAAAACGGAA AACTGAGCA AGGCCATCAG GACTCAGCTT TTATAAAAAC1500  
 AAGAGGAGTG CACTTTTGTG TTGTTTTGTT CTTTTTGGAA CTGTGCCTGG GTTGGAGGTC1560  
 TGGACAGGGA GCCAGTCCC GGGCCCCATA GTGGTGCGGG CACTGGACCC CCGGGCCCCA1620  
 CGGAGGCCGC GGTCTGAACT GCTTTCCATG CTGCCATCTG GTGGTGATTT CGGTCACTTC1680  
 AGGCATTGAC TCAAGGCCTG CCTAACTGGC TGGGTGCTTT CTTCCATCCG ACCTCGTTTC1740  
 TTTTCTTTCC TATGTTCTTT TGTTCACTGA ATATCCCTAG AGCTCCTACC ATATGTCAGG1800  
 CCCTATGCCC CACCTGTAGA ACGCAGTGAG CATGAGGTGG ACCTGTTTGC TGGGAACCCC1860  
 AGGTCAACCT CTTTTCTTCC CAACTTGGT GCCTTGAAG AATCAGGTCC AGCCCTGAAG1920  
 ATCCTTGGGG AAGAAAATGT TTATGTTGCA GGGTATTGCA TGGTCACGAG TGAGGGGAG1980  
 GCCCCTGGGG GACACATCTG CCCACAGCTG CACAGGCCAG GGGCACAGGC ACATCTGTTG2040  
 GTTCTCAGGC CTCAGATAAA ACCATCTCCG CATCATATGG CCAGTGACCG CTTTCTCCCT2100  
 TCAAGAAAAT TCTGTGGCTG TGCAGTACTT TGAAGTTTAA ATTATTAACC TGCTTTAATT2160  
 AAAGCAGTTT CTTTTCTTAT AAAGTGGAAAT CACCAAATCT TATCACACAG AGCACAGTCC2220  
 TGTAAGTACC CAGCCCGCTC CAGCAGTGCG GGAGATTGTA AGGAAGCGGT GCGGCTGGT2280  
 GAAGCAAGTC TCACATGTCG GCGTCTTGG CCAATGGATA CAAAGATAAA GAAAATGTTG2340  
 CCTTTTTCTA GGAACGTCA GAAATCCTCA TGCCTTCAA GACTTCTGTG AATGACTTGA2400  
 ATTTTTTATT CCCTGCCTAG GGTCTGTGAA CGAGGCCTGT CTCTTCCCTG GGGTTTCTTT2460  
 CCATGGCCTT TATTTCTCCT CTTCCAGTGG GAGTTTTGCA GGCTCTTCTC TGTGGAAAAC2520  
 TCACGAGCGT TGGCTGGGCC TCGGCTTCGC TGGAGTGTA TCCAGGGTGA AGGCAGAGTG2580  
 GGATTTGAGA CCCAGGTTAG GCACGACCCA GGCTGAGAAG GGACGTTTCC ATCATTCACA2640  
 GTGCCCTCCC CACAGCAACT ACCTCACCCC GACCCCCACC CTCACTCCTA CCCCACCCCG2700  
 CGATCGTCAG GGGTGCCACG GTGGGCCGGA GGGTGCCGGC TCTGGCTGTC CCTGTGCCGG2760  
 TCCCTCACAA ACCTCTCCCC CTTTGAAACT CAAGCACAGC TGCGAGGAGG GCAGCGAGGA2820  
 GGGACCCCTC TCTCATGGTT GTCTCTTCC CCGCTATGT CATAGGTAGT GGAGGAAGCG2880  
 AAGGAAGTGA ACGCTGAATG TGACGCATT CTGAAGAGCT CAGCTGTCAC CCGGCTAGC2940  
 CTGGAAGCCC CAAGTCTGTT CTGACTTTGC TGGCTGTCT CTTTGACCCG CCTCCTAGAT3000  
 CATTGTCTTT GATGTCCAGG CTGGGTCAAT TAAAATAGAG ATGCAATCAG GAAGGTTGGG3060  
 GGAAGTGGGA CTGTGGCTGA ATTGAGACCT TGCTGATGTA TTCATGTCAG CACCTGAGTC3120  
 ACAGCCAGG TGCCCGGAAG CAGCCTCTTC GCATAGGCAG TGATTTGCGA TTACTTTAAA3180  
 GCTCACCTTT TTTCTTCCCC TCTCTGTTCC CTGCTGTCAG CATAATGATT GTGTTCTTC3240  
 CCTATGGGAT CCATCTGTTT TGTAACCAAT AAAGCGTCTG AGGGAGTGTA AAAAACAGAT3300  
 GGAT

## (2) INFORMATION ON SEQ ID NO. 599:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

```

GCGGCCGCGC CAGTCTCGCT TCATGACGCA GCCGGTGACC TTCGACGAGA TCCAGGAGGT 60
GGAGGAGGAG GGGGTGTCCC CCATGGAGGA GGAGAAGGCC AAGAAGTCGT TCCTGCAGAG120
CCTGGAGTGC CTGCGCCGCA GCACGCAGAG CCTGTCGCTG CAGCGGGAGC AGCTCAGCAG180
CTGCAAACTG AGGAACAGCC TGGACTCCAG CCACTCCGAC TCGGCCCTGT AAGGGGCGCC240
GCCCCGCGGG GGGACGCGCG CGTCCGCGGT CCGCGCGGGG ACCGGCGTGT GAACCCCGAG300
AGTGCCCGCG CCCTGCTCCC GGGGGACCCG CAAGGACCCG GGACCGCCGC TCCTCGCGCG360
CTCGGACTCC CGCCCCGCTG CGAACCGGTC GGTGCGCCCC TCGCCGCGCT CGCCCTGGCC420
CGGGAGCGCC GGGAGCGGGG CCGCTTTCCT CGTCCTTGTA AATGTTTATT TTTTAACTCT480
TCCCAGTGCG AACTCTGCTG TGAGTGTGTG CGGGGAGGCG CGCCCGCGCT GAGTCGGCGG540
CGGGTAGCCA CTCCATGCCC TTGTCCGATG GTTTGCAACT CCGATTTTGC ACACCGCTCC600
ACCGTGCCCC CCAGCGCACA CCCATTCACT CTCACGCCAA CACTCTCGCT GAACACTTTT660
ATAATTGTTA GCGGTGGCCG TTGGGACTTT GGGCGCAGCG CGGCTGCTAC TCGCTCTGGA720
GGATTGATAT TTATTTTTCG ATTGCGATGG CTGAAGGCAT TTATTTAACG ATCTTTTAC780
CTGGATATGT CTGTGAGGCT CCTGAAAGGA GACAAATAAA GTCAATATAT TTGCACAGTG840
CAAAAAAAAA AAAGAAAGAA AAGAGAAGGT TCGAGAAA

```

878

## (2) INFORMATION ON SEQ ID NO. 600:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2760 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CACCCAACCT	GTGTTGTTGC	CGCCCGGCCC	TTNCTCCAC	AGNTCTNCTT	NCTNCCGCCC	60
GGCACTTCTG	TGGACCCCTT	NTTAGTTCAC	AGGCACGGNT	GGGGCCGGTC	TGTGCTGGCG	120
NCTGCTGGCC	ACTGAGGGAC	AGGGACACGT	GCCACCTGCT	CATCTCTGCC	CTGAGGTCAC	180
CCCGTGTTCC	CTCCACGTGC	CCATCTCTCT	GCAGTGCCCT	CCTCGCCTGT	GCAGCCCGCC	240
CACCCACAGG	CTCACCCCTC	CTGCCGGCTG	CCAGAGGCCC	CCTCCAGCAG	GGCCTCTCTC	300
CGTNGCCCCA	GCTTCACTCT	CTCCCTCAGC	ACCTGCCCTG	CTGGAGGCCC	CAGCCCTCCG	360
TGGACAGCAG	GGGCCACGTG	GAGCCCGGGC	CGCTCACCCG	CCACCCAGTG	CTGGCCGCCT	420
TCTTGGTGCC	AAACCCCTT	CCCCACCCA	GAGACTGGGC	AGCTGTGTCT	GGTTCGTTCT	480
TTGCACTAAC	CACATTTGTC	ATCTCTAGGG	CAGGCTGGGG	CTGCGGGCTG	AGGGGGACCG	540
CTGGCACCCC	CCTTCCCTCC	CTTCTTGGTT	CCATTTCCAT	CCATGACAGG	TACAGCATCC	600
CAGGAGCCCG	GCCTGAGGGG	CTGGACCCGA	GCCGGCTGTG	AACATCCCTC	AGCCCTTGCT	660
GTCCCCCTT	GGGACTAACC	ACTAACCTCA	CCCCAAACT	CCACGGGTGC	CCCTAGCTGG	720
CCCAGAGCCG	GCAGTGTGAG	CCCAAGTCCG	GGCTGGAGCC	GAGGCCGGAG	CAGCTGTCTG	780
GGAGTCAAGG	CTGCAGTAGC	GTTTCTTCAT	GGGGTGCTCC	AGGGGGTGCC	ACAGACCGAC	840
AGGCAGCCCA	AGGGCCTGGA	CACCCCTCCC	CAGGCAGGTG	CTGCCCCAGG	AGGACTGTCC	900
TCGGGAATGA	ACCTCCCGCG	GGCTTTGGAC	TGAGGTCCCT	GTGGCCTCGG	TCTCCTCCCC	960
ATGAAGTGGG	AGCGAGGCTC	CCCAATGGTG	CTTTTGGCTT	TAGTGTACGA	TGTTTGTGT1020	
GCTTCCCGCC	GTGGAGGGCA	GAGCCACCCC	ACATCAGGAT	CGGACGTGCT	ACCCCTCCCG1080	
GTCCCGGCCC	TGGCCAGGCC	AGCCCAGCCC	TCCAGGCTCG	ATGCCTGTGC	CAAGGCCAGG1140	
GGCAGCCAGA	GGGCAGCTGG	ATGGCCACGT	GCAGGGGTCA	AGGCTGGGCC	CTGCAGTGGG1200	
GCGGGCCGCC	AGCCCCAGCA	GTTTACAGAC	GCATGGCTCT	TCCTCCGAGA	GCAGCCGGCA1260	
GCTACCTGGA	CCGGAAATGT	CCTCATCCCC	TCCCTGGGGC	CAGGCTCTGC	CCTGGCCTTC1320	
CTCTGTGAAC	CCCTCCTTTC	TTTGTGCTGG	TGTCTGGGAC	CAAAAAGGGG	GAATATGGGA1380	
GGGCAGAGTG	GGGAGGGGAG	TCCATGGGCC	TGGGGCCCCA	AGCCGGGGCG	TCTGAGCTCC1440	
CCAGGCATGA	CCAAACCTCA	GTGGAGGGGC	CTCTGCTTCA	GGCCCCGCCT	GGCTGACATT1500	
CTGAGCCCCC	CTCGGAGGCC	CGCCACAGC	CAACCTGCCC	AGTCTTTCCT	CTGGGCTTGA1560	
CCCGCCAGGG	GAGTTCTCCA	GGCCTAGGGC	CAGGAGAGAG	GCCCTGGCAC	CCTGGCGTGG1620	
GTGCCCCCCA	AACGCCCTGC	GACCGCTACA	GAAGCACAAA	TGCTGTCCAT	GGCCGTGAGG1680	
CTGCCTGCCA	GGTGAATGGA	CATAGCGTGA	GAGGCGGTGA	GGCCAGGGCT	TCCAGCTCG1740	
TGCTGTCTCG	GGACTCCTGA	CCGTGGTGTG	CGTGTGTGCC	CGTCTGTGAC	TTTCTACTCA1800	
CCAAGGTTGA	AGAAAGGAAA	CGGGGAAAAT	CAAAAGGGGT	TCAAACCCCA	CCTCAGTAGG1860	
TGGAGGGGAG	CGCCTGCCAT	TGGTTGTATT	TTTGTTCCTGA	GTTTTCCGTG	CCGTGTTCT1920	
AACTACTCCA	TCCCATGACC	TCGCCACACC	TACTGGGGCA	TCTGGCTGGT	GCCTGCTGCC1980	
ATGGCCAGCC	CCCACTTCTC	ACCCTGCACA	GGGGGTCTTG	CAGCCCCCAG	GGCCACAGCC2040	
TCGTTGGGAG	GACAGGGTGG	CCCTGGGGAC	AAGAGGGAGG	AGCCCAGGGG	CTTACCTCAC2100	
TGAGAGTGCT	CCCCAGCAGG	CATCCACTAC	CCCAGGGCCC	CCCACATGTC	ATGGCAAGGT2160	
TGGTAGTGAA	TGGGCCTGGT	TGGGAGCAGC	CCCTGGCCCC	TTGCCCCACC	ACCCATCTCA2220	
CTATGCAATT	CGAGTTCCAA	GCAACATTTG	CTCCTGCCCT	GGGGCCAGCT	CTGCCCCAGC2280	
CCTGAGAGGG	GTGGTGAGGC	AGCCCCCTGG	ACCCCAGAAC	CCCAGACAAG	GGGGCAGGCG2340	
GGGGACCAGG	GCCTCTCCTG	TGGGATCTTT	GTTTTGTGTT	TAACCATAAT	GGTTGTGTAC2400	
TGAACCACTT	CATATTTGTT	ATATATAATA	TATATATATA	TAATCTCCTT	AAGACTCAGC2460	
CTCCTGGTTT	ACCCCCCGG	CCTGGGCATC	TGACCTCCCC	CACCCCAGTG	TGATTTAACA2520	
TCCAGGAAT	GAGGCCTGAA	CCATTTTGCA	TTCCCCCTC	CTCCAGCCTC	TGTAGGGCCA2580	
TGGCTGTATG	TACTGTCGCT	GTGTTTTTTT	GTTTTTTTAG	AACTGGGTTT	GGGGGCTGAT2640	
TTTTATTTCT	TTGGGGGCTT	TTTTTCTTGG	CAAATACTAA	AAATCTCGTC	AATGTAATTT2700	
CTGTGGTTTC	TATTCAGCTT	GGGTTTCATG	TTTTAAAATA	AATTTTAAAA	AGCAAAAAAA2760	

## (2) INFORMATION ON SEQ ID NO. 601:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

```

GGCGGGGGCCG CGAGAGCAGT AGGTGTTAGC AGCTTGGTCG CGACAGGGGC GCTAGGTAGA 60
GCGCCGGGAC CTGTGACAGG GCTGGTAGCA GCGCAGAGGA AAGGCGGCTT TTAGCCAGGT 120
ATTTTCAGTGT CTGTAGACAA GATGGAATCA TCTCCATTTA ATAGACGGCA ATGGACCTCA 180
CTATCATTGA GGGTAACAGC CAAAGAACTT TCTCTTGTC AACAAGACAA GTCATCGGCT 240
ATTGTGGAAA TATTCTCCAA GTACCAGAAA GCAGCTGAAG AAACAAACAT GGAGAAGAAG 300
AGAAGTAACA CCGAAAATCT CTCCCAGCAC TTTAGAAAAG GGACCCTGAC TGTGTTAAAG 360
AAGAAGTGGG AGAACCCAGG GCTGGGAGCA GAGTCTCACA CAGACTCTCT ACGGAACAGC 420
AGCACTGAGA TTAGGCACAG AGCAGACCAT CCTCCTGCTG AAGTGACAAG CCACGCTGCT 480
TCTGGAGCCA AAGCTGACCA AGAAGAACAA ATCCACCCCA GATCTAGACT CAGGTCACCT 540
CCTGAAGCCC TCGTTCAGGG TCGATATCCC CACATCAAGG ACGGTGAGGA TCTTAAAGAC 600
CACTCAACAG AAAGTAAAAA AATGGAAAAT TGTCTAGGAG AATCCAGGCA TGAAGTAGAA 660
AAATCAGAAA TCAGTGAAAA CACAGATGCT TCGGGCAAAA TAGAGAAATA TAATGTTCCG 720
CTGAACAGGC TTAAGATGAT GTTTGAGAAA GGTGAACCAA CTCAAATAA GATTCTCCGG 780
GCCCCAAGCC GAAGTGCAAG TGGAAGGAAG ATCTCTGAAA ACAGCTATTC TCTAGATGAC 840
CTGGAAATAG GCCCAGGTCA GTTGTCTCT TCTACATTTG ACTCGGAGAA AAATGAGAGT 900
AGACGAAATC TGGAACCTTC ACGCCTCTCA GAAACCTCTA TAAAGGATCG AATGGCCAAG 960
TACCAGGCAG CTGTGTCCAA ACAAAGCAGC TCACCGACTA TACCAATGAG CTGAAGCCAG 1020
G

```

## (2) INFORMATION ON SEQ ID NO. 602:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2889 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60  
 GAAAAACTTC CAGATGGCTT CTATCACATC CCCCAGTCTT GTTGTGGAGT GTGGAGGAGA 120  
 AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180  
 TCTCTTCATG AAAGTGTCTT TGCCCAAGGA GGAATTGTAC ATGCCCCCAC TGGTGATCAA 240  
 GGTTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTCGTC GGCCAGTGCA CCATCGAGCG 300  
 CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAAGAG GACATCGTCC CACAGCTCAA 360  
 AGCCTCCCTG CTGTCTGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420  
 ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGACT GGTGGAGTAA 480  
 ATTTGATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTGAGA AAGGCTATTC 540  
 CAAGCTCAAG ATATATAATT GTGAAGTAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600  
 CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660  
 GGTGGAGAG TTTAAGGGCT CTTTTCGGAT CTACCCTCTG CCGGATGACC CCAGCGTGCC 720  
 AGCCCCTCCC AGACAGTTTC GGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780  
 GATTTACATT GTTCGAGGCT TAGAGCTCCA GCCCCAGGAC AACATGGCC TGTGTGACCC 840  
 TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900  
 CACTCTCAAC CCAGTCTTTG GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAAGAAAA 960  
 AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA 1020  
 AACAATTATT GATCTGGAAA ACCGATTCTT TTCCCCTTT GGGTCCCACT GCGGCATACC 1080  
 AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT 1140  
 GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG 1200  
 TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAATCCT 1260  
 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG 1320  
 GCTGGTCCCT GAGCACGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTT 1380  
 CCAGGGAAAA CTTGAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCC 1440  
 TCCTTTCAAC ATCACACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA 1500  
 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA 1560  
 CGTCAAAGGC TGGATTCTTG GCAATGAAGA AAACAAACAG AAAACAGATG TCCATTACAG 1620  
 ATCTTTGGAT GGTGAAGGGA ATTTAACTG GCGATTTGTT TTCCCGTTTG ACTACCTTCC 1680  
 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGAGCATTTC TGGAGTATTG ACCAACCGGA 1740  
 ATTTGGAATC CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA 1800  
 TGACTACTTG GGTTCCTAG AACTTGACTT GCGTCACACG ATCATTCCTG CAAAATCACC 1860  
 AGAGAAATGC AGGTTGGACA TGATTCCGGA CCTCAAAGCC ATGAACCCCC TTAAAGCCAA 1920  
 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA 1980  
 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAAATCC TCAACGAGAA 2040  
 GGAGGCCGAC GAGAGGCCAG CCGGGAAGGG GCGGGACGAA CCCAACATGA ACCCCAAGCT 2100  
 GGACTTACCA AATCGACCAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT 2160  
 GAAGTTCATC GTGTGGCGCC GCTTTAAGTG GGTCAATCAT GCTTGCTGT TCCTGCTTAT 2220  
 CCTGCTGCTC TTCGTGGCCG TGCTCCTCTA CTCTTTGCCG AACTATTTGT CAATGAAGAT 2280  
 TGTAAAGCCA AATGTGTAAC AAAGGCAAG GCTTCATTTT AAGAGTCATC CAGCAATGAG 2340  
 AGAATCCTGC CTCTGTAGAC CAACATCCAG TGTGATTTT TGTCTGAGAC CACACCCAG 2400  
 TAGCAGGTTA CGCCATGTCA CCGAGCCCCA TTGATTTCCA GAGGGTCTTA GTCCTGGAAA 2460  
 GTCAGGCCAA CAAGCAACGT TTGCATCATG TTATCTCTTA AGTATTAAAA GTTTTATTTT 2520  
 CTAAAGTTTA AATCATGTTT TTCAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT 2580  
 CATCTTTTTA TATGTGTCTT CGGTCTAGA CTTGAGCTTT TGGAAATTGC TAAATAGAAT 2640  
 TCAAAAATCT CTGCATCCTG AGGTGATATA CTTCAATTT GTAATCAACT GAAAGAGCTG 2700  
 TGCATTATAA AATCAGTTAG AATAGTTAGA ACAATTCTTA TTTATGCCCC CAACCATTCG 2760  
 TATATTTTGT ATGGATGTCA TAAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA 2820  
 TGTTTCACCT TTAAACATA GGGGGGGTGG TCGGGGGGTC GGGAGGGGGG GGGGTGGTGT 2880  
 GGGGTGTGG

## (2) INFORMATION ON SEQ ID NO. 603:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3638 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG 60  
 GTTACCAACT GGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACGGGAGA GAAGGAAGTG 120  
 GCTAAAACAT TGCACAGGAG AAGTCGGCCT GAGTGGTGCG GCGCTCGGGA CCCACCAGCA 180  
 ATGCTGCTCT TCGTGCTCAC CTGCCTGCTG GCGGTCTTCC CAGCCATCTC CACGAAGAGT 240  
 CCCATATTTG GTCCCAGGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTC CATCACGTGC 300  
 TACTACCCAC CCACCTCTGT CAACCGGCAC ACCCGGAAGT ACTGGTGCCG GCAGGGAGCT 360  
 AGAGGTGGCT GCATAACCCT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGCAGGC 420  
 AGGGCTAACC TCACCAACTT CCCGGAGAAC GGCACATTTG TGGTGAACAT TGCCAGCTG 480  
 AGCCAGGATG ACTCCGGGCG CTACAAGTGT GGCCTGGGCA TCAATAGCCG AGGCCTGTCC 540  
 TTTGATGTCA GCCTGGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC 600  
 ACAGTGGACC TGGGCAGAAC GGTGACCATC AACTGCCCTT TCAAGACTGA GAATGCTCAA 660  
 AAGAGGAAGT CTTGTACAA GCAGATAGGC CTGTACCCTG TGCTGGTCAT CGACTCCAGT 720  
 GGTATGTGA ATCCCAACTA TACAGGAAGA ATACGCCTTG ATATTCAGGG TACTGGCCAA 780  
 CGACTGTTCA GCGTTGTCAT CAACCAACTC AGGCTCAGCG ATGCTGGGCA GTATCTCTGC 840  
 CAGGCTGGGG ATGATTCCAA TAGTAATAAG AAGAATGCTG ACCTCCAAGT GCTAAAGCCC 900  
 GAGCCCAGC TGGTTTATGA AGACCTGAGG GGCTCAGTGA CTTTCCACTG TGCCCTGGGC 960  
 CCTGAGGTGG CAAACGTGGC CAAATTTCTG TGCCGACAGA GCAGTGGGGA AAAGTGTGAC1020  
 GTGGTCGTCA ACACCCTGGG GAAGAGGGCC CCAGCCTTTG AGGGCAGGAT CCTGCTCAAC1080  
 CCCCAGGACA AGGATGGCTC ATTCACTGTG GTGATCACAG GCCTGAGGAA GGAGGATGCA1140  
 GGGCGCTACC TGTGTGAGC CCATTGCGAT GGTGAGTGC AGGAAGGCTC GCCTATCCAG1200  
 GCCTGGCAAC TCTTCGTCAA TGAGGAGTCC ACGATTCCCC GCAGCCCCAC TGTGGTGAAG1260  
 GGGGTGGCAG GAGGCTCTGT GGCGTGCTC TGCCCTACA ACCGTAAGGA AAGCAAAAGC1320  
 ATCAAGTACT GGTGTCTCTG GGAAGGGGCC CAGAATGGCC GCTGCCCCCT GCTGGTGGAC1380  
 AGCGAGGGGT GGGTTAAGGC CCAGTACGAG GGCGCCTCT CCCTGCTGGA GGAGCCAGGC1440  
 AACGGCACCT TCACTGTCTAT CCTCAACCAG CTCACCAGCC GGGACGCCGG CTTCTACTGG1500  
 TGTCTGACCA ACGGCGATAC TCTCTGGAGG ACCACCGTGG AGATCAAGAT TATCGAAGGA1560  
 GAACCAAACC TCAAGGTACC AGGGAATGTC ACGGCTGTGC TGGGAGAGAC TCTCAAGGTC1620  
 CCCTGTCACT TTCCATGCAA ATTCTCCTCG TACGAGAAAT ACTGGTGCAA GTGGAATAAC1680  
 ACGGGCTGCC AGGCCCTGCC CAGCCAAGAC GCAAGGCCCTT CGTGAAGTGT1740  
 GACGAGAACA GCCGGCTTGT CTCCCTGACC CTGAACCTGG TGACCAGGGC TGATGAGGGC1800  
 TGGTACTGGT GTGGAGTGAA GCAGGGCCAC TTCTATGGAG AGACTGCAGC CGTCTATGTG1860  
 GCAGTTGAAG AGAGGAAGGC AGCGGGGTCC CGCATGTCA GCCTAGCGAA GGCAGACGCT1920  
 GCTCCTGATG AGAAGGTGCT AGACTCTGGT TTTCCGGAGA TTGAGAACAA AGCCATTCTAG1980  
 GATCCCAGGC TTTTTCGAGA GGAAAAGGCG GTGGCAGATA CAAGAGATCA AGCCGATGGG2040  
 AGCAGAGCAT CTGTGGATTG CGGCAGCTCT GAGGAACAAG GTGGAAGCTC CAGAGCGCTG2100  
 GTCTCCACCC TGGTGCCCTT GGGCCTGGTG CTGGCAGTGG GAGCCGTGGC TGTGGGGGTG2160  
 GCCAGAGCCC GGCACAGGAA GAACGTGCGA CGAGTTTCAA TCAGAAGCTA CAGGACAGAC2220  
 ATTAGCATGT CAGACTTCGA GAACTCCAGG GAATTTGGAG CCAATGACAA CATGGGAGCC2280  
 TCTTCGATCA CTCAGGAGAC ATCCCTCGGA GGAAAAGAAG AGTTTGTTC CACCACTGAG2340  
 AGCACCACAG AGACCAAAGA ACCCAAGAAG GCAAAAAGGT CATCCAAGGA GGAAGCCGAG2400  
 ATGGCCTACA AAGACTTCCT GCTCCAGTCC AGCACCGTGG CCGCCGAGGC CCAGGACGGC2460  
 CCCCAGGAAG CCTAGACGGT GTCGCCGCCT GCTCCCTGCA CCCATGACAA TCACCTTCAG2520  
 AATCATGTCT ATCCTGGGGC CCTCAGCTCC TGGGGACCCC ACTCCCTGCT CTAACACCTG2580

CCTAGGTTTT TCCTACTGTC CTCAGAGGCG TGCTGGTCCC CTCCTCAGTG ACATCAAAGC2640  
 CTGGCCTAAT TGTTCTTATT GGGGATGAGG GTGGCATGAG GAGGTCCCAC TTGCAACTTC2700  
 TTTCTGTTGA GAGAACCTCA GGTACGGAGA AGAATAGAGG TCCTCATGGG TCCCTTGAAG2760  
 GAAGAGGGAC CAGGGTGGGA GAGCTGATTG CAGAAAGGAG AGACGTGCAG CGCCCCCTCTG2820  
 CACCCTTATC ATGGGATGTC AACAGAATTT TTTCCCTCCA CTCCTATCCCT CCCTCCCGTC2880  
 CTTCCCTCT TCTTCTTTCC TTACCATCAA AAGATGTATT TGAATTCATA CTAGAATTCA2940  
 GGTGCTTTGC TAGATGCTGT GACAGGTATG CCACCAACAC TGCTCACAGC CTTTCTGAGG3000  
 ACACCAGTGA AAGAAGCCAC AGCTCTTCTT GGCGTATTTA TACTCACTGA GTCTTAACCT3060  
 TTCACCAGGG GTGCTCACCT CTGCCCCAT TGGGAGAGGT CATAAAATGT CTCGAGTCCT3120  
 AAGGCCTTAG GGGTCATGTA TGATGAGCAT ACACACAGGC ATGAGCCACT GAGCCTGGCC3180  
 CAGAAGCGTT TTTCTCAAAG GCCCTCAGTG AGATAAATTA GATTTGGCAT CTCCTGTCTC3240  
 GGGCCAGGGA TCTCTCTACA AGAGCCCTG CCCCCTGTT GGAGGCACAG TTTTAGAATA3300  
 AGGAGGAGGA GGGAGAAGAG AAAATGTAAA GGAGGGAGAT CTTTCCCAGG CCGCACCATT3360  
 TCTGTCACTC ACATGGACCC AAGATAAAAG AATGGCCAAA CCCTCACAAC CCCTGATGTT3420  
 TGAAGAGTTC CAAGTTGAAG GGAAACAAAG AAGTGTGTTA TGGTGCCAGA GAGGGGCTGC3480  
 TCTCCAGAAA GCTAAAATTT AATTTCTTTT TTCCTCTGAG TTCTGTACTT CAACGAGCCT3540  
 ACAAGCTGGC ACTTGCTAAC AAATCAGAAA TATGACAATT AATGATTAAA GACTGTGATT3600  
 GCCACCAAAA AAAAAAAAAA AGACGAAAAG AAAAAGGG 3638

## (2) INFORMATION ON SEQ ID NO. 604:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2775 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

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ATAGGTTTGG ACCTTTCTTG GTAGAATTAC TGCCCTAATT TTGTTCCACT GATACTAGAA 60
ACGGTCTGAT GTTAGAGCTG GAAGGGATCT GTAGTATCAC GCAGTCCGAT TCTCTAATTT 120
TCCACATGAG AAAATGAAGG TCCAGAGGAA GCAGAGACTT AACTCACAAA TCAGAAAAGC 180
GGTTCTTGCA GAACTGAGGC CATAGTGAGG ACTTTCTGCT TTCCACCATA CCACCTTGCC 240
AGTCCACACA AGAGGGAGGA TGTATTTTGG GGGGCATACA CTGAGGATGG AGAAAGATGG 300
CATCAGAACT GCTGGGTGAA GTGGTGGCTT AACTGGACTT TGACAGCTGC CTTTTGAAAA 360
CCCCAAAAC AAACACACTG CATGTAATCA AAAGATGCTT ATACTAATAA TGACCTGTGC 420
TGTTCCCACT CAGTTGCTCT CTGTTTTCGA GAAGACATGA GAAGCTGCAA CATGACCTGG 480
AGTGGAACTG GAGAGTCACA TTTTGTGTTT AGCCAGCTTC TGGGCAGCAG ACCGACTCCA 540
CCTTCCCAGA AGGCTGAAGT GCTCGTGTGC TGCATCCAG TGGCATCTCT GCAGTGGTCA 600
GAGTGACCTG GTATAAGGGA GAGGGCATCA CCTTGCCCCC TGTGCTGACT CCTGCCCTTC 660
CCCTACAGGA GAGTCCATCC CGATCCGGCT CTTCTGGGCC GGGTATGAGC TCACGCCCAC 720
CATGCGGGAC ATCAACAAGA AGTTCTCTGT GCGCTATTAC CTCAACCTGG TGCTGATAGA 780
CGAGGAGGAG CGGCGCTACT TCAAGCAGCA GGAAGTGGTG TTGTGGCGGA AGGGTGACAT 840
CGTACGGAAG AGCATGTCCC ACCAGCGGCG CATCGCCTCA CAGCGCTTTG AGGGCACCAC 900

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CTCCCTGGGT GAGGTGCGGA CCCCCAGCCA GCTGTCTGAC AACAACTGCA GGCAGTAGGC 960
CCCCAGGGCC GAGAAGATGC TGGGCACCCA CCCAGCACCC CCATCTACCA ACACCAGCGG1020
CTGGGGGCGG GGGCGGACCT TGTGAGGCTC AGTTGACCCG TTA CTTGCAA CCTGAAAACA1080
AATCATGTTT TTGACTTAAA TTCTTTTCTC TGGAGAACCC AAGGGGCTTG GGGTGGGAAG1140
CAGTCTCTCC TTGGGATTCT GCGGCCGATG TGGGATAGAA GAGGTAGCAT CCTGGAAGCC1200
AGCCTCTCTG GGGAAACATGA GCCCCCTTCC TCGGGGGGCT GCCTTGCGTC TTAGAGGAGG1260
GAGAGCAGAG AGCACGCATC CTTGGCTCCT GGCTCTCTGA GCTTCCTGAT ACAGGATCTG1320
AGCATGTCCC TGGGATTCTG AGCTGCCAAC AGGGCCCTGG GTAGTCACAT CTTGTACTCC1380
CCTTTGCTGT CCCGGAGGTA GTGGCAGGAG TTGGGCCAGC CCCCCTAAG TGGCAGGGGA1440
AGACTCACGA TTGGGAAGCT ACCTCTTTTG GAATCTTGGA TGTGGTGATC TCAAGTTCCC1500
ACAGGCCACC TCCTTCTGGC CACTCACTGC TGGGACCCAG GCACCTCCCT TCTCCATCCT1560
CTCTGGATTG TCAGTAATGT CCTGGAACAG AAGCCTGTAG GATGGCCTTG GGCACGGAGA1620
AGCCCTGGGG TCAGTGTCGT GCACGGATGG CGGCAGTGTT GAACCCAGGA GGCTGAACCC1680
GGCCCAACAC GGAAGATGAG TGCATGGCAA CCGCCTGCCT TCACGTGCGT CCCTTGGTA1740
ACCCCAAGGT CTGGGCTGTT CTAGGTATTG CTTACGTGC CCCAGCAAGC CCTTAACAAG1800
AGGGCCTGGT TCCCTGAAGA ACCAATCCCA GGAAGGGGCC TTGATCCCTC CGCCTTGCTG1860
AGAGTGAACC CTCGTCTCTC CTCACCCTCC ATTTCAATTC TGGGAATTGG GGCTTAGTTT1920
CGAACCTTTG GCAAGGCTGT TCTTACTAAT GCCCAAGCCC CTTTACCCT CTCCCTATAG1980
GTTACACAGG GGAGACCAGG GCCTCGGCAG AAGACTGCTG CCACACTTCC GAATCATCT2040
GCTTGCCAAA TAGGTCATCT TCACCAGTTG ACTGACCCAA GTTTAGGACC ATTTGGTATCG2100
TGTGTTTAAA AAACACATAT AAAAAAATC TTGTGAATAT TCTTGTTATG CTAGAGAGGA2160
AGGTACTTCT CCCTCTACGG CTCTGCGCTG GGGCCTATGG TAGTAAAGTT GTTTACTGTC2220
CTTTTTCTGC TTCCCTGGA AATGACAGG ATTACTCTCC CATTGGCCTC CTTCCCTTT2280
ATAGAAAAGAC CAAGCAGGCC CCACTGGCCA AGAGGTACGG TATTTGGCAG TCTGAGTTCT2340
CAGTAATTTG GAAAGTTAAG GAGTTGGTTC CTGTGTCACC TTTCAAGTTAG TGTGGGAAAG2400
GAAGACTTCT GTTTTCCTGA GATCAGTGCA GTCTCAGGCC TTTGGCAGGG CTCATGGATC2460
AGAGCTGAGA CTGGAGGGAG AGGCATTTTC GGTAGCCTAG GAGGGCGACT GGCGGCAGCA2520
GAACCGAGGA AGGCAAGGTT GTTTCCCCCA CGCTGTGTCC TGTGTTTCAGG TGCGACACAC2580
AATCCTCATG GGAACAGGAT CACCCATGCG CTGCCCTTGA TGATCAAGGT TGGGGCTTAA2640
GTGGATAAGG GAGGCAAGTT CTGGGTTTCT TGCCTTTTCA GAGCATGAGG TCAGGCTCTG2700
TATCCCTCCT TTCCTAGCT GATATTCTAA CTAGAAGCAT TTGTCAAGTT CCCTGTGTGG2760
CCCTTCCCCC CAGAG

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2775

## (2) INFORMATION ON SEQ ID NO. 605:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 944 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

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GGGAGATGCC ACCGGGAAAT CCCCCAATGT CCACTAGGGG GCAGGAGGCC ACCGTTCTTC120
GTACTCCGGA GAACCTGGCT GGAGAGCTCT TTCTTGTTCA CCCTTCCCAC CAGACTAAAA180
GGTCATCGCA GATAACGTGA AGGACTGGAG CAAGGTCGTC CTGGCCTATG AGCCTGTGTG240
GGCCATTGGT ACTGGCAAGA CTGCAACACC CCAACAGGCC CAGGAAGTAC ACGAGAAGCT300
CCGAGGATGG CTGAAGTCCA ACGTCTCTGA TGCGGTGGCT CAGAGCACCC GTATCATTTA360
TGGAGGCTCT GTGACTGGGG CAACCTGCAA GGAGCTGGCC AGCCAGCCTG ATGTGGATGG420
CTTCCTTG TG TGGTGGCTT CCCTCAAGCC CGAATTCGTG GACATCATCA ATGCCAAACA480
ATGAGCCCCA TCCATCTTCC CTACCCTTCC TGCCAAGCCA GGGACTAAGC AGCCCAGAAG540
CCCAGTAACT GCCCTTTCCC TGCATATGCT TCTGATGGTG TCATCTGCTC CTTCTGTGG600
CCTCATCCAA ACTGTATCTT CCTTTACTGT TTATATCTTC ACCCTGTAAT GGTGGGGACC660
AGGCCAATCC CTTCTCCACT TACTATAATG GTTGGAAC TA AACGTCACCA AGGTGGCTTC720
TCCTTGGCTG AGAGATGGAA GCGGTGGTGG GATTTGCTCC TGGGTTCCT AGGCCCTAG780
GAGGGCAGAA GAGAAACCAT CCTCTCCCTT CTTACACCGT GAGGCCAAGA TCCCCTCAGA840
AGGCAGGAGT GCTGCCCTCT CCCATGGTGC CCGTGCCTCT GTGCTGTGTA TGTGAACCAC900
CCATGTGAGG GAATAAACCT GGCCTAGGA AAAAAAAAAA AAAA 944

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(2) INFORMATION ON SEQ ID NO. 606:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1939 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

CCAGTCAAGA ATCTCCCACT AAGCTTCAAA GTAGTGGATT ACAGCATGGC AACCATGCCA 60  
 GTAATTTGAA ATTTAGTAGA GAGGCTTTTCG CTTAGTAGAG ATGGGTTTTT GCAGGCTGCT 120  
 CCCGAACCTC TGACCTCACC CCACCCGCGG CAACCCCCC ATCGGGCCCC CAAAGTGCTG 180  
 GGGTTACAGG CTTAAGCCAC CAAGCCCGGG CGACCTTCTT CTATTTTTC ATTCTCCTTT 240  
 CCAAAGCCAT GGCCATGCGC TCCTGTGTAC AGGTGCATAA ACACATCAGT GTGCCATCCC 300  
 TCACATGCAT GTCGTTCCCC ACCCTCCTT CCCAGGGCTT CTCTTGCTC CAGCGTTCCT 360  
 CTGGGACCTT CTGCAGATAC AGCCTGTGCT GGACCCCGAG CCAGGGTGAG GGCTCATTCT 420  
 GCTCTGTCTT CCCCCTGCC TCAGTTTCCC CCAAAAGCTG ETTTCACGTC CTTCTAGTAG 480  
 GGGGCTCCC ATGGGGGCAA GGATCCCCCT TAGGATTCAA TCTTTCCTCT TTGGGCAGTT 540  
 TTGGCTTTGA GTCCCCCAGG GATCAGGGTG AGAATGAAGA AGAGCTCAGT GAGCGGAATG 600  
 ACAGCAGCTG GGTGGGTGGT GTGGGGAGAG GCTGAGGGGA AGGCAGCTCT AAGACTGGGA 660  
 GTGGAGTTCC TGGAGGTGTG GGGAGGGGGG CGTGTTTCA ATTTAGAAAA ATCTCAGCCA 720  
 GCTCGAGCCG AGAGAGAATG CGAAAGAGGA AGTTCGGAAG GAGCGAGGAA TGGGGTGGGT 780  
 GGCAGCGGGG GCCGCTCAGT CGCTGTGCT CTTGTCCACC AGCACGGCGT CCGACTCCTC 840  
 GGTGATCTCC AGCAGCGCGT GCACGTCGGG GCTGCTCCCG CGCCGAGGT CGCCGGCCTC 900  
 CCCCCGCTCC GCGCCGCCCT CGTCGTCGTC GGCGCCACC TCCACCATCT CCGTGGCCTT 960  
 GAGCACTTCC ACCTGGCCCT CGCGGATCTT CTTGACGTGG AAGGTGAAGG GTGGCACCTT 1020  
 GTAGACCGCG GTCTTGAGC GCGCGTACAC CACGTGGTCG GCGTGAAGG ATTTGCGCAA 1080  
 CTTGTCCCGC GACGTCTTCA GTTCTCGCG CCGCTCGCG GGCACCAGGC GCGTGCCAG 1140  
 CTTGTTTCATG CGCTTCTCCA GGGTGTGCC CGTCTTCTCC AGGTTTTCTT TGGTCTTGAG 1200  
 GCGCGTCTTC TCCAGGTTCT CGCGGGTACG CACCTTGGTC TTCTCCATCT TCTCCTTGA 1260  
 GAAGGCCTTC TTGAAGTCGT CCACGCGCGG CAGGCCCTGC GCTTGATACG CTCTGCGCGG 1320  
 GACTCCTCAA TAACCTCCTC AACCTCCACC GCCTCGTCCG ACGAAAGCTC CAGCGCCGCT 1380  
 GCGTCCTCCT CGGGCCGCTC GCCCTCGCCC AGCTCCTCGC CCTCCTTCTC TGGCAGCGCC 1440  
 TCCGACTCTT TCAGCGATTT GCTGATGCTC AGTTTGGCCG GCAGCTTCAC TTCATCCTGG 1500  
 TAGATCATGA CTTTAAAGTT GCGGCGCCGC AGCAGCTCGG CCTCGTTGAC CTCCAGCTTC 1560  
 TTGATCTGCC CCGCCTGGCG CTCCAGGCTG CCGCGCACGG TCTTCACGTT GACGCTGACC 1620  
 TTGCGCACCT TCTCCAGCAG CTTGCTCACC GTATTGCTCG TGGTGGCGTG CGCCTTGCCC 1680  
 AGCTTGCTCA GCTCGCCCTG GATGCTCTGC ACTGCGCCCT CCATCTCCGC CTGCCGCTCC 1740  
 TCCAGCTGTG CTTGAGTCAG CTGGATCTGG TCTACGGCCC CGATGATTTT GTCCAGGAGG 1800  
 CTCAGCACCA GCACGCCGT CACCTGGTCC GACTTGATCA GCTCTTCTGA GCCGGCCCCC 1860  
 GACGGCTCCT CCGCTGCCTG AGCCCCAGCG GAGGAAGCTC CGGGGCCTCG GCGATCGGGG 1920  
 TACCCGGGCA AGCGGCCG 1939

## (2) INFORMATION ON SEQ ID NO. 607:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1570 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

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GGCACGAGGA AGTTAAGATC ATACATGCGG ATGTGCTGGT AACCTGCAAG AAGCAATCAT 60
GCTGCGGTCC GGTGTGACCT CCCAAGGCAT TCACCCTGGG AGTCCCTGGT GCTGCACCCC 120
AACCCAGGCA GAGCTCATCG TGGGTGACCA GAGCGGGGCT ATCCACATCT GGGACTTGAA 180
AACAGACCAC AACGAGCAGC TGATCCCTGA GCCCGAGGTC TCCATCACGT CCGCCACAT 240
CGATCCCGAC GCCAGCTACA TGGCAGCTGT CAATAGCACC GGAAACTGCT ATGTCTGGAA 300
TCTGACGGGG GGCATTGGTG ACGAGGTGAC CCAGCTCATC CCCAAGACTA AGATCCCTGC 360
CCACACGCGC CGTACGCCCT GCAGTGTGCG TTCAGCCCCG ACTCCACGCT CCTCGCCACC 420
TGCTCGGCCCT GATTAAGACG GTGCAAGATC TGGAAGGACG TCCAACCTTC TCCCTGATGA 480
CGGAGCTGAA GCATCAAGAG CGGCAACCCC GGGGAAGTCC TCCCGCGGCT TGGATGTGGG 540
GGCCTGCGCT CTCATCGGGG GACTCCCAGT ACATCGTCAC TGCTTCCTCG GACAACCTGG 600
CCCGGCTCTG GTGTGTGGAG ACTGGAGAGA TCAAGAGAGA GTACGGCGGC CACCAGAAGG 660
CTGTTGTCTG CCTGGCCTTC AATGACAGTG TGCTGGGCTA GCCTGTGACC CCTCGGGACN 720
TGCCTGGTGC AGGTGGTGGC AGCNTGGAGG GACCCATGCA GCACCCAGGT CAGAGCAGAC 780
CCNTNCCCT NGCCNGGCCT GCGCCANGCT GGNACCTGAT GGCCCCCTGT GCGCCTTGA 840
CCTGCTGGGC CAGGCTGNCC CTGGGACTCT CAGCCCCCAN GTTGCTTATC CANGATGTGA 900
CAGAGCTCGA CCCAAGCCAG GCTGCACACT CCTGGACNTG GGCTAGCCTG CACTGCCNTG 960
GGAAAGNTCN GCCGAGGGCC CANAAGCTGC TGAGGGGTNC TGAGGCTGGT GCCCACCCCC1020
AAGCTAGTGT GTTCTCTGCC CCTCCCTGCC CGCGTTTCAG GGCCTCGGTC CATAGAGAAC1080

ACCACCACCA TGGCCAGGTG GAAGGGTTTA TTAGTCCCTG CCAGCAGCTG TCCTCCCTGG1140
TGCAGGTGGC CTGGCCAGCC CACTGGATTG GGGACGGGCC AGGCTGGGCC AGGTGCGGGG1200
CTCAGTCTGG GAGGTAATAA AAGCAGACCG ACACGCAGAT GTTGCTCGGG AAAAAAAAAA1260
AAAAAAAAAA AAAAAAAGC CGCTGTCTCC GGGGCCCTC TGCTCGCCGG GCCAGTAGA1320
TGGGGGTCTT CATGCACAGG CGCTGCACCA AAGCCCCCGC CTGGGCGGTA GCCACTTACG1380
AGGCTCCCTT GCACTGCCAG CAGCTCCTGG GTGTGGTGGG TGTCTGGCT GGGGACCCAA1440
GCCTCTTGGG CCTTGGAGGT ATCCACCAGC AGCCGCAGGT CTCCCGATCA CTGTCTCTCA1500
TCAGGCGGAG GAAGCAGACC TGGTGCTCCT CAGGGCGGTA ACAGATGCAG CCGCTCTGCC1560
CGTCGAACAG                                     1570

```



## (2) INFORMATION ON SEQ ID NO. 608:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

```

GCACAATCCC GGCTCACTGC AACCTCCAAC TCCTGGGTTT AAGCGATTCT CCCGTCTCTA 60
CAAAGTATAC AAAAAAATTA GCCAGGCATG GTGGTGCGTG CCTGTAATCC CAGCTACTTG 120
GGAGGCTGGG GCACAGGAAT CCTTTGAACT TGGGAGGCAG AGGTTGCAGT GAGCTGAAAT 180
CACACTACTG CCCCCAGCC TGGGCAACAG AGCAAGACTC TGTCTCGAAA AAAAAAAG 240
AAAACAATGA AGGAAAAGGA GGGTGAGTTA GCTGGAGTAG AATAGAGGTA TAGAATCGTT 300
CCTAAATAAC CGGCTGCATT GGTTCCTGG AGACTTGCTA AAAACCCAGA TTCCCAGGCC 360
CCACTTCTTG GTGCTCCTAA TTCAGTAGCA TCACAGTAGG GTTCCAGAAG CGGTATTTTT 420
AACAGCTCC CAGGTAATTC TGATGTGCAC CTAGATTTGG AAATCACTGT GTTAAAAAAT 480
ATTGTGAGGT AAGTTGGTCA GTTAGGTTGG GCAGCTTTTA TTTCATTGCT AAGGGATTG 540
GACTTGATGG TGTAATAAAG CATTAAATGA ACAAATATTT ATGGAGCCTG TACTATGTAC 600
CAGATGCAGA CTGTGCTAGC GGTGGGGAT ACAGTGATGA CTTGGTCTGC CTCTAGGTGG 660
CAGGGAGCCA TTTTGGGTTT TCGAACAGAA AAGTGACATA ATGAATGCTG AGTTCTTAGG 720
AAGATTAATC CAGGAGTAGT CTCCAGGATG TACTGGAAGG AGAGAAGCTG AAACCAGGGA 780
GGCTGCTGTG TTTGCAGTTG GCTGCCAGT GCTACCTCTG CAGAGACAAT CAATGTCCCTG 840
AAGGTAGCTG GTATGTCTGT GTGCACTGAC ACGAGCCTTC CTACCAAGCC CCAGGGGCTC 900
CATGCTGGAG AATGCACGTA GGGCTAGGGT GAGCACTAAC TTCACCTCAG GAGAGCAAGG 960
AACAGTGTGG CTCTTCCATT TTTCAGTTCT GTAAGCACAT CACCCTTTTC TCCTCCCCTT1020
GAGCTGTGTT CTCTGACAGC TGTTTGTTGG TAAAGCCAGC AGCCCCTAAA GCACGTCCCA1080
GCCTTGCTCT CTCTGTGCTT TCCCCACCA CTGCTGCTGC ACGCCTCATT TGCTGGGCA1140
CTTTAGTGGT GGAACCATT A GAGGCTGAGT GACTTAAAGG AGATTGAGTC TGTCTCGACC1200
CCGAGAGAGA GTGGGATGGA TGGATGCATC GTCTCATTTA GAAAGTGTG CCTCTGACTC1260
TAACACACTC TTCTCTCTTT CTTTACCGCC CTCCCTGTGT GCGTCCCTGG GGGGGCGTGG1320
GCTAAACCCC TTCCGTCCTT CTTTCTCCTT CTCTCTCACA GTGTAGGCAC CACTTCTCTT1380
ACAATTTAGG CTTTCTCTCT GCCTTGGGCT GAGTGAGGAA GAGGAGTGCT GTTCCTGCCT1440
TCCTAGCCCA GCTGGGTCTG ACCAGAGGCT ACTGTGTACC CATTTACCAT GCGTGATTGT1500
TAACTCAGAG TGGGGTGTAG CCAGGTATTG ACTGAATGTA TGTTCTTGCT GACCTGTGTT1560
TTTTTCTGTA GGGACCAAAG CAGTATCCTT ACAATAATCT GTACCTGGAA CGAGGCGGTG1620
ATCCCTCCAA AGAACCAGAG CGGGTGGTTC ACTATGAGAT CTGAGGAGGC TTCGTGGGCT1680
TTTGGGTCTT CTAAC TAGGA CTCCCTCATT CCTAGAAATT TAACCTTAAT GAAATCCCTA1740
ATAAACTCA GTGCTGTGTT AAAAAAA

```

1768

## (2) INFORMATION ON SEQ ID NO. 609:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

```

TAAGGAGACT GAAAGGTGAT TCATTTAGTG AGTAGCGATT ACAGAATTTT TAAACAGTG 60
GGGCGGGGGG GGGCGGCGGG GAGGAGGGCT GGAATTGTCC TCCAGCGCAT ACAAGGTTGT 120
TGCTGCCAGA GAAATCCAGC AGGAAAGAGC AGCATTCTTT CACCTTTTCC GCCTCTGAAG 180
CGGAGGAGAA CTTCAATTCC CAGCAGCCCT TAAGATTCCT CCGCGCACTG CGTAGCGTCT 240
CCGGCATTCT GCTTTCCGGC GCTCTGCCTT CCGGTGCGTC GTTTACGGCC AGTTTGAACC 300
AAAGACGCCC AANGGTTGAG GCCGAGNTTC CAGAGCATGG GGTCTCGGTT GTCCCAGCCT 360
TTTGAGTCCT ATATCACTGC GCCTCCCGGT ACCGCCGCCG CGCCCGCCAA ACCTGCGNCC 420
CCCAGCTACA CCCGAGCGC CGACCTNCCC CNAGCAGAAC ACCGCCTNGT TGAAGANCCT 480
GCTGGAGCTG TCGNCGTNGC TTTCTGGGTT GGGGCTGATG GGGGNNCGGG CGGGTACGTG 540
TACNTGGGTG GCANCGGAAG CCCATGAAGA TNGGGATACC CCCCAGTNC CATGGACCNA 600
TTACNGCAGA TGGTCATCGN NGCCTCANGC NATTGCCACC TNGGGGTANT CGTTGTNCAT 660
NGGCAGACCC CAAAGGGAAN GGCCTANCCG CGTTGTTTNG AAAGNTACCA CCANGTGAAT 720
NCTGTCTTCT GTCTNCTNGT CCCNTTTNCC CCGTGACACA CAGAGCAGGC ATGGAATTTA 780
ATGGGNTGTT CTGGNACNAG ACACTTGATC ATGGACAGAC ATCACTACTN NGTGGATACT 840
NNACAAGACT GAAAAGNAAA ATCGTATGTT GTCATTCTNTC TGGCTANTGG AGTGTGTTGTG 900
GCCTTCACAG ATTTACACAG AACCAATAAA TCCCTCAGAG AAGTAAAAAA NAAAAAAA 960
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 1001

```

## (2) INFORMATION ON SEQ ID NO. 610:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2515 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

```

GGTGTGGAAA CTACTGCAAA TAGTAGCACT TCACTGAGAT CTACAACTCT TGAAAAAGAA 60
GTTCTGTGCA TCTTCATCCA CCCTTTAAAC ACTGGATTAT TCCGGATAAA AATTCAAGGA 120
GCCACTGGAA AATTTAATAT GGTCATCCCT CTGTGGATG GGATGATTGT CAGCAGGCGA 180
GCTCTTGGCT TTCTGGTGAG GCAGACTGTA ATTAACATT GTAGAAGAAA GAGACTGGAA 240
AGTGA CTCT ACAGTCCCC CATGTCCGCC GGAAACAGAA AATCACCAGC ATTGTCAACA 300
AGTACCGGAA CAAGCAGCTG GAGCCAGAGT TTTATACTTC ACTTTTCCAG GAGGTTGGAC 360
TCAAGAACTG CAGTTCTTAG ACCACTGAAT TTCTAAGACT GTTGAAGTCC AGTTTGGGAA 420
CTATAACACA GCAGAACAGT TTGATAGGTG ATCACTGTAA AAATAAAAAC AAATCACTCC 480
CAAGAGCTTA CTGTTTAAATC ACCAGAATAG AAGAAACACA TTATAACCCA TTTGATAGAA 540
GACTTTGGGC TATCTAGTGA AATGGGCTCC CAGACACAAT CATACTCCTG CTGATAATGA 600
TGATATACAT TTTAGCCATA AACTTTCTTT TAAAAGTGAC AATTTTAGTT AAACATAAGC 660
CTTTTGAGGA GAAAGGCTTT TATGCATCTC AGTTAAACAC GTGCATTGGT AGTATCAACA 720
AATTTGCAAT TAGAAGTTG AAGATAGTTT TTTNCCTCAC TTTTAGGAG GCTGTATTCA 780
AAATTAATAA CTCAGAATCT TACAGGACAT TTAAAGGACT CATGTTGATA GCATGGAGGA 840
GAAGGAAAGA AGTCACAGCC TTCTACTCAG TTGTAGGTCT TCTTGTCATC CAGCTGTCAC 900
ACTGACAAAA AGAAAAGATG ATANCATGTT TTTTGTCTCA GATAAGAAGC CTGACATTAA 960
AAGATGTCAT ATTTTTTTCT CCACATTTCA AAAAGTTGTC CTCTCATCA CTGCACAGAT 1020
CTGTCTGAAA GCCTCAGTTT CTGAGTGACC CAGGAACAGA TCAGAAATGG AGCATGGCCT 1080
TGTCCTTTAA TGGGGATGCA AATAAAGTTT GTGGGGTTAA AAGTTATAAG ACAGCAGTGA 1140
TACCCCACTC TCTCCATTAT TGTCCAGCGG GGTGACATAA TGACAGGTTA AATATTGTG 1200
ATTCAATTGAT TAAATATTAT TTAAAGAAAT GTAAAAAATA AAAAAAGGTT GAAAATTATT 1260
TGGTTTCATC CATTGTCTCT TATTTAGGGA CCAAGCAGCA AACTGCAGTA GTTTGTGAAG 1320
GATTCTAATA TGGGGTTTCA GAATAGCCTC TCAACGCTAC TAATTCAGAT CTCTCCAGAA 1380
GAAGTACTGG ATTTCTCAT AATTGACAAA CATGAGTGAC CACCTCTTTG GGTGGCTACT 1440
GTTAGAAATG GCTGTTGTCA TGTTTTCTGG ACTTTGCCAG CCAACAGATC CCTGCCAGGT 1500
TTTGGAATAA CTTCTATTAC CTCGCTGCTA CTTTTCTGCA GGGATAAAAC TTTTGNAGGT 1560
GGCCAGACCC AGAACATCCA AGGATTCCTG TTACAGTGCT ACAGTATACA CTGCTCATTT 1620
ATCCTATTCT CATGTGCTTT CTTCTTTAGT AAGATTATTT TAAGAAAATA AGTGATATTT 1680
AAAGTCCAAA GAGGAATGAT CACAGTTGTA TAAGGGGTGT TTTCCCACTT GAAGTCTGAT 1740
GTCAGTCGAC TGTGGGTCAG AGCTACAACC ATCTGTTTGG TTTGATGTTT TGGTGGTTTA 1800
CTTACGGAGT GGGGATAGTG TGAGACCTAA TTCCCTGTGC AAATGTCTCT TATTCCAGAA 1860
ATGTGCATTT TGTCATCTAT AAGCAAGAAA TATGGGCATA GCAGCTCTTG GTTTAAANGT 1920
TTGCCATAAC CTGTTTCATG TTGTTTTAAG CTCAGGTAAG GATAACCTCC NTCTTTCTAT 1980
GACTCCAGTT TCCATTTCAGG TTATAGTATT ATTCAATAGT TGATTTTCTT TTTAAGCTNG 2040
GGCAATAAAT TGATGTTTCC AGATGGTAAC ATGGGGANGAG GGCATATAGG ATAAAGATNG 2100
AGCAAATCTT ACCCTAAAAA TGNTTCTAGT AGTTCACAGG AAGAAGATGA GGTTTAATAA 2160
CTTTCAAGGT AATTCTAGAT TGACATTTTN GAGGGGAAAA TGGGCTCTTG TTCTAGTTGA 2220
AGTGAGCAGA GAANGGCTAT NAAATTAATA TGTAANCTTA CAGCATTTCA GAGGTTAAAA 2280
ATAACTGATG CAGATGTACT TCTTCAGTGT GATTCTTCAG ATCAAACCTT TACTTTTGGC 2340
ATAGTTAATT TCAGAAAAAT GTGCTGTATG TGTGTGTGTA TGAGGGTTGG TCTTGCTGAT 2400
CCTTCAGTTA GCTCTAAATT CTGGCAACTC CTTGTAATTC CCATGTATTT GATACCATGA 2460

```

## (2) INFORMATION ON SEQ ID NO. 611:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 818 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

```

TTTTTTTTTT ATTTAAAGCC TGGATTGTAA CCAGATTTTC TTTTTTCCCC CTTCTCAGCT 60
GTAGATATGA TATCTCCTTT CAGGGCCCCA GCTTAAGGGC AAAGTGAGTT AATGTGTAGA120
CAAAGGCGAG GGACAAGAGA GAGTTAACAT CTAGACAGTG GAAAAAGCCA TGGTGTGTGG180
TTTCTGGGAA CCACCAACAC TTGCAGGTTT AGCTTTTTTC CAGGGTTGAC TACAAGAAAG240
AAAACCATGT TTTTGCAAGA TTAAAATGTG GTTGAGTGTG CCTAAATTAA CCATCCCCAT300
TTTTATCATA TTTCCACCAT CACTTCAGGG TTTTAAGAGT CAGTGCTCAC CTGGGCGGAG360
CTGGTAGTAC ATTTTGCTTC TTAGAAAGCT AAGTCCTGGG TTCCGTCTGA TTTTAGGTTT420
CAGGAAC TTCGAGAACAC CCGATCGCAG AGGGTAATTT TCTGGAGTTT GTTTTGCAGG480
GATAGCTGGG AGTATGGCCA CCCTGCTCCA CGATGCGGTA ATGAATCCAG CAGAAGTGGT540
GAAGCAGCGC TTGCAGATGT ACAACTCGCA GCACCGGTCA GCAATCAGCT GCATCCGGAC600
GGTGTGGAGG ACCGAGGGGT TGGGGGCCTT CTACCGGAGC TACACCACGC CAGCTGACCA660
TGAACATCCC CTTCCAGTCC ATCCACTTCA TCACCTATGA GTTCCTGCAG GAGCAGGTCA720
ACCCCCACCG GACCTACAAC CCGCAGTCCC ACATCATCTC AGGCGGGCTG GCCGGGGCCC780
TTGCCGCGGC GCGAGGGGC CCCCTGGACG TTSTAAGA
818

```

## (2) INFORMATION ON SEQ ID NO. 612:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

```

GCGGTCGGTA GTGCGGCGCT GTTTAAAGAT GGCGGCGGAG GAACCTCAGC AGCAGAAGCA 60
GGAGCCGCTG GGCAGCGACT CCGAAGTGTT AACTGTCTGG CCTATGATGA AGCCATCATG 120
GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180
CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240
ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300
TTCTATCGGG CTTTCGGATT CTCCCACTTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360
CAGCGGTTCA AGGCTGTGTC TGCCAAGAGC AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420
GAATTCACAA TTGAGGATTT CCACAACACG TTCATGGACC TGATTGAGCA GGTGGAGAAG 480
CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540
GTGGTCTACC TGCGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600
CACTTCATCG AGGGTGGACG GACTGTCAAG GAGTTCTGCC AGCAGGAGGT GGAGCCCATG 660
TGCAAGGAGA GCGACCACAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720
CAGGTGGAGT ACATGGACCG CGGCGAGGGC GGCACCACCA ATCCGCACAT CTTCCCTGAG 780
GGCTCCGAGC CCAAGGTCTA CCTTCTCTAC CGGCCTGGAC ACTACGATAT CCTCTACAAA 840
TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCCT CTGCCAGGCG CTAGACATGT 900
ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTTACC CCCTTCTTCC TGTCACATGA 960
CCCCCCCCCA TGTTTTATTA AAGGGGGTGC TGGTGGTGAA AAAAAAAAAA AAAAAAAAAA 1020
AAAA

```

1024

## (2) INFORMATION ON SEQ ID NO. 613:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1322 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

```

GCTGACCACG ACATGTGTCT CCTCCTCTGC ACCTTCCAAG ACCTCCTTAA TAATGAACCC 60
ACATGCCTCT ACCAATGGAC AGCTCTCAGT CCACACTCCC AAAAGGGAAA GTTTGTCCCA 120
TGAGGAGCAC CCCCATAGCC ATCCTCTCTA TGGACATGGT GTATGCAAGT GGCCAGGCTG 180

TGAAGCAGTG TGCGAAGATT TCCAATCATT TCTAAAACAT CTCAACAGTG AGCATGCGCT 240
GGACGATAGA AGTACAGCCC AATGTAGAGT ACAAATGCAG GTTGTACAGC AGTTAGAGCT 300
ACAGCTTGCA AAAGACAAAG AGCGCCTGCA AGCCATGATG ACCCACCTGC ATGTGAAGTC 360
TACAGAACCC AAAGCCGCCC CTCAGCCCTT GAATCTGGTA TCAAGTGTCA CTCTCTCCAA 420
GTCCGCATCG GAGGCTTCTC CACAGAGCTT ACCTCATACT CCAACGACCC CAACCGCCCC 480
CCTGACTCCC GTCACCCAAG GCCCCTCTGT CATCACAACC ACCAGCATGC ACACGGTGGG 540
ACCCATCCGC AGGCGGTACT CAGACAAATA CAACGTGCCC ATTCGTCAG CAGATATTGC 600
GCAGAACCAA GAATTTTATA AGAACGCAGA AGTTAGACCA CCATTTACAT ATGCATCTTT 660
AATTAGGCAG GCCATTCTCG AATCTCCAGA AAAGCAGCTA ACACTAAATG AGATCTATAA 720
CTGGTTCACA CGAATGTTTG CTTACTTCCG ACGCAACGCG GCCACGTGGA AGAATGCAGT 780
GCGTCATAAT CTTAGTCTTC ACAAGTGTTT TGTGCGAGTA GAAAACGTTA AAGGGGCAGT 840
ATGGACAGTG GATGAAGTAG AATTCCAAA ACGAAGGCCA CAAAAGATCA GTGGTAACCC 900
TTCCCTTATT AAAACATGC AGAGCAGCCA CGCCTACTGC ACACCTCTCA ATGCAGCTTT 960
ACAGGCTTCA ATGGCTGAGA ATAGTATACC TCTATACACT ACCGCTTCCA TGGGAAATCC1020
CACTCTGGGC AACTTAGCCA GCGCAATACG GGAAGAGCTG AACGGGGCAA TGGAGCATAAC1080
CAACAGCAAC GAGAGTGACA GCAGTCCAGG CAGATCTCCT ATGCAAGCCG TGCATCCTGT1140
ACACGTCAAA GAAGAGCCCC TCGATCCAGA GGAAGCTGAA GGGCCCCCTGT CCTTAGTGAC1200
AACAGCCAAC CACAGTCCAG ATTTTGACCA TGACAGAGAT TACGAAGATG AACCAGTAAA1260
CGAGGACATG GAGTGACTAT CGGGGCGGGC CAACCCCGAG AATGAAGATT GGAAAAAGGA1320
AA

```

## (2) INFORMATION ON SEQ ID NO. 614:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4458 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

```

GCCCCGGCGTT AACAAAGGGA GCCGATACCG ACCGGCGTGG GCGCGGAGCG GGCGGCCGCC 60
ACCGAGCGTG CTGAGCAACC GCAGCCTCCG CGGCCGAGAG TGCAGCGAGC AAGGGGACAA 120
AAAGTTCCGC AAAGCCCGCA CAACCAGCAC CACAGAGAGA AGGGAAGAAC GGCATCCAGC 180
CCACCAGAAA TGGACCGACA CACCTCAGCA TCTCCAAACC CCGCAGCACA CGTGACCATA 240
AACCAGCAAA GATGAGTTTT GATCATCCTG AGAAAAATGG GCCTTGGCCT GCAGACCCAA 300
TAAACCTTCC CTCCCATGGA TAATAGTGCT AATTCCTGAG GACCTGAAGG GCCTGCCGCC 360
CCTGGGGGAT TAGCCAGAAG CAGGCTTGTT TTCCTGCTCA GAACAAAGTG ACTTCCCTGA 420
ACACATCTTC ATTATGATTC ACACCAACCT GAAGAAAAAG TTCAGCTGCT GCGTCCTGGT 480
CTTTCTTCTG TTTGCAGTCA TCTGTGTGTG GAAGGAAAAG AAGAAAGGGA GTTACTATGA 540
TTCCTTTAAA TTGCAAACCA AGGAATTCCA GGTGTTAAAG AGTCTGGGGA AATTGGCCAT 600
GGGGTCTGAT TCCCAGTCTG TATCCTCAAG CAGCACCCAG GACCCCCACA GGGGCCGCCA 660
GACCCCTCGGC AGTCTCAGAG GCCTAGCCAA GGCCAAACCA GAGGCCTCCT TCCAGGTGTG 720
GAACAAGGAC AGCTCTTCCA AAAACCTTAT CCCTAGGCTG CAAAAGATCT GGAAGAATTA 780

```

CCTAAGCATG AACAAAGTACA AAGTGTCTTA CAAGGGGCCA GGACCAGGCA TCAAGTTCAG 840  
 TGCAGAGGCC CTGCGCTGCC ACCTCCGGGA CCATGTGAAT GTATCCATGG TAGAGGTCAC 900  
 AGATTTTCCC TTCAATACCT CTGAATGGGA GGGTTATCTG CCCAAGGAGA GCATTAGGAC 960  
 CAAGGCTGGG CCTTGGGGCA GGTGTGCTGT TGTGTCTGCA GCGGGATCTC TGAAGTCCTC1020  
 CCAACTAGGC AGAGAAATCG ATGATCATGA CGCAGTCCTG AGGTTTAATG GGGCACCAC1080  
 AGCCAACTTC CAACAAGATG TGGGCACAAA AACTACCATT CGCCTGATGA ACTCTCAGTT1140  
 GGTACCACA GAGAAGCGCT TCCTCAAAGA CAGTTTGTAC AATGAAGGAA TCCTAATTGT1200  
 ATGGGACCCA TCTGTATACC ACTCAGATAT CCCAAAGTGG TACCAGAATC CGGATTATAA1260  
 TTTCTTTAAC AACTACAAGA CTTATCGTAA GCTGCACCCC AATCAGCCCT TTTACATCCT1320  
 CAAGCCCCAG ATGCCTTGGG AGCTATGGGA CATTCTTCAA GAAATCTCCC CAGAAGAGAT1380  
 TCAGCCAAAC CCCCCATCCT CTGGGATGCT TGGTATCATC ATCATGATGA CGCTGTGTGA1440  
 CCAGGTGGAT ATTTATGAGT CCCTCCCATC CAAGCGCAAG ACTGACGTGT GCTACTACTA1500  
 CCAGAAGTTC TTCGATAGTG CCTGCACGAT GGGTGCCTAC CACCCGCTGC TCTATGAGAA1560  
 GAATTTGGTG AAGCATCTCA ACCAGGGCAC AGATGAGGAC ATCTACCTGC TTGGAAAAGC1620  
 CACACTGCCT GGCTTCCGGA CCATTCACTG CTAAGCACAG GCTCCTCACT CTTCTCCATC1680  
 AGGCATTAAA TGAATGGTCT CTTGGCCACC CCAGCCTGGG AAGAACATTT TCCTGAACAA1740  
 TTCCAGCCTG CTCCTTTTAC TCTAGGGGCC TCTGTGAGCA AGACCATGGG GACTTCAAGA1800  
 GCCTGTGGTG AGGAAATCAG GTCCAGCCTT CCCTGTAGCC AGACAGTTTA TGAGCCCCAG1860  
 GGCTCTGCTC ACACACATGC ACACATATCT AGCATTTCTT CCAGACAGCA TCCTCCCCGC1920  
 CTTCCACCTT GGTAGATGCA AGGTCTATCT CTCCCATCAG GGCTGCCAAA GCTGGGCTTT1980  
 GTTTTCCCA GCAGAATGAT GCCATTCTCA CAAACCAATG CTCTATATTG CTTNGAAGTC2040  
 TGCATCTAAA TATTGATTTT ACGNTTTTAA AGNAAATTCT NNCTTAAATT ACAATTGTGC2100  
 CCAATGCAGG GTGGNCTCTN NGGGGGGCAA GTAGGTGGTA CAGGGGATTG GAAACATCCT2160  
 CCGCGCCTCC AGAGAAAAGT TGCTCCCGAG GTCCATGCCC CTGGAACGTG TTCCTATCAC2220  
 TCTGGCTGGT TGGGCTGGTC CTTAGACTGG GTGCTTATGA TTAAAAGGGT CTTGGTTAAG2280  
 CCCACTTTCC CTCTCCATGT GGAGATGGAA GGTAGAGAAG GATACAGTGT CTATCCTCAA2340  
 GTTGCTACGG TTCAGTGAGA GAGGCAGACA TCTGAACAGG NCAGGTAGGA TTCAGTGTGC2400  
 TCAGTGCATG GGGGATTGG AGAGAGATGG GCTTGCTCTC TCTGTGCACC CAGGAGGGCC2460  
 ACGCATCTTA AACTGTGTTT GTGGATCAGA GAAGGCTTTA TAGCACAGGG GGCATTCCAG2520  
 TGAGTCTTAG AGGAAGAGAA GAAACATGGC AAGCAGATTA CATCTGAGCC GTTTGAATTG2580  
 TGTTTTTCTT TCTTCCCATG TTTATTTTCT AAGATCTACC TGAACCTAGN AGACTCAAGA2640  
 TATTTTTTTA GGAAACCTCC TACCCATGTC TGAGGTAGCA AGTGCAGCCT CACGACAGAT2700  
 ACCAGGCAAT CCAGAGCCAC AAAACGTGAT TCCTCCAGGC TCTGCCTGGC CTGACCCTGT2760  
 CCTGTGAGCT GGGTTTACAT ACCAGTCCCA TTCTTCCTTT TCAATACCTA CCCCCAAATC2820  
 TTCTCCTAAC CACCATCTGT TTTTTTTTGG TTAAGCATT TTTTGCTTTA AAAGCATCCT2880  
 GACCCCAATT TCTTTGAGCT CACGGGCCTT TTGCTGAAGG TCTCTCAGGG TGTAGTGGT2940  
 TGGCTCTCTG GACTTAACGT CACTCTCAGN AGGTCAGAAC CTTNGGAGAT CAGAAGTGA3000  
 TCTCACCAGG TGTGAGAGGT GTGGNTANGC AGATTGCAAT GCTCTGCACC TCTTNCCTTG3060  
 CAAGTGAGNC AACTTNCAGG NCTCTCTGGG NCAGAGGCTG GCCCACTGTA GTTTGCAGAC3120  
 ATGCTCTCCA GATGGNTTTT ACTAAGTCCC CTCTCCCTGN ATANGGGAAT CCTGNCTGGN3180  
 ACCAGCGCAN GCCCTNNGGT GTNGGANNGA GGTNAAAAG ACTTGNCACA GGNATACCA3240  
 AGTNCATGCT GNTAGANGCC AGGATTCCTA GACCCAGGGC TCTGCACTCT CAAGGCTGGC3300  
 CCCATGTGCT CAAGGGGGTC TAATGTTTGG GCTCCAAACT AACCATCTCG GAGCTGGGCT3360  
 CCTCATTTAC TGCCAAACCC TCAGNCTTAT GTAGCNTAGA AAGGGCCCTG GANGTGNAGA3420  
 AAGCCTGGAT TTTCAAATTG ATGCTCCCTT ACTNGACTAG NCTGTGCCAC TCNTGGGCAA3480  
 ATGCTCTTCC TTGAGCCTGT TTCCACACCT GTAAAGTGGG GATGATGATC CTATCTCACT3540  
 GCTTTTNGTG NAGGATTACA GGNAAAAGCA CCTGTCTGGG CTCTGTACCT GGCACGTAGT3600  
 ANGGTGCTCA GTTCATGCTG GTTTCCTTCC TGCTTTAGT AGGGACCTGC TCTGTGCTCA3660  
 CACCTCGGCT GCATGCACCC TGCTGTGACG GAGGCTAGTG TGGAAGAGGT CCTGTCTCA3720  
 GGGAAATTAAC TGTCTTATTG GGAGACAACA ACTGTCCCTC TTGGAACACC CAAGAAACCA3780  
 TGNCAAAGCA GTGGACAACA CAGAACACGN CCCTCCTCCT CGCTGCCTGC AGCTNCCAAT3840  
 CTGATTCTGC TTGGGAATGG GCGGANACAG NTGGGCTGCT TAACTGCTGT ATAGGACAAG3900  
 CCCCTTACCC CTCTCTGGGC CCATGAATTC CTGGCTTGGT TTATGTTCTG ATTTGACACA3960  
 CTGATTTTAA TTTTCGAATC ATGACACTGA GTGCAGAGGA GGTGGCATTG CGACAGCAGG4020  
 ACATACATGT TNGGTGTGAA GACTGGGACG AACTGGGTA GAATCTAGTT TTTAATTATT4080  
 ATTAATATAA AGGATCAAAAT TAATTTAAAT ATGAATCTGA AGTCCACAGA ACTTTNNNNN4140  
 AAGTGCTGTC CAGGCCAACA CTTTGGTAAA ATGCAAATTA TGATATGGAC GTTATCATTG4200  
 GTCTGGTGAG ATGTTTCATA TTTGTGACAG TTAATTTAAA AATTATGACT TAATGCTGCC4260  
 TGTGTCTATG GGGTTCTGTC TTCTTTGATA GCCATCTATT CATCTGGATC ATGGGACCCT4320  
 CTCTAATCCT TCCACCAATC AAATAAGCTA TTGCTATTGG TTTGGAGTTG AGATATCAGT4380  
 CTCGGAAACT TCTGAAAAAT GCTAATAATT ACCCAAGGAT TATGTCAAAT TTTAAAATAA4440  
 ATGTGTGTGT GTTTCTTT



## (2) INFORMATION ON SEQ ID NO. 615:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1562 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

```

TGGAGGCAGC TAGCGCGAGG GTGGGGAGCG CTGAGCCGCG CGTCGTGCCC TGCCTGCCCC 60
AGACTAGCGA ACAATACAGT CAGGATGGCT AAAGGTGACC CCAAGAAACC AAAGGGCAAG 120
ATGTCCGCTT ATGCCTTCTT TGTGCAGACA TGCAGAGAAG AACATAAGAA GAAAAACCCA 180
GAGGTCCCTG TCAATTTTGC GGAATTTTCC AAGAAGTGCT CTGAGAGGTG GAAGACGATG 240
TCCGGGAAAG AGAAATCTAA ATTTGATGAA ATGGCAAAGG CAGATAAAGT GCGCTATGAT 300
CGGGAAATGA AGGATTATGG ACCAGCTAAG GGAGCAAGA AGAAGAAGGA TCCTAATGCT 360
CCCCAAAGGC CACCGTCTGG ATTCTTCTTG TTCTGTTTCTG AATTCCGCCC CAAGATCAAA 420
TCCACAAACC CCGGCATCTC TATTGGAGAC GTGGCAAAAA AGCTGGGTGA GATGTGGAAT 480
AACTTAAATG ACAGTGAAAA GCAGCCTTAC ATCACTAAGA CGGCAAAGCT GAAGGAGAAG 540
TACGAGAAGG ATGTTGCTGA CTATAAGTCG AAAGGAAAGT TTGATGGTGC AAAGGGTCCT 600
GCTAAAGTTG CCCGGAAAAA GGTGGAAGAG GAAGATGAAG AAGACGGGGG GGGGGGGGGG 660
GGGGGGGGGG GGGGGACGTA TAGTCGGGTC GGCTGGTGGA GTAGCCCAA AGAAGGGGAG 720
CGCCGTAATT GACACATCTC TTATTTGAGA AGTGTCTGTT GCCCTCATT GGTTTAATTA 780
CAAAATTTGA TCACGATCAT ATTGTAGTCT CTCAAAGTGC TCTAGAAATT GTCAGTGGTT 840
TACATGAAGT GGCCATGGGT GTCTGGAGCA CCCTGAAACT GTATCAAAGT TGTACATATT 900
TCCAAACATT TTTAAATGA AAAGGCACTC TCGTGTTCTC CTCACTCTGT GCACTTTGCT 960
GTTGGTGTGA CAAGGCATT AAAGATGTT CTGGCATTCT CTTTTTATTT GTAAGGTGGT1020
GGTAACTATG GTTATTGGCT AGAAATCCTG AGTTTTCAAC TGTATATATC TATAGTTTGT1080
AAAAAGAACA AAACAACCGA GACAAACCTT TGATGCTCCT TGCTCGGCGT TGAGGCTGTG1140
GGGAAGATGC CTTTTGGGAG AGGCTGTAGC TCAGGGCGTG CACTGTGAGG CTGGACCTGT1200
TGACTCTGCA GGGGGCATCC ATTTAGCTTC AGGTGTCTTT GTTTCTGTAT ATAGTGACAT1260
AGCATTCTGC TGCCATCTTA GCTGTGGACA AAGGGGGGTC AGCTGGCATG AGAATATTTT1320
TTTTTTTAAG TGCGGTAGTT TTTAACTGT TTGTTTTTAA ACAAACTATA GAACTCTTCA1380
TTGTCAGCAA AGCAAAGAGT CACTGCATCA ATGAAAGTTC AAGAACCCTC TGTACTTAAA1440
CACGATTCGC AACGTTCTGT TATTTTTTTT GTATGTTTAG AATGCTGAAA TGTTTTTTGA1500
GTAAATAAAA CAGTATTACA TTTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA1562
AA

```

1562

## (2) INFORMATION ON SEQ ID NO. 616:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2278 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

```

GGCAATTTCC GTTAGGTGCT GAAGGCTGTG GCGCGCGGCT GTCCCCATTC CCACGTGAAG 60
CGCTACGCTA GCATCGCTCG GCTGGCGGCT CCCAGCTCGC CGCGGAGCAG TCCCGGCAGC 120
AGCGGGGGAC CGGAAGTGCG TCGCGGAGGC TCAGAAGCTA GTCCCGGAGC CCGGCGTGTG 180
GCGCCTCGGA GCACGGTGAC GCGCGCATGT CCCTAATCTG CTCCATCTCT AACGAAATGC 240
CGGAGCACCC ATGTGTATCC CCTGTCTCTA ATCATGTTTA TGAGCGGCGG CTCATCGAGA 300
AGTACATTGC GGAGAATGGT ACCGACCCCA TCAACAACCA GCCTCTCTCC GAGGAGCAGC 360
TCATCGACAT CAAAGTTGCT CACCCAATCC GGCCCAAGCC TCCCTCAGCC ACCAGCATCC 420
CGGCCATTCT GAAAGCTTTG CAGGATGAGT GGGATGCACT CATGCTGCAC AGCTTCACTC 480
TGCGCCAGAG CTGCAGACAA CCCGCCAAGA GCTGTACAC GCTCTGTACC AGCAGCATGC 540
CGCCTGCCGT GTCATTGCCC GTCTCACCAA GGAAGTCACT GCTGCCCGAG AAGCTCTGGC 600
TACCCTGAAA CCACAGGCTG GCCTCATTGT GCCCCAGGCT GTGCCAAGTT CCCAACCAAG 660
TGTTGTGGGT GCGGGTGAGC CAATGGATT TGGTGAGCTG GTGGGAATGA CCCAGAGAT 720
TATTCAGAAG CTTCAAGACA AAGCCACTGT GCTAACCACG GAGCGCAAGA AGAGAGGGAA 780
GACTGTGCCT GAGGAGCTGG TGAAGCCAGA AGAGCTCAGC AAATACCGGC AGGTGGCATC 840
CCACGTGGGG TTGCACAGTG CCAGCATTC TGGGATCCTG GCCCTGGACC TCTGCCCGTC 900
CGACACCAAC AAGATCCTCA CTGGTGGGGC GGATAAAAAT GTCGTTGTGT TTGACAAAAG 960
TTCTGAACAA ATCCTGGCTA CCCTCAAAGG CCATACCAAG AAGGTCACCA GCGTGGTGT 1020
TCACCTTCC CAGGACCTGG TGTTTTCTGC FTCCCCCGAT GCCACTATCA GGATTTGGTC 1080
GGTCCCAAT GCCTCTTGTG TACAGGTGGT TCGGGCCCAT GAGAGTGCTG TGACAGGCCT 1140
CAGCCTTCAT GCCACTGGCG ACTATCTCTC GAGCTCCTCC GATGATCAGT ACTGGGCTTT 1200
CTCTGACATC CAGACAGGGC GTGTGCTCAC CAAGGTGACA GATGAGACCT CCGGCTGCTC 1260
TCTCACCTGT GCACAGTTCC ACCCTGACGG ACTCATCTTT GGAACAGGAA CCATGGACTC 1320
TCAGATCAAG ATCTGGGACT TGAAGGAACG TACTAATGTG GCCAACTTCC CTGGCCACTC 1380
GGGCCCCATC ACTAGCATCG CCTTCTCTGA GAATGGTTAC TACCTGGCTA CAGCGGCTGA 1440
TGACTCCTCT GTCAAGCTCT GGGATCTGCG CAAGTTAAGA ACTTTAAGAC TTTGCAGCTG 1500
GATAACAAC TTAGGTTAAA GTCATGATC TTTGACCAGA GTGGTACCTA CCTGGCTCTT 1560
GGGGGCACGG ATGTCCAGAT CTACATCTGC AAACAATGGA CGGAGATTCT TCACTTTACA 1620
GAGCATAGCG GCCTGACCAC AGGGGTGGCC TTCGGGCATC ACGCCAAGTT CATCGCTTCA 1680
ACAGGCATGG ACAGAAGCCT CAAGTTCTAC AGCCTGTAGG CCCTGGCCCT TCTGATGGAA 1740
GCTGGGCCTC ATCTCAGTAG AGGGGTAGAA TTAGGGTTTG GGGGGGGTGG GGGGGAATCT 1800
ATGGGGGGAG GGGGCTCTGT GGGGTGGGAC ATTACATCA TTTCACTCTG GTCTGAGTGG 1860
TGGCCTGAGA ACCATGGTGG CATGGACCAC CCTCATCCAT GCAACTCCAG GCCCCATGGG 1920
AACGGATGTG GAAGGAAGAA CTGTCACCTT CTTAAGGCCC AGGGTCGGAG CCCAGGGCCT 1980
CTCCCTTCTT GTCGTTCAAT GGACGTGGTG GTGGCTGTTT CACACCCATT TTGTTGCAGT 2040
TCCTGTGAGA CAGGAGAGGC TGAGCCAAGG GAACTGTGAA GGGGATGGGC AGGAGGGCTT 2100
GTGCAGGGTT TTGTAAGCAG TGATCTAGTT TCATTAAAAA AAGAAAACAA TAACCATAAC 2160
CACCTCCCCG TGTCTGTCTG CACCAGGAGC ACCTGGGACT GGGGAAGTCAA GGGGAGGGAG 2220
CACACACTGG GACACTGGCT TCCGGGAAGC CCATCTTCCT TTCCTTTCAC AGCTCTTA 2278

```

## (2) INFORMATION ON SEQ ID NO. 617:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 931 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

```

CAGGGGCGTG CAGCCCGCTT GCCAATCAGA GCGCGGCTGA GCGGCCCCGC AGCCAACCCC 60
CGAGGAGCGG CCGGCTGGCG TCCGCCGCGC CCAGGAGTTG GGGATGTCCT ACAAACCCAT120
CGCCCCTGCT CCCAGCAGCA CCCCTGGCTC CAGCACCCCT GGGCCGGGCA CCCCAGTCCC180
TACAGGAAGC GTCCCGTCGC CGTCGGGCTC AGTGCCAGGA GCCGCGCTC CTTTCAGACC240
GCTGTTTAAC GACTTTGGAC CGCCTTCCAT GGGCTACGTG CAGGCGATGA AGCCACCCGG300
CGCCCAGGGC TCCCAGAGCA CCTACACGGA CCTGCTGTCA GTCATAGAGG AGATGGGCAA360
AGAGATCCGG CCTACCTATG CTGGCAGCAA GAGCGCCATG GAGCGCCTGA AGAGAGGTAT420
CATCCATGCC CGGGCCCTAG TCAGAGAGTG CCTGGCAGAG ACAGAGCGGA ACGCCCGCAC480
GTAACAGGAA GCGCCTCGGC CTCAGCGTCT GGACCTATCC GGCCACTGCA GAGCACCCGC540
TTCTCCCTGG CCTTCATCCC GAGTTGCACT AACCATCCTG GGCTTCCTGT CCTGTGTCCC600
TTGGTGGGTC CCCTCCAGGA ACCAAGGAGT GGCCCTCCAG GTGGCAGCAC TAAGGACACC660
CCCCACAAC AAGAGTTAGC AGCGAGGTCC GCATGAGTCC CACCCATGAC CTGCCGACAG720
TGTTGCCCCA CGGAACTTTT GTGGCCCCTA CCGCTCAGCC CTTCCCAGCA CTTCTCCCAC780
TTTGTCCCGA GCCTCCTTCT CGCCCAGCAG GGGCACAGGC CTGGCACCTC CCTGCCTTGT840
GTCCTGAGCC ATAGTGACTC TTTTATCTGT GTGTCTTTTG CTAAATATGC CCTTTTTATA900
TTAATAAAAG ATGATTTGGA GTTGTGCTCT C

```

931

## (2) INFORMATION ON SEQ ID NO. 618:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 447 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

```

ELPSSPPFGL PEVAPDATST GLPDTPAAPE TSTNYPVECT EGSAGPQSLP LPILEPVKNP 60
CSVKDQTPLQ LSVEDTTSPN TKPCPPTPTT PETWGGGGGG APSSTPCSAH LTPSSLFPSS120
LESSSEQKFY NFVILHARAD EHIALRVREK LEALGVDPGA TFCEDFQVPG RGELSCLQDA180
IDHSAFIILL LTSNFDCLRS LHQVNQAMMS NLTRQGSFDC VIFFLPLESS PAQLSSDTAS240
LLSGLVRLDE HSQIFARKVA NTFKPHRLQA RKAMWRKEQD TRALREQSQH LDGERMQAAA300
LNAAYSAYLQ SYLSYQAQME QLQVAFGSHM SFGTGAPYGV RMPFQGQGPL GAPPPFPTWP360
GCPQPPPLHA WQAGTPPPPS PQPAAFPQSL PFPQSPAFPT ASPAPPQSPG LQPLIIHHAQ420
MVQLGLNNHM WNQRGSQAPE DKTQEAE                                     447

```

## (2) INFORMATION ON SEQ ID NO. 619:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 205 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

```

ADAGGGTERS LLSLPPELLV LPGTDGAAPG GFWEPHVIWD WGALWGQNAL WGPAGPGSPA 60
TLSHLAGVPA AATPARMAGW HPPTALPTAS SLSTVTALPA VPSLPYGLTR TPSEPRATP120
HYPPRTDGTG GAEQPHVEPE RVPGARGQDA GGRMTACPCL TTWGTPLDPG IGQDPIEH180
LPCALWTVED EVICHFQDIV REPFI                                     205

```

## (2) INFORMATION ON SEQ ID NO. 620:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 409 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

```

KSRLSVTLMP VQLSEHPewn ESMHSLRISV GGLPVLASMT KAADPRFRPR WKVILTFEFG 60
AAILWLLCSH RPAPGRPPTH NAHNWRLGQA PANWYNDTYP LSPPQRTAG IRYRIAVIAD120
LDTEPTAQDE NTWRSOLKKG YLTLSDSGDK VAVEWDKDHG VLESHLAEG RGMELSDLIV180
FNGKLYSDD RTGVVYQIEG SKAVPWVILS DGDGTVEKGF KAEWLAVKDE RLYVGGLGKE240
WTTTGDVVN ENPEWVKVVG YKGSVDHENW VSNYNALRAA AGIQPPANLI HESACWSDTL300
QRWFFLPRA SQERYSEKDD ERKGANLLS ASPDFGDIIV SHVGAVVPTH GFSSFKFIPN360
TDDQIIVALK SEEDSGRVAS YIMAFTLDGR FLLPETKIGS VKYEGIEFI 409

```

## (2) INFORMATION ON SEQ ID NO. 621:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 249 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

```

KLSPDGLAQC FRFELNELDA FVFHASDLGL RQOEAPVQRE GHDVGGDSAA VLLGFEGHND 60
LVVGVGDELE GREAVSGDHR PDVAHSDVAE VRGGAQQQVG ALALVVLLAV ALLAGAARQE120
EPALQRVTPA GRMLDEVSWR LDAGSSPQGV VVGHPVLVH AALVAHHLHP LRVLVHHITR180
SGRPLLAQAA HVQTLVLHCQ PFGLEAFLHG AVAVGQNHG HGFAAFDLVD DPRPVIHGVE240
FPIENNQVG 249

```

## (2) INFORMATION ON SEQ ID NO. 622:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 255 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

```

AAPVSLHDA AGDLRRDPGG GGGGGVPHGG GEGQEVVPAE PGVPAPQHA E PVAAGAAQQ 60
LQTEEQPGLQ RLRLGPFVGA ARGGDARVRG PRGDRRVNPE SARALLPGDP QGPGTAAPRA120
LGLPPRCEPV GAPLAALALA RERRERGRFP RPCKCLFFNS SQCELCCECV RGGAPALSRR180

RVATPCPCPM VCNSDFAHRS TVPPSAHPFT LTPTLSLNTF IIVRRGRWDF GRSAAATASG240
GLIFIFALRW LKAFT                                     255

```

## (2) INFORMATION ON SEQ ID NO. 623:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 196 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

```

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIKVFSE SVGVSVNGCA LGGTVERCAK 60
SELQTIGQGH GVATRRRLSA GAPPRTHSQQ SSHWHEELKNK HLQGRGKRPR SRRSRARASA120
ARGAPTGSQR GGSPSARGAA VPGPCGSPGS RARALSGFTR RSPRGPRTRA SPPRAAPLTG180
PSRSRWSPGC SSVCS C                                     196

```

## (2) INFORMATION ON SEQ ID NO. 624:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 242 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

```
VESHRAHATH TTVRSPETAR GWKPWPHRLS RYVHSPGRQP HGHGQHLFC SGRRAFGGHP 60
RQGARASLLA LGLENSPGGS SPEERLGRLA VAGPPRGAQN VSQAGPEAEA PPLRFGHAWG120
AQTPRLGAPG PWTPLPTLPS HIPFFWSQTP AQRKEGFTEE GQGRAWPQGG DEDISGPGSC180
RLLWEEEPVCV CKLLGLAARP TAGPSLDPCT WPSSCPLAAP GLGTGIEPRG LGWLGGQRDR240
EG                                         242
```

(2) INFORMATION ON SEQ ID NO. 625:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 216 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

```
GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSRQKARA EPGPREGMRT 60
FPVQVAAGCS GRKSHASVNC WGWRRPAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120
WARAGTGRGS TSDPDVGWLC PPRREAQOTS YTKAKSTIGE PRSHFMGRRP RPQGPQSKAR180
GRFIPEDSPP GAAPAWGGVS RPLGCLSVCG TPWSTP                               216
```

(2) INFORMATION ON SEQ ID NO. 626:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 299 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

PGISVSVDKM ESSPFNRRQW TSLSLRVTA ELSLVNKNKS SAIVEIFSKY QKAAEETNME 60  
 KKRSTENLS QHFRKGTITV LKKKWENPGL GAESHTDSL NSSTEIRHRA DHPPAEVTSH120  
 AASGAKADQE EQIHPRSLR SPPEALVQGR YPHIKDGEDL KDHSTESKMM ENCLGESRHE180  
 VEKSEISENT DASGKIEKYN VPLNRLKMMF EKGEPTQTKI LRAQSRASG RKISENSYSL240  
 DDLEIGPGQL SSSTFDSEKN ESRRNLELPR LSETSIKDRM AKYQAAVSKQ SSSPTIPMS 299

(2) INFORMATION ON SEQ ID NO. 627:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 94 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

DSAPSPGFSH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLLT60  
 RESSLAVTLN DSEVHCRLN GDDSILSTDT EIPG 94

(2) INFORMATION ON SEQ ID NO. 628:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 765 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

```

IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTFFNFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEIVDWWSK FDASSGEHEK CGQYIQKGY180
KLKIYNCELE NVAEFEGLTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPEQCTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
TLNPFVFGMY ELSCYLPQEK DLKISVYDYD TFTRDEKVG E TIIDLENRFL SRFGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDGS RIRYGGRDYS LDEFANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYYLRLVIWN TKDVILDEKS ETGEEMSDIY VKGWIPGNEE NKQKTDVHYR540
SLDGEGNFW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPRLLIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPCL DLPNRPETSF LWFTNPCKTM720
KFIVWRRFKW VIIGLLFLLI LLLFVAVLLY SLPNYLSMKI VKPNV 765

```

## (2) INFORMATION ON SEQ ID NO. 629:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 289 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

```

ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFLGFPG120
CDVERRAWWP QTLGENIHPH LKESLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSKPLFRG180
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240
NTVLLWYAAV GPKAGKESVF QINNCFSYFF IPGKGVIID RNFQVFFLR 289

```

## (2) INFORMATION ON SEQ ID NO. 630:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 824 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

```

RVSVLAAASS ALPVAPREAG VTNWPAGCVP EVRSTGEKEV AKTLHRRSRP EWCGARDPPA 60
MLLFVLTCLL AVFPAISTKS PIFGPPEVNS VEGNSVSITC YYPPTSVNRH TRKYWCRQGA120
RGGCITLISS EGYVSSKYAG RANLTNFPEN GTFVVNIAQL SQDDSGRYKC GLGINSRGLS180
FDVSLEVSQG PGLLNDTKVY TVDLGRVTI NCPFKTENAQ KRKSLYKQIG LYPVLVIDSS240
GYVNPNYTGR IRLDIQGTGQ RLFSVVINQL RLSDAGQYLC QAGDDSNSENK KNADLQVLKP300
EPELVYEDLR GSVTFHCALG PEVANVAKFL CRQSSGENCD VVVNTLGKRA PAFEGRILLN360
PQDKDGSFSV VITGLRKEDA GRYLCGAHSD GQLQEGSPIQ AWQLFVNEES TIPRSPTVVK420
GVAGGSVAVL CPYNRKESKS IKYWCLWEGA QNGRCPLLVD SEGWVKAQYE GRSLLEEPG480
NGTFTVILNQ LTRDAGFYW CLTNGDTLWR TTVEIKIIEG EPNLKVPNGV TAVLGETLKV540
PCHFPCKFSS YEKYWCKWNN TGCQALPSQD EGPSKAFVNC DENSRLVSLT LNLVTRADEG600
WYWCQGVKQGH FYGETAAVYV AVEERKAAGS RDVSLAKADA APDEKVLD SG FREIENKAIQ660
DPRLFAEEKA VADTRDQADG SRASVDSGSS EEQGGSSRAL VSTLVPLGLV LAVGAVAVGV720
ARARHRKNVD RVSIRSYRTD ISMSDFENSR EFGANDNMGA SSITQETSLG GKEEFVATTE780
STTETKEPKK AKRSSKEEAE MAYKDFLLQS STVAAEAQDG PQEA 824

```

(2) INFORMATION ON SEQ ID NO. 631:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 267 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

```

ADIAGPRCLP LFNCHIDGCS LSIEVALLHS TPVPALISPG HQVQGQGD KP AVLVTVHEGL 60
AGAFVLAGQG LAARVIPLAP VFLVRGEFAW KVTGDLESLS QHSRDIPWYL EVWFSFDNLD120
LHGGPPESIA VGQTPVEAGV PAGELVEDDS EGAVAWLLQQ GEALVLGLN PPLAVHQQA180
AAILGPFPEP PVLDAFAFLT VVGAEHGHR SCHPLHSGA AGNRGLLIDE ELPGLDORRAF240
LQLTIRMGST QVAPCILLPQ ACDHTE 267

```

(2) INFORMATION ON SEQ ID NO. 632:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLLPC 60  
THLPWWAGFS LLGSTLPSPV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120  
GQKEVACGNL RSPHPRFPKR 140

(2) INFORMATION ON SEQ ID NO. 633:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 127 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSGSSE SQEPRMRALC 60  
SPSSKTQGSP PRKGAHVPRQ GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120  
DLFSGCK 127

(2) INFORMATION ON SEQ ID NO. 634:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

HHQKHMQGKG SYWASGLLSP WLGRKGREDG WGSLEFGIDDV HEFGLEGSTT HKEAIIHRLA 60  
 QLLAGCPSH RASINDTGAL SHRIDVGLQ PSSELLVYFL GLLGCCSLAS TNGPHRLIGQ120  
 DDLAPVLHVI CDDLLVWVEG 140

## (2) INFORMATION ON SEQ ID NO. 635:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 101 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

KVIADNVKDW SKVVLAYEPV WAIGTGKTAT PQQAQEVHEK LRGWLKSNVS DAVAQSTRII 60  
 YGGSVTGATC KELASQPDVD GFLVGGASLK PEFVDIINAK Q 101

## (2) INFORMATION ON SEQ ID NO. 636:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 329 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

DSIFPLWAVL ALSPPGIRVR MKKSSVSGMT AAGVVWGEA EGKAALRLGV EFLEVWGGGR 60  
 VFNLEKSQPA RAERECERGS SEGARNVGG SGGRSVAVAL VHQHGVRLLG DLQQRVHVGA120  
 APAPQVAGLP PLRAALVVVG AHLHHLGGLE HFHLALADLL DVEGEGWHLV DRGLGARVHH180  
 VVGREGFAQL VPRRLQFLAP LGGHQARAQL VHALLOGVPR LLQVFLGLEA RLLQVLAGTH240  
 LGLLHLLLGE GLLEVHAPQ ALRLIRSARD SSITSSTSTA SSDESSSAAA SSSGRSPSPS300  
 SSPSFSGSAS DSFSDLLMLS LAGSFTSSW 329

## (2) INFORMATION ON SEQ ID NO. 637:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 263 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

```
GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60
TQAQLEERQA EMEGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSRLER120
QAGQIKKLEV NEAELLRRRN FKVMYQDEV KLPKLSISK SLKESEALPE KEHEELGE180
RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSTRPSPRRR WRRPRCVPAR240
TWRRRASRPR KTWRRRGTPW RSA 263
```

## (2) INFORMATION ON SEQ ID NO. 638:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

```
SGDLRLLVDT SKVQEAWVPS QDTHHTQELL AVQGSLSVSGY RPPGGGFGAAP VHEDPHLLGP 60
ASRGAPETAA FFFFFFFFEP EQHLRVGLLL LPPRLSPRPG PAWPVPNPVG WPGHLHQGGQ 120
LLAGTNKPFH LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLXTPQQLXG PRXXFPXAVQ 180
ASPXPGVCSL AWVELCHIXD KQXGG 205
```

## (2) INFORMATION ON SEQ ID NO. 639:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

```
PVTPRDXPGA GGSXEGPMQ HPGQSRPXPL AXPAPXWXL APCGALTCWA RLXLGLSAPX 60
LLIXDVTELD PSQAAHSWTW ASLHCXGKXX PRAXKLLRGX EAGAHPOASV FSAPPCPRFR120
ASVHREHHHH GQVEGFISPC QQLSSLVQVA WPAHWIGDGP GWARSGAQSG R 171
```

## (2) INFORMATION ON SEQ ID NO. 640:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

```
ISRNEGVLVR GPKSPRSLLR SHSEPPALVL WRDHRLVPGT DYCKDTALVP TEKNTGQQEH 60
TFSQYLATPH SELTITHGKW VHSSLWSDPA GLGRQEQHSS SSLSPRQRES LNCKRSGAYT120
VREKEKGGRK GFSPPRPRDA HREGGKEREK SVLESEATLS K 161
```

## (2) INFORMATION ON SEQ ID NO. 641:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 127 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAYRTEKWKS HTPVCSPEVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60  
RGSTGQPTAN TAASLVASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120  
HHCIPNR 127

(2) INFORMATION ON SEQ ID NO. 642:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 136 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

WGXHRVRVVG WXRKPMKXGI PPEXHGPITA DGHRLXXLP PXGXRCXXAD PKGXGLXALF 60  
XKXPPXEXCL LSXXPPXPVT HRAGMEFNGX FWXXTLVHGQ TSLXGYXTR LKXKIVCCHS120  
SGXWSVCG LH RFHRNQ 136

(2) INFORMATION ON SEQ ID NO. 643:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

GRXSRAWGLG CPSLLSPISL RLPVPPPRPP NLRPPATPGA PTXPXQNTAX LKXLLSXX 60  
LSGLGLMGXR AGTCTWAXE AHEDXDTPRV PWTXYXRWSS XPXAIATGX SLXXGRPQRE120  
XPXRVVXKXT TX 132

## (2) INFORMATION ON SEQ ID NO. 644:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

```

GVETTANSST SLRSTTLEKE VPVIFIHPLN TGLFRIKIQG ATGKFNMVIP LVDGMIVSRR 60
ALGFLVRQTV INICRRKRLE SDSYSPMSA GNRKSPTLST STGTSSWSQS FILHFSRRLD120
SRTAVLRPLN F                                     131
  
```

## (2) INFORMATION ON SEQ ID NO. 645:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

```

LTNMSOHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLP RCYFSAGIKL LXVARPRTSK60
DSCYSATVYT AHLSSHVLS SLVRLF                                     86
  
```

## (2) INFORMATION ON SEQ ID NO. 646:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60  
LRSGVLRKFL EPKIRRNPGI SFLRSKMYQ LRPGEH 96

(2) INFORMATION ON SEQ ID NO. 647:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 92 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

SSACRCTTRS TGQQAASGR CGGPRGWGPS TGATPRQLTM NIPFQSIHFI TYEFLQEQVN60  
PHRTYNPQSH IISGGLAGAL AAAARGPLOW LR 92

(2) INFORMATION ON SEQ ID NO. 648:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 280 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

AVGSAALFKD GGGGTSAAEA GAAGQRLRSV NCLAYDEAIM AQQDRIQQEI AVQNPLVSR 60  
LELSVLYKEY AEDDNIYQK IKDLHKKYSY IRKTRPDGNC FYRAFGFSL EALLDDSKEL120  
QRFKAVSAKS KEDLVSQGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180  
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDHIHII ALAQALSVSI240  
QVEYMDRGEG GTTNPHIFPE GSEPKVYLLY RPHGYDILYK 280

## (2) INFORMATION ON SEQ ID NO. 649:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 244 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

DHLQPQKNLC TCLAPGRGGQ QGSSGLEPAL FVEDIVVSRP VEKVDLGLGA LREDVRIGGA 60  
 ALAAVHVLHL DGHAEGLGQR NDVDVVALLA HGLHLLLAEL LDSPSTLDEV LEELALALQV120  
 ARGEQPQVDH KVVGGALVIE GGQQVGDRGL LLHLLNQVHE RVVEILNCEF SEALGHQVFL180  
 ALGRHSLEPL QLLAVIQQCL QVGESESPIE TVAVRPGAD VRVLFVEVLD LLLIDVVIFS240  
 ILLV 244

## (2) INFORMATION ON SEQ ID NO. 650:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 424 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

LTTTCVSSSA PSKTS LIMNP HASTNGQLSV HTPKRESLSH EEHPHSHPLY GHGVCKWPGC 60  
 EAVCEDFQSF LKHLNSEHAL DDRSTAQCRV QMQVVQLEL QLAKDKERLQ AMMTHLHVKS120  
 TEPKAAPQPL NLVSSVTLSK SASEASQSL PHTPTTPTAP LTPVTQGPSV ITTSMHTVG180  
 PIRRRYSOKY NVPISADIA QNQEFYKNAE VRPPFTYASL IRQAILESPE KQLTLNEIYN240  
 WFTRMFAYFR RNAATWKNV RHNLSLHKCF VRVENVKGAV WTVDEVEFQK RRPQKISGNP300  
 SLIKMQSSH AYCTPLNAAL QASMAENSIP LYTTASMGNP TLGNLASAIR EELNGAMEHT360  
 NSNESDSSPG RSPMQAVHPV HVKEEPLDPE EAEGPLSLVT TANHSPDFDH DRYEDEPVN420  
 EDME 424

## (2) INFORMATION ON SEQ ID NO. 651:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 117 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

STNAGCTAVR ATACKRQRAP ASHDDPPACE VYRTQSRPSA LESGIKCHSL QVRIGGFSTE 60  
 LTSYSNDPNR PPDSRHPRPL CHNHQHAGH GTHPQAVLRQ IQRAHFVSRY CAEPRIL 117

## (2) INFORMATION ON SEQ ID NO. 652:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 426 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

PEAGLFSCSE QSDFPHEIFI MIHTNLKKKF SCCVLVLLF AVICVWKEKK KGSYYDSFKL 60

QTKEFQVLKS LGKLAGSDS QSVSSSSTQD PHRGQTLS LRGLAKAKPE ASFQVWNKDS120  
 SSKNLIPRLQ KIWKNYLSMN KYKVSYPGPG PGIKFSAEAL RCHLRDHVNV SMVEVTDFFP180  
 NTSEWEGYLP KESIRTKAGP WGRCAVVSSA GSKSSQLGR EIDDHDAVLR FNGAPTANFQ240  
 QDVGTKTTIR LMNSQLVTE KRFLKDSLYN EGILIVWDPS VYHSDIPKWY QNPDYNFFNN300  
 YKTYRKLHPN QPFYILKPOM PWELWDILQE ISPEEQPNP PSSGMLGIII MMTLCDQVDI360  
 YESLPSKRKT DVCYYYQKFF DSACTMGAYH PLYEKNLVK HLNQGTDEDI YLLGKATLPG420  
 FRTIHC 426

## (2) INFORMATION ON SEQ ID NO. 653:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 139 amino acids  
 (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

```
RCVQGSHEFVL SRKTSLLLAN PPGAAGPSGP QELALLSMGG KVYWVCRPRP IFLRMKTHL 60
CWFMVTCAAG FGDAEVCRSI SGGLDVLPF SLWCWLCGLC GTFCPLARCT LGRGGCGCSA120
RSVAAARSAP TPVGIGSLC                                     139
```

(2) INFORMATION ON SEQ ID NO. 654:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 243 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

```
WRQLARGWGA LSRASCPALP RLANNTVRMA KGDPKKPKGK MSAYAFFVQT CREEHKKKNP 60
EVPVNFAEFS KKCSEWKTMT SGKEKSKFDE MAKADKVRD REMKDYGPAK GGKKKKDPNA120
PKRPPSGFFL FCSEFRPKIK STNPGISIGD VAKKLGEMWN NLNDSEKQPY ITKTAKLKEK180
YEKDVADYKS KGKFDGAKGP AKVARKKVEE EDEEDGGGGG GGGGGTYSRV GWWSSPKEGE240
RRN                                     243
```

(2) INFORMATION ON SEQ ID NO. 655:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 110 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

TEQEESSRRWP FGSIRILLLL ASLSWSIILH FPIIAHFICL CHFIKFRFLF PGHRLPPLRA 60  
LLGKFRKIDR DLWVFLLMFF SACLHKEGIS GHLALWFLGV TFSHPDCIVR 110

(2) INFORMATION ON SEQ ID NO. 656:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 356 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

VGCSHAAQLH SAPELQTTRO ELSHALYQHD AACRVIA RL T KEVTAAREAL ATLKPQAGLI 60  
VPQAVPSSQP SVVGAGEPMD LGELVGMTPE IIQKLODKAT VLTTERKKRG KTVPEELVKP120  
EELSKYRQVA SHVGLHSASI PGILALDLCP SDTNKILTGG ADKNVVVFDK SSEQILATLK180  
GHTKKVTSVV FHPSQDLVFS ASPDATIRIW SVPNASCVQV VRAHESAVTG LSLHATGDYL240  
LSSSDQYWA FSDIQTGRVL TKVTDETS GC SLTCAQFH PD GLIFGTGTMD SQIKIWDLKE300  
RTNVANFP GH SGPITSIAFS ENGYYLATAA DDSSVKLWDL RKLRTLRLCS WITTLR 356

(2) INFORMATION ON SEQ ID NO. 657:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 240 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

LAQIPELDRG VISRCSQVVT ILREGDASDG ARVAREVGHI STFLQVPDLD LRVHGSCSKD 60  
 ESVRVELCTG ERAAGGLICH LGEHTPCLDV RESPVLIIGG AQEIVASGMK AEACHSTLMG120  
 PNHLYTRGIG DRPNPDSGIG GSRKHQVLGR VKHHAGDLLG MAFEGSQDLF RTFVKHNDIF180  
 IRPTSEDLVG VGRAEVQGD PRNAGTVQPH VGCHLPVFAE LFWLHQLLRH SLPSLLALRG240

(2) INFORMATION ON SEQ ID NO. 658:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 162 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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 (A) ORGANISM: HUMAN

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 (A) LENGTH: 148 amino acids  
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 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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 (A) ORGANISM: HUMAN

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WO 99/55858

PCT/DE99/01258

**Claims**

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-88, 90-96, 98-120, 123-140, 142-144, and 597-617,

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-157, 597-617, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID Nos. 1-157 and 597-617, characterized in that they are expressed elevated in pancreas tumor tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-157 and 597-617 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.



16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-157 and 597-617, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 158-596 and 618-659.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 158-596 and 618-659 as tools for finding active ingredients against the pancreas tumor.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-157 and 597-617 for expression of polypeptides that can be used as tools for finding active ingredients against the pancreas tumor.

29. Use of nucleic acid sequences Seq. ID Nos. 1-157 and 597-617 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 158-596 and 618-659 as pharmaceutical agents in gene therapy for treatment of the pancreas tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 158-596 and 618-659 for the production of a pharmaceutical agent for treatment of the pancreas tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 158-596 and 618-659.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-157 and 597-617.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

09/674266

526 Rec'd PCT/PTO 30 OCT 2000

## Sequence Listing

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<211> 2155

<212> DNA

<213> homo sapiens

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<213> homo sapiens

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1743

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<213> homo sapiens

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<212> DNA

<213> homo sapiens

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<211> 2279

<212> DNA

<213> homo sapiens

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<211> 761

<212> DNA

<213> homo sapiens

<400> 17

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<212> DNA

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<211> 1702

<212> DNA

<213> homo sapiens

<400> 19

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<212> DNA  
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<212> DNA  
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<400> 21

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<400> 22

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<211> 1259

<212> DNA

<213> homo sapiens

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<212> DNA

<213> homo sapiens

<400> 24

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agcagcgca gggcaccatc caggtgcagg gccaggccct cttcttccga gaggccctgc 180
ccggcagtg gacaggtcgc ttctctgtac tgctgctgca tggatttcgc ttctcctccg 240
```



```

agacctggca gaacctgggt acactgcaca ggctggccca ggctggctac cgggctgtgg 300
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cggggcaccg ctgttacctg gacaaaccag aggagtggca tacagggctg ctggacttcc 720
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c
1021

```

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<210> 25
<211> 1407
<212> DNA
<213> homo sapiens

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<400> 25
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1407

```

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<210> 26
<211> 286
<212> DNA
<213> homo sapiens

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<400> 26
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ctctcggtc cgcctggcag cagctccgcc gccagaggc gtccgagacc ctccgactcg 60
tgggtacgca taggcctcgc cagcgagcct tgcccaggca acgagtcgcc agcccggccc 120
ctcgccgcgg gctaggtctc acctcgccac cagtacgtct tggacaagta gtgccaggct 180
tgatgccggg tgtggtgagt gccgccggga cccaggtgcg ccgcctcgat gaggtcccgg 240
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286

```

```

<210> 27
<211> 815
<212> DNA

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<213> homo sapiens

<400> 27

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agttcgccac ttccggttct cctgggtatc caatagcatc gagtggagca tccccggaag180
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gttgatctat accctgtttc cgaattctgc cgtgtgtatc cccaaccctt gacccaatga720
caccaaacac agtggttttg agctcgggat tatatatatt tttctcatta aaggtttaaa780
acaaaaaaa aaaaaaaaaa aaaaaaaagt cgacg                                     815
```

<210> 28

<211> 548

<212> DNA

<213> homo sapiens

<400> 28

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agccatcgca atgcaaaaat aaatatcaat cctccagacg cagtagcagc cgcgctgcgc180
ccaaagtccc aacggccacg cctaacaatt ataaaagtgt tcagcgagag tgttggcggt240
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cgcacacact cacagcagag ttgcactgg gaagagttaa aaaataaaca tttacaagga420
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ccgaccgggt cgcagcgggg cgggagtcgc aagcgcgccg ggagcgggcg gtccccgggtc540
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```

<210> 29

<211> 493

<212> DNA

<213> homo sapiens

<400> 29

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tctgccacgc ctggctgatc tggactggag agtggatatc aaaacctcct cagacagcat420
cagccgcatg gccgttgccc cacctggcct ggttcagat ggaaggttcc aaggaggttc480
ccaggctatg ggg                                     493
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<210> 30

<211> 1063

<212> DNA

<213> homo sapiens

<400> 30

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cgctcgagg tcccgaggag cgcagactgt gtccctgaca atgggaacag ccgacagtga 120
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tgagatggcc	ccggaggccc	cacagcacac	ccacatcgat	gtgcacatcc	accaggagtc	180
tgccttggcc	aagctcctgc	tcacctgctg	ctctgcgctg	cgccccggg	ccaccaggg	240
caggggcagc	agccggctgc	tgggtggcctc	gtgggtgatg	cagatcgctg	tggggatcct	300
gagtgcagtc	ctaggaggat	ttttctacat	ccgcgactac	accctcctcg	tcacctcggg	360
agctgccatc	tggacagggg	ctgtggctgt	gctggctgga	gctgctgcct	tcatttaaga	420
gaaacggggt	ggtacatact	gggccctgct	gaggactctg	ctagcgctgg	cagctttctc	480
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gctcttcaac	agccccagtt	atcctggccc	catgaccgtg	gccacagccc	tgctccagca	960
gcacttgccc	attccttaca	ccccctcccc	atcctgctcc	gcttcatgtc	ccctcctgag	1020
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<210> 31

<211> 472

<212> DNA

<213> homo sapiens

<400> 31

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cgtttggggg	gaacaacccg	ttcttgccctc	aggccagctg	cctccaggcc	aagagggatc	180
cttcaccctg	gtctggaccc	gtgcactctc	tccgactctc	gggcaagtgc	ttcagcctgg	240
tggagtccac	gtacaagtat	gagttctgcc	cgttccacaa	cgtgacccag	cacgagcaga	300
ccttccgctg	gaacgcctac	agtgggatcc	tccgcatctg	gcacgagtgg	gagatcgcca	360
acaacacctt	cacgggcatg	tggatgaggg	acggtgacga	ctgccgttcc	cggagccggc	420
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<210> 32

<211> 2568

<212> DNA

<213> homo sapiens

<400> 32

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tcttgcaaaa tactaaaaat ctgctcaatg taatttctgt ggtttctatt cagcttgggt2520
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```

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<210> 33
<211> 239
<212> DNA
<213> homo sapiens

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<400> 33

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cgcgccggca ggtgcagcga agatgaagggt ggtggaggag cccaacgcgt ttgggtgagc120
agcctcgcgg gctggcggct cgagcggggg acggcccggg cccgttcccc gctgaccttg180
ccgcttcccc taggtggaac aaccgcttct tgcctcaggc cagtcgcctc caggccaag 239

```

```

<210> 34
<211> 482
<212> DNA
<213> homo sapiens

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<400> 34

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aa

```

482

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<210> 35
<211> 641
<212> DNA
<213> homo sapiens

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<400> 35

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tgtagacaag atggaatcat ctccatttaa tagacggcaa tggacctcac tatcattgag180
ggtaacagcc aaagaacttt ctcttgtaa caagaacaag tcatcggtta ttgtggaaat240
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```

gaacccaggg ctgggagcag agtctcacac agactctcta cggaacagca gcaactgagat420
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agctgaccaa gaagaacaaa tccaccccag atctagactc aggtcacctc ctgaagccct540
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aagtaaaaaa atggaaaatt gtctaggaga atccaggcat g
641

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<210> 36  
 <211> 381  
 <212> DNA  
 <213> homo sapiens

<400> 36

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aagttgatga cctacgctct tacttctgct tgccaggagt aactgaaagc aaacaccaca 60
gtctgttgtt tattagcttt taaaggcttg tcaacattcc ttgttaacaa tttctttttg120
ggtagccttt tataaaatgc gtaggtgatg agtgatccag cagacaaggc ggctcgagcc180
gattcggctc gagcggctcg aggtaaaaga aaaaaaaatg tggaggaaaa catggcctac240
tcagctttga tggaagtggc tggttactgc ttaatagaga gaatgctttg gaatcctatg300
ttgaaaataa aaagtgtttg gttgtgcagt tatgcgggtca tggtcattcc cagacagttg360
gctaagggtt agtggctctc t
381

```

<210> 37  
 <211> 1539  
 <212> DNA  
 <213> homo sapiens

<400> 37

```

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cctggggccc agaggtaaaa gagagaacaa ggatgaacaa gcagcagaac tctcccttgg 120
ccaagagcaa gccaggcagc acggggcctg agccccccag cccccaggcc tccccagggc 180
ccccaggcct cccctgggcc cccaaaccct accacaaatt catggccttc aagtcctttg 240
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tccccaacac cgacggcatg gagatgctgc tgtgctacga ggacgagggt gtctacgtca 480
acacgtacgg gcgcatcatt aaggatgtgg tctgctcagt gggggagatg cctacttctg 540
tggcctacat ctgctccaac cagataatgg gctgggggtg gaaagccatt gagatccgct 600
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1539

```

<210> 38  
 <211> 2195  
 <212> DNA  
 <213> homo sapiens

<400> 38

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gggcccagcc	gagcaacgtg	gggcgaaggc	ggcgcggaag	gcccgggctg	ggagcggttg	180
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<400> 44

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<211> 1612

<212> DNA

<213> homo sapiens

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<211> 1106

<212> DNA

<213> homo sapiens

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<210> 47

<211> 1370

<212> DNA

<213> homo sapiens

<400> 47

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<211> 617

<212> DNA

<213> homo sapiens

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<210> 49

<211> 1899

<212> DNA

<213> homo sapiens

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<211> 1398

<212> DNA

<213> homo sapiens

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<211> 1340

<212> DNA

<213> homo sapiens

<400> 51

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<211> 315

<212> DNA

<213> homo sapiens

<400> 52

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<210> 53

<211> 1162

<212> DNA

<213> homo sapiens

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<211> 1826

<212> DNA

<213> homo sapiens

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<211> 1114

<212> DNA

<213> homo sapiens

<400> 55

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<211> 1644

<212> DNA

<213> homo sapiens

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<211> 1510

<212> DNA

<213> homo sapiens

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<211> 1188

<212> DNA

<213> homo sapiens

<400> 59

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<211> 2208

<212> DNA

<213> homo sapiens

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<211> 283

<212> DNA

<213> homo sapiens

<400> 61

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<211> 184

<212> DNA

<213> homo sapiens

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<212> DNA

<213> homo sapiens

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<211> 1085

<212> DNA

<213> homo sapiens

<400> 65

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<211> 1393

<212> DNA

<213> homo sapiens

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<211> 774

<212> DNA

<213> homo sapiens

<400> 69

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<210> 70

<211> 426

<212> DNA

<213> homo sapiens

<400> 70

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<210> 71

<211> 1417

<212> DNA

<213> homo sapiens

<400> 71

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<211> 691

<212> DNA

<213> homo sapiens

<400> 72

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<211> 1705

<212> DNA

<213> homo sapiens

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<212> DNA

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<212> DNA

<213> homo sapiens

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<210> 77  
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<400> 78

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<400> 79

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<210> 80  
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<212> DNA  
<213> homo sapiens

<400> 80

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<213> homo sapiens

<400> 81

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<212> DNA

<213> homo sapiens

<400> 82

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<210> 83

<211> 1890

<212> DNA

<213> homo sapiens

<400> 83

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<400> 84

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<211> 2358

<212> DNA

<213> homo sapiens

<400> 85

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<212> DNA

<213> homo sapiens

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<212> DNA
<213> homo sapiens

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<400> 92

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<400> 94

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<211> 1015

<212> DNA

<213> homo sapiens

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<211> 2532

<212> DNA

<213> homo sapiens

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<211> 776

<212> DNA

<213> homo sapiens

<400> 98

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<211> 629

<212> DNA

<213> homo sapiens

<400> 99

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<212> DNA
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<400> 100

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<212> DNA
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<400> 101

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<210> 102
<211> 1281
<212> DNA
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<400> 102

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<210> 103

<211> 716

<212> DNA

<213> homo sapiens

<400> 103

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<211> 1160

<212> DNA

<213> homo sapiens

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<211> 1040

<212> DNA

<213> homo sapiens

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<211> 1336

<212> DNA

<213> homo sapiens

<400> 106

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<212> DNA  
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<211> 1407

<212> DNA

<213> homo sapiens

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<211> 1376

<212> DNA

<213> homo sapiens

<400> 110

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<211> 854

<212> DNA

<213> homo sapiens

<400> 111

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<211> 1681

<212> DNA

<213> homo sapiens

<400> 112

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<211> 852

<212> DNA

<213> homo sapiens

<400> 113

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<210> 114

<211> 1739

<212> DNA

<213> homo sapiens

<400> 114

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<211> 805

<212> DNA

<213> homo sapiens

<400> 115

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<211> 1483

<212> DNA

<213> homo sapiens

<400> 116

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<211> 1347  
<212> DNA  
<213> homo sapiens

<400> 117

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<212> DNA  
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<400> 118

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<400> 120

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 <212> DNA  
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<400> 123

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<212> DNA

<213> homo sapiens

<400> 125

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<210> 126

<211> 1202

<212> DNA

<213> homo sapiens

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<211> 1014

<212> DNA

<213> homo sapiens

<400> 127

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<210> 128

<211> 1171

<212> DNA

<213> homo sapiens

<400> 128

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<211> 353

<212> DNA

<213> homo sapiens

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<210> 130

<211> 205

<212> DNA

<213> homo sapiens

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<210> 131

<211> 211

<212> DNA

<213> homo sapiens

<400> 131

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<210> 132

<211> 867

<212> DNA

<213> homo sapiens

<400> 132

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<211> 257

<212> DNA

<213> homo sapiens

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<211> 204

<212> DNA

<213> homo sapiens

<400> 134

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204

<210> 135

<211> 245

<212> DNA

<213> homo sapiens

<400> 135

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cccatattccc tttgtaatca gaggaattct gtttcaagat tattgttggtg tgtgatctgt180
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<210> 136

<211> 1637

<212> DNA

<213> homo sapiens

<400> 136

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cattgtcact gccctctccc caacctctcc tctaaccac tagagattgc ctgtgtcctg1560
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<210> 137

<211> 260

<212> DNA

<213> homo sapiens

<400> 137

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tacagacgac aagagtatca ggtagaattc aacatatggt gcttgaagtg ggctcttgtt180
ttatcagtta tggcatatgt aaataacagt gtaccaagtt agtgtggtgt ttatgaagat240
gagtttaate ttttgtgatg                                         260
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<210> 138  
<211> 957  
<212> DNA  
<213> homo sapiens

<400> 138

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tgacatcata cccagtccaa cagacaccag ctgccgtcaa gaaactccag cctttgagcg900
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```

<210> 139  
<211> 760  
<212> DNA  
<213> homo sapiens

<400> 139

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ttatgtttct gggttccttt tttagctgta aaaatacttc gtcactaaag catgaaattt120
aatcagcagt tgttcttcaa gttcctgaaa gctataaaaag tttctcatga cttgagtgg180
tttttccctg cccaccagag gagaaagccc ttgtagaatt ctgcagtgtt acaagtgttc240
cctacaaaaa ctgaaaccat cagctcctct ttaacaagtt ggctttttaa aagcacgtaa300
ttacaattta atggtattct gtaaagtggg gctctaggca taatttaa at tctttttaat360
gactatattt cttcaaaact ttgaaagaaa aatgtgttct ttttgcgtga tcttttgtaa420
gaagactgcc aacagaggaa aaaggacttt acaaattaag accatcttgg tttcatttcc480
acaaagatga gaacaaatca tgggtgtagg aaaggatcct tagaagaaca caagaatttg540
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aataaaactg agtaagtaat gaaaaaaaaa aaaaaaaaaa 760
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<210> 140  
<211> 280  
<212> DNA  
<213> homo sapiens

<400> 140

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tgctgtcttc ccctaagtag aatgttgatt cctgtcaaac acacagccta gccctgattc180
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<210> 141  
<400> 141  
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<210> 142  
<211> 461  
<212> DNA  
<213> homo sapiens

<400> 142

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tatcgtagcg cctggtgttg gtgttgccct actcctctga gctcttctt ctgatcaagc420
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```

<210> 143  
<211> 436  
<212> DNA  
<213> homo sapiens

<400> 143

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tagaggtgtg agttgggaag ttgttaaata caagagggtt tgagcttctg gagaagagga120
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caaataagcc aacattttcca aagaaacacg aatgtctatg gcagagttaa cataagggtca360
gaaaatcctc tggaagaaat ttccggtatca atgtttataa tctctgcatt taggggtttg420
ccagtttggg caaaaa 436
```

<210> 144  
<211> 287  
<212> DNA  
<213> homo sapiens

<400> 144

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ttagggaggt ggagaagggg tggaatagat caagcaagac cttggccctg gtagggatct240
gggatttaaa gtgagaggac aaccgttggg atgttgtgag cacagaa 287
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<210> 145  
<211> 555  
<212> DNA  
<213> homo sapiens

<400> 145

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ggcctgcgac gcgtcgctgg aggaacccga ttccctttcc cgagacgttt gacggcgata180
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cgttctccag cgacgccttg aagggtgacgt tcctcatcac ccgcctcaca gggcccgccc300
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ccctgcggtg ctgtt 555
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<210> 146  
<211> 1790  
<212> DNA  
<213> homo sapiens

<400> 146

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ccaccatgaa cggacagttg gatctaagt ggaagctaata catcaaagct caacttgggg 180
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<210> 147  
<211> 2357  
<212> DNA  
<213> homo sapiens

<400> 147

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<211> 907  
<212> DNA  
<213> homo sapiens  
<400> 148

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<210> 149  
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<212> DNA  
<213> homo sapiens  
<400> 149

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<212> DNA

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<212> DNA

<213> homo sapiens

<400> 154

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<211> 965

<212> DNA

<213> homo sapiens

<400> 155

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<211> 3101

<212> DNA

<213> homo sapiens

<400> 156

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3101

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<211> 983

<212> DNA

<213> homo sapiens

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<210> 158

<211> 293

<212> PRT

<213> homo sapiens

<400> 158

Phe 1	Ile	Asp	Ser	Tyr 5	Arg	Cys	Phe	Gln	Pro 10	Lys	Gln	Glu	Gly	Ala 15	Phe
Thr	Cys	Trp	Ser 20	Ala	Val	Thr	Gly	Ala 25	Arg	His	Leu	Asn 30	Tyr	Gly	Ser
Arg	Leu	Asp 35	Tyr	Thr	Leu	Gly	Asp 40	Arg	Thr	Leu	Val	Ile 45	Asp	Thr	Phe
Gln	Ala 50	Ser	Phe	Leu	Leu	Pro 55	Glu	Val	Met	Gly	Ser 60	Asp	His	Cys	Pro
Val 65	Gly	Ala	Val	Leu	Ser 70	Val	Ser	Ser	Val	Pro 75	Ala	Lys	Gln	Cys	Pro 80
Pro	Leu	Cys	Thr	Arg 85	Phe	Leu	Pro	Glu	Phe 90	Ala	Gly	Thr	Gln	Leu 95	Lys
Ile	Leu	Arg	Phe 100	Leu	Val	Pro	Leu	Glu 105	Gln	Ser	Pro	Val	Leu 110	Glu	Gln
Ser	Thr	Leu 115	Gln	His	Asn	Asn	Gln 120	Thr	Arg	Val	Gln	Thr 125	Cys	Gln	Asn
Lys	Ala 130	Gln	Val	Arg	Ser	Thr 135	Arg	Pro	Gln	Pro	Ser 140	Gln	Val	Gly	Ser
Ser 145	Arg	Gly	Gln	Lys	Asn 150	Leu	Lys	Ser	Tyr	Phe 155	Gln	Pro	Ser	Pro	Ser 160

Cys	Pro	Gln	Ala	Ser 165	Pro	Asp	Ile	Glu	Leu 170	Pro	Ser	Leu	Pro	Leu 175	Met	
Ser	Ala	Leu	Met 180	Thr	Pro	Lys	Thr	Pro 185	Glu	Glu	Lys	Ala	Val 190	Ala	Lys	
Val	Val	Lys 195	Gly	Gln	Ala	Lys	Thr 200	Ser	Glu	Ala	Lys	Asp 205	Glu	Lys	Glu	
Leu	Arg 210	Thr	Ser	Phe	Trp	Lys 215	Ser	Val	Leu	Ala	Gly 220	Pro	Leu	Arg	Thr	
Pro 225	Leu	Cys	Gly	Gly	His 230	Arg	Glu	Pro	Cys	Val 235	Met	Arg	Thr	Val	Lys 240	
Lys	Pro	Gly	Pro	Asn 245	Leu	Gly	Arg	Arg	Phe 250	Tyr	Met	Cys	Ala	Arg 255	Pro	
Arg	Gly	Pro	Pro 260	Thr	Asp	Pro	Ser	Ser 265	Arg	Cys	Asn	Ser	Ser 270	Ser	Gly	
Ala	Gly	Pro 275	Ala	Glu	Pro	Met	Glu 280	Ala	Trp	Gly	His	Leu 285	Ala	Trp	Ser	
Pro	Leu 290	His	Met	Ile												

<210> 159

<211> 131

<212> PRT

<213> homo sapiens

<400> 159

Glu 1	Thr	Leu	Arg	Glu 5	Lys	Gln	Glu	Ala	Ala 10	Gln	Gly	Arg	Gly	Ala 15	Gly	
Leu	Arg	Ser	Cys 20	Ala	Gly	Val	Thr	Met 25	Pro	Asp	Val	Pro	Arg 30	Pro	Pro	
Leu	Val	Gln 35	Leu	Gly	Leu	Leu	Gln 40	Arg	Lys	Asn	Cys	Thr 45	Gly	Arg	Arg	
Gly	Gln 50	Trp	Glu	Asp	Pro	Gly 55	Ala	Trp	His	Thr	Cys 60	Arg	Ser	Gly	Gly	
Pro 65	Ser	Trp	Val	Leu	Ala 70	Ser	Ser	Gln	Tyr	Ala 75	Ser	His	Met	Ala	Pro 80	
Cys	Gly	Pro	His 85	Arg	Gly	Val	Cys	Ala	Arg 90	Ala	Pro	Pro	Ala	Gln 95	Thr	
Ser	Arg	Met	Arg 100	Ser	Val	Thr	Pro	Ser 105	His	Leu	Trp	Leu	Leu 110	Lys	Ser	
Trp	Pro	Ala 115	Pro	Ser	Pro	Leu	Trp 120	Pro	Leu	Pro	Ser	Leu 125	Leu	Glu	Ser	
Ser	Gly 130	Ser														

<210> 160

<211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 160

Lys 1	Arg	Arg	Pro	Lys 5	Leu	Gly	Pro	Gly	Phe 10	Phe	Thr	Val	Arg	Ile 15	Thr
His	Gly	Ser	Leu 20	Trp	Pro	Pro	Gln	Arg 25	Gly	Val	Arg	Lys	Gly 30	Pro	Ala
Ser	Thr	Asp 35	Phe	Gln	Asn	Glu	Val 40	Arg	Asn	Ser	Phe	Ser 45	Ser	Leu	Ala
Ser	Glu 50	Val	Leu	Ala	Cys	Pro 55	Phe	Thr	Thr	Leu	Ala 60	Thr	Ala	Phe	Ser
Ser 65	Gly	Val	Phe	Gly	Val 70	Met	Arg	Ala	Leu	Ile 75	Ser	Gly	Arg	Leu	Gly 80
Ser	Ser	Met	Ser	Gly 85	Glu	Ala	Trp	Gly	Gln 90	Leu	Gly	Glu	Gly		

<210> 161  
 <211> 136  
 <212> PRT  
 <213> homo sapiens

<400> 161

Leu 1	His	Gln	Leu	Ala 5	Ala	Gln	Arg	Leu	Tyr 10	Leu	Arg	Pro	Val	Arg 15	Val
Gly	Ala	Trp	Ala 20	Leu	Ser	Leu	Pro	Gly 25	Glu	Arg	Arg	Ala	Glu 30	Ile	Ser
Asn	Gln	Trp 35	Ser	Ala	Leu	Val	Thr 40	Trp	Ile	Pro	Glu	Gly 45	Arg	Glu	Gly
Ser 50	Thr	Val	Ser	Ser	Ala	Ala 55	Asp	Cys	Cys	Ser	Lys 60	Asn	Val	Phe	Ser
Thr 65	Ser	Phe	Glu	Ser	Pro 70	Ser	His	Gly	Asn	Pro 75	Ser	Thr	Pro	Thr	Arg 80
Asp	Pro	Thr	Pro	Ala 85	Val	Ser	Arg	Ile	Ser 90	Ser	Thr	Cys	Thr	Ser 95	Arg
Asp	Pro	Asn	Asp 100	Ser	Cys	Thr	Asn	Glu 105	His	Tyr	Gly	Ser	Cys 110	Ser	Asn
Cys	Leu	Ser 115	Thr	His	Cys	Val	Tyr 120	Gly	Trp	Lys	Ala	Phe 125	Gly	Arg	Lys
Lys	Gly 130	Ser	Ser	Arg	Leu	Lys 135	Gly								

<210> 162  
 <211> 281  
 <212> PRT  
 <213> homo sapiens

<400> 162

Pro 1	Gly	Ser	Gln	Lys 5	Val	Ala	Lys	Ala	Val 10	Pro	Phe	Pro	Gln	Arg 15	Arg
Thr	Ala	Ala	Val 20	Arg	Met	Ser	Phe	Pro 25	Pro	His	Leu	Asn	Arg 30	Pro	Pro
Met	Gly	Ile 35	Pro	Ala	Leu	Pro	Pro 40	Gly	Ile	Pro	Pro	Pro 45	Gln	Phe	Pro
Gly	Phe 50	Pro	Pro	Pro	Val	Pro 55	Pro	Gly	Thr	Pro	Met 60	Ile	Pro	Val	Pro
Met 65	Ser	Ile	Met	Ala	Pro 70	Ala	Pro	Thr	Val	Leu 75	Val	Pro	Thr	Val	Ser 80
Met	Val	Gly	Lys	His 85	Leu	Gly	Ala	Arg	Lys 90	Asp	His	Pro	Gly	Leu 95	Lys
Ala	Lys	Glu	Asn 100	Asp	Glu	Asn	Cys	Gly 105	Pro	Thr	Thr	Thr	Val 110	Phe	Val
Gly	Asn	Ile 115	Ser	Glu	Lys	Ala	Ser 120	Asp	Met	Leu	Ile	Arg 125	Gln	Leu	Leu
Ala	Lys 130	Cys	Gly	Leu	Val	Leu 135	Ser	Trp	Lys	Arg	Val 140	Gln	Gly	Ala	Ser
Gly 145	Lys	Leu	Gln	Ala	Phe 150	Gly	Phe	Cys	Glu	Tyr 155	Lys	Glu	Pro	Glu	Ser 160
Thr	Leu	Arg	Ala	Leu 165	Arg	Leu	Leu	His	Asp 170	Leu	Gln	Ile	Gly	Glu 175	Lys
Lys	Leu	Leu	Val 180	Lys	Val	Asp	Ala	Lys 185	Thr	Lys	Ala	Gln	Leu 190	Asp	Glu
Trp	Lys	Ala 195	Lys	Lys	Lys	Ala	Ser 200	Asn	Gly	Asn	Ala	Arg 205	Pro	Glu	Thr
Val	Thr 210	Asn	Asp	Asp	Glu	Glu 215	Ala	Leu	Asp	Glu	Glu 220	Thr	Lys	Arg	Arg
Asp 225	Gln	Met	Ile	Lys	Gly 230	Ala	Ile	Glu	Val	Leu 235	Ile	Arg	Glu	Tyr	Ser 240
Ser	Glu	Leu	Asn	Ala 245	Pro	Ser	Gln	Glu	Ser 250	Asp	Ser	His	Pro	Gln 255	Glu
Glu	Glu	Glu	Gly 260	Lys	Glu	Gly	Gly	His 265	Phe	Pro	Gln	Ile	Ser 270	Ser	Gly
Pro	Thr	Asp 275	Pro	Leu	Ser	Thr	His 280	His							

<210> 163

<211> 103

<212> PRT

<213> homo sapiens

<400> 163

Cys 1	Ser	Leu	Val	Gln 5	Glu	Ser	Leu	Gly	Ser 10	Leu	Glu	Val	Gln	Val 15	Glu
Glu	Ile	Leu	Glu 20	Thr	Ala	Gly	Val	Gly 25	Ser	Leu	Val	Gly	Val 30	Leu	Gly
Phe	Pro	Trp 35	Glu	Gly	Asp	Ser	Asn 40	Glu	Val	Glu	Lys	Thr 45	Phe	Leu	Leu
Gln	Gln 50	Ser	Ala	Ala	Glu	Glu 55	Thr	Val	Leu	Pro	Ser 60	Arg	Pro	Ser	Gly
Ile 65	Gln	Val	Thr	Ser	Ala 70	Leu	His	Trp	Phe	Glu 75	Ile	Ser	Ala	Arg	Arg 80
Ser	Pro	Gly	Arg	Leu 85	Ser	Ala	Gln	Ala	Pro 90	Thr	Arg	Thr	Gly	Arg 95	Lys
Tyr	Ser	Arg	Cys 100	Ala	Ala	Ser									

<210> 164  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 164

Asn 1	Ile	Ser	Leu	Leu 5	Asp	His	Pro	Gly	Leu 10	Gln	Ser	Cys	Leu	Tyr 15	Phe
Leu	Phe	Trp	Ile 20	Leu	Phe	Thr	Asn	Arg 25	Glu	Arg	Tyr	Ile	Ser 30	Ala	Trp
Lys	Trp	Pro 35	Asp	Val	Trp	Lys	Leu 40	Asp	Ile	Trp	His	Phe 45	Gly	Leu	His
Ser	His 50	Gly	Tyr	Tyr	Ser	His 55	Asn	Lys	Asp	Gly	Ser 60	Gly	Asn	Ser	Phe
Leu 65	Asp	Leu	Asp	Gln	Pro 70	Ser	Arg	Tyr	Leu	Gly 75	Ile	Tyr	Tyr	Ile	Leu 80
Phe	Cys	Ile	Phe	Leu 85	Val	Leu	Trp	Arg	Asp 90	Ser	Leu	Ala	Ile	Phe 95	Gly
Leu	Pro	Glu	Tyr 100	Val	Phe	Cys	Val	Tyr 105	Ser	Ala	Pro	Val	Lys 110	Trp	Phe
Cys	Leu	Val 115	Cys	His	Asn	Pro	His 120	Gly	Cys	Tyr	Met	Ser 125	Ile	Ser	

<210> 165  
 <211> 382  
 <212> PRT  
 <213> homo sapiens

<400> 165

His 1	Glu	Val	Leu	Cys 5	Cys	Arg	Met	Ala	Pro 10	Leu	Gln	Lys	Ala	Lys 15	Val
Ile	Arg	Leu	Ile	Lys	Ile	Ser	Pro	Glu	Lys	Pro	Ile	Thr	Leu	Ala	Val



			20					25					30				
Gly	Asp	Gly 35	Ala	Asn	Asp	Val	Ser 40	Met	Ile	Gln	Glu	Ala 45	His	Val	Gly		
Ile	Gly 50	Ile	Met	Gly	Lys	Glu 55	Gly	Arg	Gln	Ala	Ala 60	Arg	Asn	Ser	Asp		
Tyr 65	Ala	Ile	Ala	Arg	Phe 70	Lys	Phe	Leu	Ser	Lys 75	Leu	Leu	Phe	Val	His 80		
Gly	His	Phe	Tyr	Tyr 85	Ile	Arg	Ile	Ala	Thr 90	Leu	Val	Gln	Tyr	Phe 95	Phe		
Tyr	Lys	Asn	Val 100	Cys	Phe	Ile	Thr	Pro 105	Gln	Phe	Leu	Tyr	Gln 110	Phe	Tyr		
Cys	Leu	Phe 115	Ser	Gln	Gln	Thr	Leu 120	Tyr	Asp	Ser	Val	Tyr 125	Leu	Thr	Leu		
Tyr	Asn 130	Ile	Cys	Phe	Thr	Ser 135	Leu	Pro	Ile	Leu	Ile 140	Tyr	Ser	Leu	Leu		
Glu 145	Gln	His	Val	Asp	Pro 150	His	Val	Leu	Gln	Asn 155	Lys	Pro	Thr	Leu	Tyr 160		
Arg	Asp	Ile	Ser	Lys 165	Asn	Arg	Leu	Leu	Ser 170	Ile	Lys	Thr	Phe	Leu 175	Tyr		
Trp	Thr	Ile	Leu 180	Gly	Phe	Ser	His	Ala 185	Phe	Ile	Phe	Phe	Phe 190	Gly	Ser		
Tyr	Leu	Leu 195	Ile	Gly	Lys	Asp	Thr 200	Ser	Leu	Leu	Gly	Asn 205	Gly	Gln	Met		
Phe	Gly 210	Asn	Trp	Thr	Phe	Gly 215	Thr	Leu	Val	Phe	Thr 220	Val	Met	Val	Ile		
Thr 225	Val	Thr	Ile	Lys	Met 230	Ala	Leu	Glu	Thr	His 235	Phe	Trp	Thr	Trp	Ile 240		
Asn	His	Leu	Val	Thr 245	Trp	Gly	Ser	Ile	Ile 250	Phe	Tyr	Phe	Val	Phe 255	Ser		
Leu	Phe	Tyr	Gly 260	Gly	Ile	Leu	Trp	Pro 265	Phe	Leu	Gly	Ser	Gln 270	Asn	Met		
Tyr	Phe	Val 275	Phe	Ile	Gln	Leu	Leu 280	Ser	Ser	Gly	Ser	Ala 285	Trp	Phe	Ala		
Ile	Ile 290	Leu	Met	Val	Val	Thr 295	Cys	Leu	Phe	Leu	Asp 300	Ile	Ile	Lys	Lys		
Val 305	Phe	Asp	Arg	His	Leu 310	His	Pro	Thr	Ser	Thr 315	Glu	Lys	Ala	Gln	Met 320		
Tyr	Ser	Asn	Thr	Val 325	Ala	Leu	Ser	Asp	Glu 330	Phe	Ile	Ala	Leu	Gln 335	Pro		
Leu	Ser	Arg	Ala 340	Arg	Asn	Gln	Leu	Ser 345	Lys	Leu	Ser	Leu	Leu 350	Lys	Gln		
Met	Gln	Val	Ser	Ser	Ala	Trp	Thr	Pro	Cys	Ala	Val	Ser	Arg	Lys	Glu		

355						360						365				
Lys	Gln	Arg	Val	His	Leu	Leu	Glu	Glu	Cys	Trp	Asn	Glu	Leu			
	370					375					380					
<210> 166																
<211> 85																
<212> PRT																
<213> homo sapiens																
<400> 166																
Gln	Glu	Leu	Asn	Lys	His	Lys	Ile	His	Ile	Leu	Gly	Ala	Gln	Lys	Trp	
1				5					10					15		
Pro	Glu	Asn	Pro	Ser	Ile	Lys	Gln	Gly	Lys	Tyr	Lys	Ile	Lys	Tyr	Asn	
			20					25					30			
Arg	Ser	Pro	Gly	Asn	Glu	Met	Val	Asp	Pro	Ser	Pro	Lys	Met	Ser	Phe	
		35					40					45				
Gln	Ser	His	Leu	Tyr	Cys	Asp	Cys	Asn	Asn	His	Asp	Cys	Glu	Asp	Gln	
	50					55					60					
Ser	Ala	Lys	Cys	Pro	Val	Ser	Lys	His	Leu	Ala	Ile	Ser	Lys	Gln	Arg	
65					70					75					80	
Cys	Ile	Phe	Pro	Tyr												
				85												
<210> 167																
<211> 496																
<212> PRT																
<213> homo sapiens																
<400> 167																
Arg	Leu	Glu	Lys	Gly	Pro	Leu	Pro	Phe	Gln	Met	Pro	Gly	Met	Arg	Leu	
1				5					10					15		
Pro	Glu	Thr	Gln	Val	Leu	Pro	Gly	Glu	Ile	Asp	Glu	Thr	Pro	Leu	Ser	
			20					25					30			
Lys	Pro	Gly	His	Asp	Leu	Ala	Ser	Met	Glu	Asp	Lys	Thr	Glu	Lys	Trp	
		35					40					45				
Ser	Ser	Gln	Pro	Glu	Gly	Pro	Leu	Lys	Leu	Lys	Ala	Ser	Ser	Thr	Asp	
	50					55					60					
Met	Pro	Ser	Gln	Ile	Ser	Val	Val	Asn	Val	Asp	Gln	Leu	Trp	Glu	Asp	
65					70					75					80	
Ser	Val	Leu	Thr	Val	Lys	Phe	Pro	Lys	Leu	Met	Val	Pro	Arg	Phe	Ser	
				85					90					95		
Phe	Pro	Ala	Pro	Ser	Ser	Glu	Asp	Asp	Val	Phe	Ile	Pro	Thr	Val	Arg	
			100					105					110			
Glu	Val	Gln	Cys	Pro	Glu	Ala	Asn	Ile	Asp	Thr	Ala	Leu	Cys	Lys	Glu	
		115					120					125				
Ser	Pro	Gly	Leu	Trp	Gly	Ala	Ser	Ile	Leu	Lys	Ala	Gly	Ala	Gly	Val	
	130					135					140					

Pro 145	Gly	Glu	Gln	Pro	Val 150	Asp	Leu	Asn	Leu	Pro 155	Leu	Glu	Ala	Pro	Pro 160
Ile	Ser	Lys	Val	Arg 165	Val	His	Ile	Gln	Gly 170	Ala	Gln	Val	Glu	Ser 175	Gln
Glu	Val	Thr	Ile 180	His	Ser	Ile	Val	Thr 185	Pro	Glu	Phe	Val	Asp 190	Leu	Ser
Val	Pro	Arg 195	Thr	Phe	Ser	Thr	Gln 200	Ile	Val	Arg	Glu	Ser 205	Glu	Ile	Pro
Thr	Ser 210	Glu	Ile	Gln	Thr	Pro 215	Ser	Tyr	Gly	Phe	Ser 220	Leu	Leu	Lys	Val
Lys 225	Ile	Pro	Glu	Pro	His 230	Thr	Gln	Ala	Arg	Val 235	Tyr	Thr	Thr	Met	Thr 240
Gln	His	Ser	Arg	Thr 245	Gln	Glu	Gly	Thr	Glu 250	Glu	Ala	Pro	Ile	Gln 255	Ala
Thr	Pro	Gly	Val 260	Asp	Ser	Ile	Ser	Gly 265	Asp	Leu	Gln	Pro	Asp 270	Thr	Gly
Glu	Pro	Phe 275	Glu	Met	Ile	Ser	Ser 280	Ser	Val	Asn	Val	Leu 285	Gly	Gln	Gln
Thr	Leu 290	Thr	Phe	Glu	Val	Pro 295	Ser	Gly	His	Gln	Leu 300	Ala	Asp	Ser	Cys
Ser 305	Asp	Glu	Glu	Pro	Ala 310	Glu	Ile	Leu	Glu	Phe 315	Pro	Pro	Asp	Asp	Ser 320
Gln	Glu	Ala	Thr 325	Thr	Pro	Leu	Ala	Asp	Glu 330	Gly	Arg	Ala	Pro	Lys 335	Asp
Lys	Pro	Glu	Ser 340	Lys	Lys	Ser	Gly	Leu 345	Leu	Trp	Phe	Trp	Leu 350	Pro	Asn
Ile	Gly	Phe 355	Ser	Ser	Ser	Val	Asp 360	Glu	Thr	Gly	Val	Asp 365	Ser	Lys	Asn
Asp	Val 370	Gln	Arg	Ser	Ala	Pro 375	Ile	Gln	Thr	Gln	Pro 380	Glu	Ala	Arg	Pro
Glu 385	Ala	Glu	Leu	Pro	Lys 390	Lys	Gln	Glu	Lys	Ala 395	Gly	Trp	Phe	Arg	Phe 400
Pro	Lys	Leu	Gly	Phe 405	Ser	Ser	Ser	Pro	Thr 410	Lys	Lys	Ser	Lys	Ser 415	Thr
Glu	Asp	Gly	Ala 420	Glu	Leu	Glu	Glu	Gln 425	Lys	Leu	Gln	Glu	Glu 430	Thr	Ile
Thr	Phe	Phe 435	Asp	Ala	Arg	Glu	Ser 440	Phe	Ser	Pro	Glu	Glu 445	Lys	Glu	Glu
Gly	Glu 450	Leu	Ile	Gly	Pro	Val 455	Gly	Thr	Gly	Leu	Asp 460	Ser	Arg	Val	Met
Val 465	Thr	Ser	Ala	Ala	Arg 470	Thr	Glu	Leu	Ile	Leu 475	Pro	Glu	Gln	Asp	Arg 480

Lys	Ala	Asp	Asp	Glu	Ser	Lys	Gly	Ser	Gly	Leu	Gly	Pro	Asn	Glu	Gly
				485					490					495	

<210> 168  
 <211> 125  
 <212> PRT  
 <213> homo sapiens

<400> 168

Ser	Leu	Pro	Ala	Ser	Met	Tyr	Trp	Asp	Ser	Lys	His	Ser	His	Leu	Lys
1				5					10					15	
Phe	Leu	Leu	Ala	Thr	Ser	Leu	Gln	Thr	Ala	Val	Gln	Met	Arg	Ser	Gln
			20					25					30		
Gln	Lys	Phe	Leu	Ser	Phe	Pro	Leu	Met	Ile	Ala	Lys	Arg	Gln	Pro	His
		35					40					45			
His	Trp	Gln	Met	Lys	Ala	Gly	Leu	Gln	Lys	Thr	Asn	Gln	Lys	Val	Lys
	50					55					60				
Asn	Leu	Val	Cys	Ser	Gly	Phe	Gly	Phe	Gln	Thr	Leu	Gly	Phe	Pro	Leu
65					70					75					80
Leu	Leu	Met	Arg	Gln	Val	Leu	Ile	Pro	Lys	Met	Thr	Ser	Arg	Asp	Leu
				85					90					95	
Leu	Pro	Phe	Lys	His	Ser	Leu	Arg	His	Asp	Gln	Arg	Gln	Asn	Cys	Leu
			100					105					110		
Lys	Asn	Arg	Arg	Arg	Gln	Ala	Gly	Ser	Asp	Phe	Pro	Asn			
		115					120					125			

<210> 169  
 <211> 130  
 <212> PRT  
 <213> homo sapiens

<400> 169

Met	Gly	Ala	Asp	Leu	Trp	Thr	Ser	Phe	Leu	Glu	Ser	Thr	Pro	Val	Ser
1				5					10					15	
Ser	Thr	Glu	Glu	Glu	Asn	Pro	Met	Phe	Gly	Ser	Gln	Asn	Gln	Ser	Arg
		20						25					30		
Pro	Asp	Phe	Leu	Leu	Ser	Gly	Leu	Ser	Phe	Gly	Ala	Leu	Pro	Ser	Ser
		35					40					45			
Ala	Ser	Gly	Val	Val	Ala	Ser	Trp	Leu	Ser	Ser	Gly	Gly	Asn	Ser	Arg
	50					55					60				
Ile	Ser	Ala	Gly	Ser	Ser	Ser	Glu	Gln	Leu	Ser	Ala	Ser	Trp	Trp	Pro
65				70						75					80
Glu	Gly	Thr	Ser	Asn	Val	Ser	Val	Cys	Cys	Pro	Ser	Thr	Leu	Thr	Leu
				85					90					95	
Glu	Glu	Ile	Ile	Ser	Asn	Gly	Ser	Pro	Val	Ser	Gly	Trp	Arg	Ser	Pro
			100					105					110		

Glu	Met	Glu	Ser	Thr	Pro	Gly	Val	Ala	Cys	Met	Gly	Ala	Ser	Ser	Val
		115					120					125			

Pro	Ser
	130

<210> 170

<211> 123

<212> PRT

<213> homo sapiens

<400> 170

Val	Val	Tyr	Arg	Gly	Val	Lys	Cys	Phe	Ile	Asp	Lys	Lys	Lys	Lys	Thr
1				5					10					15	
Ala	Leu	Glu	Pro	Thr	Tyr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
			20					25						30	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
		35					40					45			
Ser	Ser	Ser	Ser	Phe	Phe	Phe	Leu	Leu	Phe	Ser	Ala	Leu	Thr	Thr	Pro
	50					55					60				
Phe	Phe	Ala	Ala	Ser	Gly	Phe	Pro	Leu	Ala	Arg	Tyr	Ala	Ala	Ile	Ser
65					70					75					80
Phe	Ser	Tyr	Phe	Ser	Phe	Thr	Ser	Gln	Pro	Ser	Phe	His	Lys	Ala	Ala
				85					90					95	
Cys	His	Leu	Gln	Gln	Cys	Tyr	Ser	Thr	Ser	Leu	Pro	Val	Ser	Ser	Gln
			100					105					110		
His	His	Gln	Trp	Thr	Gly	Gln	Asp	Val	Leu	Leu					
		115					120								

<210> 171

<211> 157

<212> PRT

<213> homo sapiens

<400> 171

Lys	Lys	Leu	Tyr	Leu	Leu	Arg	Ser	Ile	Gln	Asn	Val	Asn	Lys	Thr	Ala
1				5					10					15	
Ala	Ile	Phe	Phe	Leu	Gln	Leu	Gln	Ser	Gly	Ile	Gln	Leu	Thr	Glu	Gln
			20					25					30		
Gln	Leu	Ser	Ser	Tyr	Lys	Leu	His	Gln	Arg	Gln	Leu	Lys	Met	Lys	Lys
		35					40					45			
Ile	Lys	Pro	Lys	Lys	Lys	Thr	Lys	Arg	Lys	Lys	Lys	Lys	Lys	Gln	Lys
	50					55					60				
Thr	Lys	Leu	Pro	Ser	Pro	Tyr	Ile	Thr	Asn	Leu	Cys	Cys	Ala	Pro	Thr
65					70					75					80
Arg	Thr	Cys	Phe	Lys	Phe	Pro	Cys	Gln	Phe	Thr	Thr	Pro	Ile	Leu	Tyr
				85					90					95	
Gln	Ala	Arg	Leu	Val	Ala	Ile	Glu	Asn	Thr	Thr	Arg	Thr	Gly	Leu	Ser

100							105				110				
Lys	Asp	Thr	Phe	Gly	Ser	Val	Leu	Thr	Ile	Gln	Lys	Lys	Thr	Leu	Tyr
		115					120					125			
Ser	Leu	Lys	Thr	Asn	Leu	Thr	Gln	Pro	Tyr	Ile	Ser	Ile	Phe	Phe	Phe
	130					135					140				
Lys	Arg	Ser	Glu	Leu	Cys	Thr	Gly	Gly	Leu	Asn	Ala	Leu			
145					150					155					

<210> 172  
 <211> 152  
 <212> PRT  
 <213> homo sapiens

<400> 172

Leu	Asn	Met	Gly	Lys	Gly	Asp	Pro	Lys	Lys	Pro	Arg	Gly	Lys	Met	Ser
1				5					10					15	
Ser	Tyr	Ala	Phe	Phe	Val	Gln	Thr	Cys	Arg	Glu	Glu	His	Lys	Lys	Lys
			20					25					30		
His	Pro	Asp	Ala	Ser	Val	Asn	Phe	Ser	Glu	Phe	Ser	Lys	Lys	Cys	Ser
		35					40					45			
Glu	Arg	Trp	Lys	Thr	Met	Ser	Ala	Lys	Glu	Lys	Gly	Lys	Phe	Glu	Asp
	50					55					60				
Met	Ala	Lys	Ala	Asp	Lys	Ala	Arg	Tyr	Glu	Arg	Glu	Met	Lys	Thr	Tyr
65					70					75					80
Ile	Pro	Pro	Lys	Gly	Glu	Thr	Lys	Lys	Lys	Phe	Lys	Asp	Pro	Asn	Ala
				85					90					95	
Pro	Lys	Arg	Pro	Pro	Ser	Ala	Phe	Phe	Leu	Phe	Cys	Ser	Glu	Tyr	Arg
			100					105					110		
Pro	Lys	Ile	Lys	Gly	Glu	His	Pro	Gly	Leu	Ser	Ile	Gly	Asp	Val	Ala
		115					120					125			
Lys	Lys	Leu	Gly	Glu	Met	Trp	Asn	Asn	Thr	Ala	Ala	Asp	Asp	Lys	Gln
	130					135					140				
Pro	Tyr	Glu	Lys	Lys	Ala	Ala	Lys								
145					150										

<210> 173  
 <211> 281  
 <212> PRT  
 <213> homo sapiens

<400> 173

Ser	Gly	Ser	Ala	Gly	Pro	Gly	Pro	Arg	Gly	Pro	Arg	Ala	Thr	Glu	Ser
1				5					10					15	
Gly	Lys	Arg	Met	Asp	Cys	Pro	Ala	Leu	Pro	Pro	Gly	Trp	Lys	Lys	Glu
			20					25					30		
Glu	Val	Ile	Arg	Lys	Ser	Gly	Leu	Ser	Ala	Gly	Lys	Ser	Asp	Val	Tyr
		35					40					45			

Tyr	Phe	Ser	Pro	Ser	Gly	Lys	Lys	Phe	Arg	Ser	Lys	Pro	Gln	Leu	Ala	
	50					55					60					
Arg	Tyr	Leu	Gly	Asn	Thr	Val	Asp	Leu	Ser	Ser	Phe	Asp	Phe	Arg	Thr	
65					70					75					80	
Gly	Lys	Met	Met	Pro	Ser	Lys	Leu	Gln	Lys	Asn	Lys	Gln	Arg	Leu	Arg	
				85					90					95		
Asn	Asp	Pro	Leu	Asn	Gln	Asn	Lys	Gly	Lys	Pro	Asp	Leu	Asn	Thr	Thr	
			100					105					110			
Leu	Pro	Ile	Arg	Gln	Thr	Ala	Ser	Ile	Phe	Lys	Gln	Pro	Val	Thr	Lys	
		115					120					125				
Val	Thr	Asn	His	Pro	Ser	Asn	Lys	Val	Lys	Ser	Asp	Pro	Gln	Arg	Met	
	130					135					140					
Asn	Glu	Gln	Pro	Arg	Gln	Leu	Phe	Trp	Glu	Lys	Arg	Leu	Gln	Gly	Leu	
145					150					155					160	
Ser	Ala	Ser	Asp	Val	Thr	Glu	Gln	Ile	Ile	Lys	Thr	Met	Glu	Leu	Pro	
				165					170					175		
Lys	Gly	Leu	Gln	Gly	Val	Gly	Pro	Gly	Ser	Asn	Asp	Glu	Thr	Leu	Leu	
			180					185					190			
Ser	Ala	Val	Ala	Ser	Ala	Leu	His	Thr	Ser	Ser	Ala	Pro	Ile	Thr	Gly	
		195					200					205				
Gln	Val	Ser	Ala	Ala	Val	Glu	Lys	Asn	Pro	Ala	Val	Trp	Leu	Asn	Thr	
	210					215					220					
Ser	Gln	Pro	Leu	Cys	Lys	Ala	Phe	Ile	Val	Thr	Asp	Glu	Asp	Ile	Arg	
225					230					235					240	
Lys	Gln	Glu	Glu	Arg	Val	Gln	Gln	Val	Arg	Lys	Lys	Leu	Glu	Glu	Ala	
				245					250					255		
Leu	Met	Ala	Asp	Ile	Leu	Ser	Arg	Ala	Ala	Asp	Thr	Glu	Glu	Met	Asp	
			260					265					270			
Ile	Glu	Met	Asp	Ser	Gly	Asp	Glu	Ala								
		275					280									

<210> 174

<211> 102

<212> PRT

<213> homo sapiens

<400> 174

Ile	Ile	Asp	Ile	Tyr	Ile	Lys	Asn	Thr	Ser	Lys	Lys	Ala	Leu	Val	Ser	
1				5					10					15		
Ala	Ile	Lys	Lys	Leu	Tyr	Val	Leu	Gly	Tyr	Ile	Phe	Phe	Leu	Thr	Gly	
			20					25					30			
Lys	Ser	Gln	Trp	Lys	His	Phe	Cys	Ser	Ile	Ser	Arg	Asn	Phe	Leu	Leu	
		35					40					45				
Gly	Lys	Val	Gly	Arg	Lys	Leu	Pro	Asp	His	Ile	Leu	Arg	Leu	His	Leu	

	50					55						60				
His	Cys	Pro	Phe	Gln	Tyr	Pro	Ser	Leu	Leu	Tyr	Gln	Gln	Leu	Ala	Thr	
65					70					75					80	
Arg	Cys	Leu	Pro	Ser	Val	Leu	Leu	Pro	Ile	Ser	Cys	Val	Leu	Ala	Val	
				85					90					95		
Leu	Ala	Leu	Pro	Val	Ser											
			100													

<210> 175  
 <211> 147  
 <212> PRT  
 <213> homo sapiens

<400> 175

Ile	Tyr	Thr	Ser	Lys	Ile	His	Leu	Lys	Arg	His	Trp	Leu	Val	Leu	Leu	
1				5					10					15		
Lys	Ser	Ser	Met	Cys	Ser	Gly	Thr	Phe	Phe	Phe	Leu	Gln	Ala	Lys	Ala	
			20					25					30			
Ser	Gly	Asn	Ile	Phe	Val	Gln	Phe	Leu	Gly	Ile	Phe	Ser	Trp	Gly	Lys	
		35					40					45				
Ser	Val	Glu	Ser	Tyr	Leu	Ile	Ile	Phe	Leu	Gly	Phe	Ile	Ser	Thr	Val	
	50					55					60					
His	Phe	Asn	Ile	His	Leu	Phe	Cys	Ile	Ser	Ser	Ser	Arg	Gln	Asp	Val	
65					70					75					80	
Cys	His	Gln	Cys	Phe	Phe	Gln	Phe	Leu	Ala	Tyr	Leu	Leu	Tyr	Ser	Leu	
				85					90					95		
Phe	Leu	Phe	Pro	Asp	Val	Phe	Ile	Cys	Asp	Asn	Lys	Ser	Phe	Ala	Glu	
			100					105					110			
Gly	Leu	Arg	Cys	Val	Lys	Pro	Asn	Ser	Arg	Val	Leu	Phe	His	Ser	Ser	
		115					120					125				
Gly	Asp	Leu	Pro	Cys	Asp	Trp	Arg	Arg	Ala	Cys	Val	Gln	Ser	Thr	Gly	
	130					135					140					
Asn	Ser	Arg														
145																

<210> 176  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 176

Glu	Cys	Pro	Leu	Gly	Ala	Arg	Gly	Pro	Trp	Glu	Pro	Arg	His	Pro	Phe	
1				5					10					15		
Pro	Leu	Gly	Arg	Gly	Ala	Arg	Ser	Arg	His	Pro	Cys	Thr	His	Gly	Arg	
			20					25					30			
Leu	Ala	Pro	Pro	Gln	Ser	Pro	Pro	His	Ser	Gln	Gln	Pro	Phe	His	Ser	
		35					40					45				



His	Cys	Pro	Ser	Arg	Ser	Pro	Gln	Pro	Ser	Leu	Arg	Pro	His	Pro	His
	50					55					60				
Pro	Leu	Arg	Ala	Gln	Gly	Cys	Asn	Pro	Ser	Leu	Ser	Thr	Thr	His	Arg
65					70					75					80
Trp	Tyr	Ser	Trp	Gly											
				85											

<210> 177  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 177

Asn	Ala	Leu	Trp	Gly	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Ala	Thr	Leu	Ser
1				5					10					15	
His	Leu	Ala	Gly	Val	Pro	Ala	Ala	Ala	Thr	Pro	Ala	Arg	Met	Ala	Gly
			20					25					30		
Trp	His	Pro	Pro	Arg	Ala	Leu	Pro	Thr	Ala	Ser	Ser	Leu	Ser	Thr	Val
		35					40					45			
Thr	Ala	Leu	Pro	Ala	Val	Pro	Ser	Leu	Pro	Tyr	Gly	Leu	Thr	Arg	Thr
	50					55					60				
Pro	Ser	Glu	Pro	Arg	Ala	Ala	Thr	Pro	His	Tyr	Pro	Pro	Arg	Thr	Asp
65					70					75					80
Gly	Thr	Ala	Gly	Ala	Glu	Gln	Pro	His	Val	Glu	Pro	Glu	Arg	Val	Pro
				85					90					95	
Gly	Ala	Arg	Gly	Gln	Asp	Ala	Gly	Gly	Arg	Met	Thr	Ala	Cys	Pro	Cys
			100					105					110		
Leu	Thr	Ser	Trp	Gly	Thr	Thr	Leu	Asp	Arg	Gly	Ile	Gly	Gln	Asp	Pro
		115					120					125			

<210> 178  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

<400> 178

Met	Pro	Phe	Gly	Gly	Gln	Gly	Pro	Leu	Gly	Ala	Pro	Pro	Pro	Phe	Pro
1				5					10					15	
Thr	Trp	Pro	Gly	Cys	Pro	Gln	Pro	Pro	Pro	Leu	His	Ala	Trp	Gln	Ala
			20					25					30		
Gly	Thr	Pro	Pro	Glu	Pro	Ser	Pro	Gln	Pro	Ala	Ala	Phe	Pro	Gln	Ser
		35					40					45			
Leu	Pro	Phe	Pro	Gln	Ser	Pro	Ala	Phe	Pro	Thr	Ala	Ser	Pro	Ala	Pro
	50					55					60				
Pro	Gln	Ser	Pro	Gly	Leu	Gln	Pro	Leu	Ile	Ile	His	His	Ala	Gln	Met
65					70					75					80

Val	Gln	Leu	Gly	Leu	Asn	Asn	His	Met	Trp	Asn	Gln	Arg	Gly	Ser	Gln
				85					90					95	

Ala	Pro	Glu	Asp	Lys	Thr	Gln	Glu	Ala	Glu
			100					105	

<210> 179

<211> 77

<212> PRT

<213> homo sapiens

<400> 179

Gly	Asn	Pro	Glu	Leu	Pro	Trp	Arg	Lys	Phe	Gln	Cys	Gln	His	Ser	Cys
1				5					10					15	

Ser	Leu	Trp	Pro	Ser	Pro	Thr	Leu	Trp	Pro	Glu	Ile	Pro	Gln	Ser	Asn
			20					25					30		

Leu	Glu	Pro	Lys	Arg	Thr	Gln	Arg	Thr	Leu	Asp	Pro	Asn	Cys	Pro	Arg
		35					40					45			

Pro	Ser	Pro	Glu	Val	Gly	Val	Thr	Asn	Ser	Ser	Gly	Leu	Arg	His	Met
	50					55					60				

Lys	Lys	Leu	Tyr	Ile	Asn	Pro	Arg	Gln	Ala	Thr	Asn	Pro
65					70					75		

<210> 180

<211> 64

<212> PRT

<213> homo sapiens

<400> 180

Pro	Pro	Thr	His	Thr	Arg	Gln	Val	Gly	Glu	Glu	Ile	Gln	Ser	Cys	His
1				5					10					15	

Gly	Glu	Asn	Ser	Ser	Val	Ser	Ile	Leu	Ala	Pro	Cys	Gly	Pro	Leu	Leu
			20					25					30		

His	Ser	Gly	Gln	Arg	Tyr	His	Ser	Gln	Thr	Trp	Ser	Gln	Lys	Gly	His
		35					40					45			

Lys	Gly	Leu	Ser	Thr	Gln	Thr	Ala	Pro	Asp	Pro	Leu	Gln	Arg	Leu	Gly
	50					55					60				

<210> 181

<211> 206

<212> PRT

<213> homo sapiens

<400> 181

Arg	Leu	Ser	Cys	Ala	Gly	Thr	Leu	Ser	Gly	Ser	Gly	Pro	His	Pro	Ser
1				5					10					15	

Arg	Arg	Leu	Thr	Gln	Gly	Arg	Trp	Val	Arg	Lys	Ser	Arg	Val	Ala	Met
			20					25					30		

Glu	Lys	Ile	Pro	Val	Ser	Ala	Phe	Leu	Leu	Leu	Val	Ala	Leu	Ser	Tyr
		35					40					45			

Thr	Leu	Ala	Arg	Asp	Thr	Thr	Val	Lys	Pro	Gly	Ala	Lys	Lys	Asp	Thr
	50					55					60				
Lys	Asp	Ser	Arg	Pro	Lys	Leu	Pro	Gln	Thr	Leu	Ser	Arg	Gly	Trp	Gly
65					70					75					80
Asp	Gln	Leu	Ile	Trp	Thr	Gln	Thr	Tyr	Glu	Glu	Ala	Leu	Tyr	Lys	Ser
				85					90					95	
Lys	Thr	Ser	Asn	Lys	Pro	Leu	Met	Ile	Ile	His	His	Leu	Asp	Glu	Cys
			100					105					110		
Pro	His	Ser	Gln	Ala	Leu	Lys	Lys	Val	Phe	Ala	Glu	Asn	Lys	Glu	Ile
		115					120					125			
Gln	Lys	Leu	Ala	Glu	Gln	Phe	Val	Leu	Leu	Asn	Leu	Val	Tyr	Glu	Thr
	130					135					140				
Thr	Asp	Lys	His	Leu	Ser	Pro	Asp	Gly	Gln	Tyr	Val	Pro	Arg	Ile	Met
145					150					155					160
Phe	Val	Asp	Pro	Ser	Leu	Thr	Val	Arg	Ala	Asp	Ile	Thr	Gly	Arg	Tyr
				165					170					175	
Ser	Asn	Arg	Leu	Tyr	Ala	Tyr	Glu	Pro	Ala	Asp	Thr	Ala	Leu	Leu	Leu
			180					185					190		
Asp	Asn	Met	Lys	Lys	Ala	Leu	Lys	Leu	Leu	Lys	Thr	Glu	Leu		
		195					200					205			

<210> 182

<211> 206

<212> PRT

<213> homo sapiens

<400> 182

Arg	Val	Phe	Gln	Glu	Glu	Glu	Leu	Val	Arg	Arg	Gln	Arg	Asn	Gly	Ala
1				5					10					15	
Ser	Gly	Pro	Arg	Pro	Gly	Leu	Arg	Arg	Leu	Arg	Gly	Gly	Arg	Arg	Ala
			20					25					30		
Val	Arg	Arg	Lys	Glu	Arg	Leu	Leu	His	Arg	Gln	Leu	Pro	Ala	Val	His
		35					40					45			
Lys	Arg	Gly	Ala	Arg	Val	Lys	Leu	Ser	Ser	Pro	Glu	Arg	Asp	Val	Glu
	50					55					60				
Arg	Asp	Val	Phe	Leu	Tyr	Arg	Ala	Tyr	Leu	Ala	Gln	Arg	Lys	Phe	Gly
65					70					75					80
Val	Val	Leu	Asp	Glu	Ile	Lys	Pro	Ser	Ser	Ala	Pro	Glu	Leu	Gln	Ala
				85					90					95	
Val	Arg	Met	Phe	Ala	Asp	Tyr	Leu	Ala	His	Glu	Ser	Arg	Arg	Asp	Ser
			100					105					110		
Ile	Val	Ala	Glu	Leu	Asp	Arg	Glu	Met	Ser	Arg	Ser	Val	Asp	Val	Thr
		115					120					125			
Asn	Thr	Thr	Phe	Leu	Leu	Met	Ala	Ala	Ser	Ile	Tyr	Leu	His	Asp	Gln
	130					135					140				

Asn 145	Pro	Asp	Ala	Ala	Leu 150	Arg	Ala	Leu	His	Gln 155	Gly	Asp	Ser	Leu	Glu 160
Cys	Thr	Ala	Met	Thr 165	Val	Gln	Ile	Leu	Leu 170	Lys	Leu	Asp	Arg	Leu 175	Asp
Leu	Ala	Arg	Lys 180	Glu	Leu	Lys	Arg	Met 185	Gln	Asp	Leu	Asp	Glu 190	Asp	Ala
Thr	Leu	Thr 195	Gln	Leu	Lys	Val	Leu 200	Val	Ser	Leu	Gln	Arg 205	Val		

<210> 183  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 183

Leu 1	Pro	Arg	Pro	Arg 5	Glu	Ser	Glu	Gly	Gln 10	His	Arg	Gly	Arg	Ala 15	Gly
Pro	Arg	Asp	Glu 20	Gln	Glu	Arg	Gly	Arg 25	Asp	Gln	His	His	Leu 30	Pro	Ala
His	Gly	Arg 35	Leu	His	Leu	Ser	Pro 40	Arg	Pro	Glu	Pro	Gly 45	Cys	Arg	Pro
Ala	Cys 50	Ala	Ala	Pro	Gly	Gly 55	Gln	Pro	Gly	Val	His 60	Ser	His	Asp	Ser
Ala 65	Asp	Pro	Ala	Glu	Ala 70	Gly	Pro	Pro	Gly	Pro 75	Arg	Pro	Glu	Gly	Ala 80
Glu	Glu	Asn	Ala	Gly 85	Pro	Gly	Arg	Gly	Cys 90	His	Pro	His	Pro	Ala 95	Gln
Gly	Leu	Gly	Lys 100	Leu	Ala	Thr	Gly	Val 105	Lys	Ala	Gln	Gly	Ser 110	Phe	

<210> 184  
 <211> 165  
 <212> PRT  
 <213> homo sapiens

<400> 184

Gly 1	Thr	Ile	Leu	Pro 5	Ile	Pro	Glu	Ile	Arg 10	Arg	Ile	Leu	Glu	Leu 15	Leu
His	Pro	Leu	Gln 20	Ala	Tyr	Gln	Asp	Leu 25	Glu	Leu	Gly	Glu	Gly 30	Gly	Ile
Leu	Val	Gln 35	Val	Leu	His	Ser	Leu 40	Gln	Leu	Leu	Pro	Gly 45	Glu	Val	Gln
Ala	Val 50	Gln	Leu	Gln	Gln	Asp 55	Leu	His	Cys	His	Gly 60	Cys	Ala	Leu	Gln
Ala 65	Val	Pro	Leu	Val	Gln 70	Arg	Thr	Gln	Gly	Gly 75	Ile	Arg	Val	Leu	Val 80

Val	Glu	Ile	Asp	Gly 85	Gly	Gly	His	Glu	Gln 90	Glu	Gly	Gly	Val	Gly 95	His	
Val	His	Ala	Pro 100	Ala	His	Leu	Ser	Val 105	Gln	Leu	Gly	His	Asp 110	Ala	Val	
Pro	Pro	Thr 115	Leu	Val	Gly	Glu	Val 120	Val	Ser	Lys	His	Ala 125	His	Gly	Leu	
Glu	Leu 130	Arg	Gly	Arg	Gly	Gly 135	Leu	Asp	Leu	Ile	Gln 140	Asp	His	Thr	Glu	
Leu 145	Pro	Leu	Arg	Gln	Val 150	Arg	Ser	Ile	Gln	Glu 155	Asp	Val	Pro	Leu	His 160	
Val	Ser	Leu	Trp	Ala 165												

<210> 185

<211> 75

<212> PRT

<213> homo sapiens

<400> 185

Leu 1	Leu	Ser	Met	Arg 5	Met	Ile	Leu	Lys	Pro 10	Gln	Ser	Phe	Met	Ile 15	Leu	
Met	Met	Leu	Arg 20	Ser	Ser	Asn	Arg	Val 25	Thr	Trp	Lys	Leu	Leu 30	Leu	Ile	
Gly	Leu	Asp 35	Tyr	Ile	Arg	Tyr	Gln 40	Met	Glu	Asn	Gln	Lys 45	Thr	Ser	Leu	
Leu	Leu 50	Met	Glu	Asn	Ser	Lys 55	Thr	Arg	Leu	Leu	Leu 60	Leu	Lys	Leu	Leu	
Asn 65	Pro	Leu	Ile	Asn	Val 70	Gly	Lys	His	Cys	Leu 75						

<210> 186

<211> 340

<212> PRT

<213> homo sapiens

<400> 186

Arg 1	Thr	Val	Ile	Asp 5	Ala	Met	Ser	Ala	Leu 10	Leu	Arg	Leu	Leu	Arg 15	Thr	
Gly	Ala	Pro	Ala 20	Ala	Ala	Cys	Leu	Arg 25	Leu	Gly	Thr	Ser	Ala 30	Gly	Thr	
Gly	Ser	Arg 35	Arg	Ala	Met	Ala	Leu 40	Tyr	His	Thr	Glu	Glu 45	Arg	Gly	Gln	
Pro	Cys 50	Ser	Gln	Asn	Tyr	Arg 55	Leu	Phe	Phe	Lys	Asn 60	Val	Thr	Gly	His	
Tyr 65	Ile	Ser	Pro	Phe	His 70	Asp	Ile	Pro	Leu	Lys 75	Val	Asn	Ser	Lys	Glu 80	
Glu	Asn	Gly	Ile	Pro	Met	Lys	Lys	Ala	Arg	Asn	Asp	Glu	Tyr	Glu	Asn	

				85				90				95			
Leu	Phe	Asn	Met	Ile	Val	Glu	Ile	Pro	Arg	Trp	Thr	Asn	Ala	Lys	Met
			100					105					110		
Glu	Ile	Ala	Thr	Lys	Glu	Pro	Met	Asn	Pro	Ile	Lys	Gln	Tyr	Val	Lys
		115					120					125			
Asp	Gly	Lys	Leu	Arg	Tyr	Val	Ala	Asn	Ile	Phe	Pro	Tyr	Lys	Gly	Tyr
	130					135					140				
Ile	Trp	Asn	Tyr	Gly	Thr	Leu	Pro	Gln	Thr	Trp	Glu	Asp	Pro	His	Glu
145					150					155					160
Lys	Asp	Lys	Ser	Thr	Asn	Cys	Phe	Gly	Asp	Asn	Asp	Pro	Ile	Asp	Val
				165					170					175	
Cys	Glu	Ile	Gly	Ser	Lys	Ile	Leu	Ser	Cys	Gly	Glu	Val	Ile	His	Val
			180					185					190		
Lys	Ile	Leu	Gly	Ile	Leu	Ala	Leu	Ile	Asp	Glu	Gly	Glu	Thr	Asp	Trp
		195					200					205			
Lys	Leu	Ile	Ala	Ile	Asn	Ala	Asn	Asp	Pro	Glu	Ala	Ser	Lys	Phe	His
	210					215					220				
Asp	Ile	Asp	Asp	Val	Lys	Lys	Phe	Lys	Pro	Gly	Tyr	Leu	Glu	Ala	Thr
225					230					235					240
Leu	Asn	Trp	Phe	Arg	Leu	Tyr	Lys	Val	Pro	Asp	Gly	Lys	Pro	Glu	Asn
				245					250					255	
Gln	Phe	Ala	Phe	Asn	Gly	Glu	Phe	Lys	Asn	Lys	Ala	Phe	Ala	Leu	Glu
			260					265					270		
Val	Ile	Lys	Ser	Thr	His	Gln	Cys	Trp	Lys	Ala	Leu	Leu	Met	Lys	Lys
		275					280					285			
Cys	Asn	Gly	Gly	Ala	Ile	Asn	Cys	Thr	Asn	Val	Gln	Ile	Ser	Asp	Ser
	290					295					300				
Pro	Phe	Arg	Cys	Thr	Gln	Glu	Glu	Ala	Arg	Ser	Leu	Val	Glu	Ser	Val
305					310					315					320
Ser	Ser	Ser	Pro	Asn	Lys	Glu	Ser	Asn	Glu	Glu	Glu	Gln	Val	Trp	His
				325					330					335	
Phe	Leu	Gly	Lys												
			340												

<210> 187

<211> 131

<212> PRT

<213> homo sapiens

<400> 187

Leu	Ser	Ile	Leu	Tyr	Ile	Leu	Phe	Asn	Gly	Ile	His	Trp	Leu	Leu	Gly
1				5					10					15	
Gly	Asn	Leu	His	Phe	Ser	Ile	Cys	Pro	Pro	Arg	Tyr	Phe	Tyr	Asn	His
			20					25					30		

Ile	Lys	Gln	Ile	Leu	Ile	Phe	Ile	Ile	Ser	Cys	Phe	Leu	His	Arg	Asn	
		35					40					45				
Ala	Ile	Phe	Leu	Phe	Arg	Val	His	Leu	Gln	Arg	Asn	Ile	Met	Lys	Gly	
	50					55					60					
Gly	Asn	Val	Val	Thr	Ser	Tyr	Ile	Leu	Lys	Glu	Glu	Ala	Val	Ile	Leu	
65					70					75					80	
Arg	Ala	Gly	Leu	Ala	Ala	Leu	Leu	Ser	Val	Val	Gln	Gly	His	Ser	Thr	
				85					90					95		
Ala	Arg	Pro	Gly	Pro	Cys	Thr	Gly	Pro	Gln	Pro	Gln	Ala	Arg	Ser	Gly	
			100					105					110			
Trp	Gly	Thr	Arg	Ala	Gln	Gln	Pro	Gln	Gln	Arg	Ala	His	Gly	Val	Asn	
		115					120					125				
Asp	Gly	Pro														
	130															
<210> 188																
<211> 436																
<212> PRT																
<213> homo sapiens																
<400> 188																
Gly	Arg	Gly	Met	Gly	Arg	Val	Gln	Leu	Phe	Glu	Ile	Ser	Leu	Ser	His	
1				5					10					15		
Gly	Arg	Val	Val	Tyr	Ser	Pro	Gly	Glu	Pro	Leu	Ala	Gly	Thr	Val	Arg	
			20					25					30			
Val	Arg	Leu	Gly	Ala	Pro	Leu	Pro	Phe	Arg	Ala	Ile	Arg	Val	Thr	Cys	
		35					40					45				
Ile	Gly	Ser	Cys	Gly	Val	Ser	Asn	Lys	Ala	Asn	Asp	Thr	Ala	Trp	Val	
	50					55					60					
Val	Glu	Glu	Gly	Tyr	Phe	Asn	Ser	Ser	Leu	Ser	Leu	Ala	Asp	Lys	Gly	
65					70					75					80	
Ser	Leu	Pro	Ala	Gly	Glu	His	Ser	Phe	Pro	Phe	Gln	Phe	Leu	Leu	Pro	
				85					90					95		
Ala	Thr	Ala	Pro	Thr	Ser	Phe	Glu	Gly	Pro	Phe	Gly	Lys	Ile	Val	His	
			100					105					110			
Gln	Val	Arg	Ala	Ala	Ile	His	Thr	Pro	Arg	Phe	Ser	Lys	Asp	His	Lys	
		115					120					125				
Cys	Ser	Leu	Val	Phe	Tyr	Ile	Leu	Ser	Pro	Leu	Asn	Leu	Asn	Ser	Ile	
	130					135					140					
Pro	Asp	Ile	Glu	Gln	Pro	Asn	Val	Ala	Ser	Ala	Thr	Lys	Lys	Phe	Ser	
145					150					155					160	
Tyr	Lys	Leu	Val	Lys	Thr	Gly	Ser	Val	Val	Leu	Thr	Ala	Ser	Thr	Asp	
				165					170					175		
Leu	Arg	Gly	Tyr	Val	Val	Gly	Gln	Ala	Leu	Gln	Leu	His	Ala	Asp	Val	
			180					185					190			

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Glu	Asn	Gln	Ser	Gly	Lys	Asp	Thr	Ser	Pro	Val	Val	Ala	Ser	Leu	Leu
		195					200					205			
Gln	Lys	Val	Ser	Tyr	Lys	Ala	Lys	Arg	Trp	Ile	His	Asp	Val	Arg	Thr
	210					215					220				
Ile	Ala	Glu	Val	Glu	Gly	Ala	Gly	Val	Lys	Ala	Trp	Arg	Arg	Ala	Gln
225					230					235					240
Trp	His	Glu	Gln	Ile	Leu	Val	Pro	Ala	Leu	Pro	Gln	Ser	Ala	Leu	Pro
				245					250					255	
Gly	Cys	Ser	Leu	Ile	His	Ile	Asp	Tyr	Tyr	Leu	Gln	Val	Ser	Leu	Lys
			260					265					270		
Ala	Pro	Glu	Ala	Thr	Val	Thr	Leu	Pro	Val	Phe	Ile	Gly	Asn	Ile	Ala
		275					280					285			
Val	Asn	His	Ala	Pro	Val	Ser	Pro	Arg	Pro	Gly	Leu	Gly	Leu	Pro	Pro
	290					295					300				
Gly	Ala	Pro	Pro	Leu	Val	Val	Pro	Ser	Ala	Pro	Pro	Gln	Glu	Glu	Ala
305					310					315					320
Glu	Ala	Glu	Ala	Ala	Ala	Gly	Gly	Pro	His	Phe	Leu	Asp	Pro	Val	Phe
				325					330					335	
Leu	Ser	Thr	Lys	Ser	His	Ser	Gln	Arg	Gln	Pro	Leu	Leu	Ala	Thr	Leu
			340					345					350		
Ser	Ser	Val	Pro	Gly	Ala	Pro	Glu	Pro	Cys	Pro	Gln	Asp	Gly	Ser	Pro
		355					360					365			
Ala	Ser	His	Pro	Leu	His	Pro	Pro	Leu	Cys	Ile	Ser	Thr	Gly	Ala	Thr
	370					375					380				
Val	Pro	Tyr	Phe	Ala	Glu	Gly	Ser	Gly	Gly	Pro	Val	Pro	Thr	Thr	Ser
385					390					395					400
Thr	Leu	Ile	Leu	Pro	Pro	Glu	Tyr	Ser	Ser	Trp	Gly	Tyr	Pro	Tyr	Glu
				405					410					415	
Ala	Pro	Pro	Ser	Tyr	Glu	Gln	Ser	Cys	Gly	Gly	Val	Glu	Pro	Ser	Leu
			420					425					430		
Thr	Pro	Glu	Ser												
		435													

<210> 189  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 189

Ser	Val	Leu	Phe	Thr	Gly	Val	Val	Ser	Pro	Gly	Pro	Ser	Ser	Leu	Pro
1				5					10					15	
Pro	Pro	Pro	Gln	Pro	Gln	Gly	Glu	Glu	Gly	Gly	Cys	Arg	Gly	Ala	Gly
			20					25					30		
Arg	Gly	Trp	Ala	Gly	Pro	Glu	Trp	Ala	Arg	Leu	Gly	Gln	Glu	Arg	Arg



		35					40					45				
His	Glu	Ala	Leu	Gly	Ala	Pro	Val	Pro	Gly	Gln	Arg	Pro	Gly	Leu	Pro	
	50					55					60					
Gly	Glu	Gly	Ser	Thr	Gly	Ser	Ala	Leu	Arg	Gly	Gln	Ala	Gly	Phe	His	
65					70					75					80	
Ala	Ala	Ala	Ala	Leu	Leu	Ile	Arg	Arg	Trp	Gly	Leu	Ile	Gly	Val	Ala	
				85					90					95		
Pro	Arg	Thr	Val	Leu	Trp	Arg	Lys	Asn	Gln	Gly	Ala	Gly	Ser	Gly	His	
			100					105					110			
Trp	Pro	Pro	Gly	Ala	Leu	Cys	Lys	Val	Gly	Asp	Ser	Gly	Thr	Cys		
		115					120					125				

<210> 190

<211> 213

<212> PRT

<213> homo sapiens

<400> 190

Leu	Val	Leu	Asn	Val	Gly	Met	Gln	Leu	Gln	Cys	Leu	Pro	His	His	Ile	
1				5					10					15		
Ala	Ala	Glu	Ile	Ser	Ala	Gly	Cys	Glu	Asp	His	Ala	Ala	Arg	Leu	His	
			20					25					30			
Gln	Leu	Val	Gly	Glu	Leu	Leu	Gly	Gly	Arg	Gly	His	Val	Gly	Leu	Leu	
		35					40					45				
Asn	Val	Trp	Asp	Ala	Val	Gln	Val	Gln	Gly	Ala	Gln	Asp	Ile	Glu	His	
	50					55					60					
Glu	Ala	Ala	Leu	Val	Ile	Leu	Gly	Lys	Pro	Trp	Arg	Val	Asp	Gly	Gly	
65					70					75					80	
Pro	His	Leu	Val	His	Asp	Leu	Pro	Glu	Arg	Thr	Leu	Lys	Gly	Arg	Gly	
				85					90					95		
Cys	Ser	Gly	Arg	Lys	Gln	Glu	Leu	Glu	Gly	Glu	Ala	Val	Leu	Ser	Ser	
			100					105					110			
Gly	Gln	Ala	Pro	Leu	Val	Cys	Gln	Arg	Gln	Gly	Thr	Val	Glu	Val	Thr	
		115					120					125				
Leu	Leu	His	Tyr	Pro	Arg	Cys	Val	Ile	Ser	Leu	Val	Gly	Asp	Pro	Ala	
	130					135					140					
Gly	Thr	Tyr	Ala	Gly	His	Pro	Asp	Gly	Ser	Glu	Arg	Gln	Arg	Cys	Pro	
145					150					155					160	
Gln	Ala	His	Ala	His	Gly	Pro	Ser	Gln	Arg	Leu	Pro	Gly	Ala	Val	Asp	
				165					170					175		
Asp	Ala	Ala	Val	Ala	Gln	Ala	Asp	Leu	Glu	Glu	Leu	His	Ser	Pro	His	
			180					185					190			
Ala	Ala	Ala	Ser	Pro	Ala	Ser	Arg	Ala	Ala	Thr	Pro	Pro	Pro	Ala	Ala	
		195					200					205				

Arg Glu Ser Arg Leu  
210

<210> 191

<211> 635

<212> PRT

<213> homo sapiens

<400> 191

Gly 1	Gly	Val	Ser	Pro 5	Trp	Arg	Ala	Cys	Val 10	Gln	Gln	Arg	Met	Glu 15	Glu
Ser	Glu	Pro	Glu 20	Arg	Lys	Arg	Ala	Arg 25	Thr	Asp	Glu	Val	Pro 30	Ala	Gly
Gly	Ser	Arg 35	Ser	Glu	Ala	Glu	Asp 40	Glu	Asp	Asp	Glu	Asp 45	Tyr	Val	Pro
Tyr	Val 50	Pro	Leu	Arg	Gln	Arg 55	Arg	Gln	Leu	Leu	Leu 60	Gln	Lys	Leu	Leu
Gln 65	Arg	Arg	Arg	Lys	Gly 70	Ala	Ala	Glu	Glu	Glu 75	Gln	Gln	Asp	Ser	Gly 80
Ser	Glu	Pro	Arg	Gly 85	Asp	Glu	Asp	Asp	Ile 90	Pro	Leu	Gly	Pro	Gln 95	Ser
Asn	Val	Ser	Leu 100	Leu	Asp	Gln	His	Gln 105	His	Leu	Lys	Glu	Lys 110	Ala	Glu
Ala	Arg	Lys 115	Glu	Ser	Ala	Lys	Glu 120	Lys	Gln	Leu	Lys	Glu 125	Glu	Glu	Lys
Ile	Leu 130	Glu	Ser	Val	Ala	Glu 135	Gly	Arg	Ala	Leu	Met 140	Ser	Val	Lys	Glu
Met 145	Ala	Lys	Gly	Ile	Thr 150	Tyr	Asp	Asp	Pro	Ile 155	Lys	Thr	Ser	Trp	Thr 160
Pro	Pro	Arg	Tyr	Val 165	Leu	Ser	Met	Ser	Glu 170	Glu	Arg	His	Glu	Arg 175	Val
Arg	Lys	Lys	Tyr 180	His	Ile	Leu	Val	Glu 185	Gly	Asp	Gly	Ile	Pro 190	Pro	Pro
Ile	Lys	Ser 195	Phe	Lys	Glu	Met	Lys 200	Phe	Pro	Ala	Ala	Ile 205	Leu	Arg	Gly
Leu	Lys 210	Lys	Lys	Gly	Ile	His 215	His	Pro	Thr	Pro	Ile 220	Gln	Ile	Gln	Gly
Ile 225	Pro	Thr	Ile	Leu	Ser 230	Gly	Arg	Asp	Met	Ile 235	Gly	Ile	Ala	Phe	Thr 240
Gly	Ser	Gly	Lys	Thr 245	Leu	Val	Phe	Thr	Leu 250	Pro	Val	Ile	Met	Phe 255	Cys
Leu	Glu	Gln	Glu 260	Lys	Arg	Leu	Pro	Phe 265	Ser	Lys	Arg	Glu	Gly 270	Pro	Tyr
Gly	Leu	Ile 275	Ile	Cys	Pro	Ser	Arg 280	Glu	Leu	Ala	Arg	Gln 285	Thr	His	Gly

Ile	Leu	Glu	Tyr	Tyr	Cys	Arg	Leu	Leu	Gln	Glu	Asp	Ser	Ser	Pro	Leu
	290					295					300				
Leu	Arg	Cys	Ala	Leu	Cys	Ile	Gly	Gly	Met	Ser	Val	Lys	Glu	Gln	Met
305					310					315					320
Glu	Thr	Ile	Arg	His	Gly	Val	His	Met	Met	Val	Ala	Thr	Pro	Gly	Arg
				325					330					335	
Leu	Met	Asp	Leu	Leu	Gln	Lys	Lys	Met	Val	Ser	Leu	Asp	Ile	Cys	Arg
			340					345					350		
Tyr	Leu	Ala	Leu	Asp	Glu	Ala	Asp	Arg	Met	Ile	Asp	Met	Gly	Phe	Glu
		355					360					365			
Gly	Asp	Ile	Arg	Thr	Ile	Phe	Ser	Tyr	Phe	Lys	Gly	Gln	Arg	Gln	Thr
	370					375					380				
Leu	Leu	Phe	Ser	Ala	Thr	Met	Pro	Lys	Lys	Ile	Gln	Asn	Phe	Ala	Lys
385					390					395					400
Ser	Ala	Leu	Val	Lys	Pro	Val	Thr	Ile	Asn	Val	Gly	Arg	Ala	Gly	Ala
				405					410					415	
Ala	Ser	Leu	Asp	Val	Ile	Gln	Glu	Val	Glu	Tyr	Val	Lys	Glu	Glu	Ala
			420					425					430		
Lys	Met	Val	Tyr	Leu	Leu	Glu	Cys	Leu	Gln	Lys	Thr	Pro	Pro	Pro	Val
		435					440					445			
Leu	Ile	Phe	Ala	Glu	Lys	Lys	Ala	Asp	Val	Asp	Ala	Ile	His	Glu	Tyr
	450					455					460				
Leu	Leu	Leu	Lys	Gly	Val	Glu	Ala	Val	Ala	Ile	His	Gly	Gly	Lys	Asp
465					470					475					480
Gln	Glu	Glu	Arg	Thr	Lys	Ala	Ile	Glu	Ala	Phe	Arg	Glu	Gly	Lys	Lys
				485					490					495	
Asp	Val	Leu	Val	Ala	Thr	Asp	Val	Ala	Ser	Lys	Gly	Leu	Asp	Phe	Pro
			500					505					510		
Ala	Ile	Gln	His	Val	Ile	Asn	Tyr	Asp	Met	Pro	Glu	Glu	Ile	Glu	Asn
		515					520					525			
Tyr	Val	His	Arg	Ile	Gly	Arg	Thr	Gly	Arg	Ser	Gly	Asn	Thr	Gly	Ile
	530					535					540				
Ala	Thr	Thr	Phe	Ile	Asn	Lys	Ala	Cys	Asp	Glu	Ser	Val	Leu	Met	Asp
545					550					555					560
Leu	Lys	Ala	Leu	Leu	Leu	Glu	Ala	Lys	Gln	Lys	Val	Pro	Pro	Val	Leu
				565					570					575	
Gln	Val	Leu	His	Cys	Gly	Asp	Glu	Ser	Met	Leu	Asp	Ile	Gly	Gly	Glu
			580					585					590		
Arg	Gly	Cys	Ala	Phe	Cys	Gly	Gly	Leu	Gly	His	Arg	Ile	Thr	Asp	Cys
		595					600					605			
Pro	Lys	Leu	Glu	Ala	Met	Gln	Thr	Lys	Gln	Val	Ser	Asn	Ile	Gly	Arg
	610					615					620				

Lys	Asp	Tyr	Leu	Ala	His	Ser	Ser	Met	Asp	Phe
625					630					635

<210> 192  
 <211> 147  
 <212> PRT  
 <213> homo sapiens

<400> 192

Lys	Pro	Ser	Arg	Arg	Cys	Arg	Pro	Cys	Cys	Arg	Cys	Cys	Ile	Ala	Gly
1				5				10						15	
Met	Ser	Pro	Cys	Trp	Thr	Leu	Glu	Glu	Ser	Ala	Ala	Val	Pro	Ser	Ala
			20					25					30		
Gly	Ala	Trp	Val	Ile	Gly	Ser	Leu	Thr	Ala	Pro	Asn	Ser	Arg	Leu	Cys
		35					40					45			
Arg	Pro	Ser	Arg	Ser	Ala	Thr	Ser	Val	Ala	Arg	Thr	Thr	Trp	Pro	Thr
	50					55					60				
Ala	Pro	Trp	Thr	Ser	Glu	Pro	Thr	Val	Phe	Pro	Ser	Leu	Gln	Glu	Ala
65					70				75						80
Ser	Val	Pro	Lys	Thr	Ala	Thr	Ser	Leu	His	Ile	Gln	Gln	Pro	Pro	Gly
				85					90					95	
Gln	Asn	Gln	His	Phe	Ser	Ser	Ala	Gly	Leu	Glu	Trp	Ala	Arg	Leu	Val
			100					105					110		
Leu	Ala	Ala	Cys	Ser	Leu	Cys	Ser	Ser	Glu	Leu	Leu	Phe	Leu	Phe	Pro
		115					120					125			
Phe	Thr	Pro	Ala	Ala	Ile	Lys	Ala	Gln	Thr	Ser	Ser	Pro	Lys	Lys	Lys
	130					135					140				
Lys	Lys	Lys													
145															

<210> 193  
 <211> 150  
 <212> PRT  
 <213> homo sapiens

<400> 193

Asp	Ile	Leu	Leu	Ala	Leu	Pro	Glu	Cys	Leu	Asp	Gly	Leu	Ser	Pro	Phe
1				5					10					15	
Leu	Leu	Val	Phe	Ala	Pro	Met	Asp	Gly	Tyr	Gly	Leu	Asn	Pro	Leu	Glu
			20					25					30		
Gln	Gln	Val	Leu	Val	Asp	Gly	Val	His	Val	Cys	Leu	Leu	Leu	Cys	Lys
		35					40					45			
Asp	Glu	Tyr	Arg	Arg	Gly	Cys	Leu	Leu	Gln	Ala	Leu	Glu	Gln	Val	His
	50					55					60				
His	Leu	Gly	Leu	Leu	Leu	His	Ile	Phe	Tyr	Leu	Leu	Asp	Asp	Ile	Gln
65					70					75					80

Ala	Gly	Ser	Pro	Ser 85	Ala	Pro	His	Ile	Asp 90	Gly	His	Arg	Leu	Tyr 95	Lys
Gly	Thr	Leu	Ser 100	Lys	Val	Leu	Asn	Leu 105	Leu	Arg	His	Gly	Gly 110	Thr	Glu
Glu	Gln	Gly 115	Leu	Ser	Leu	Ala	Leu 120	Glu	Val	Gly	Glu	Asp 125	Gly	Thr	Asp
Val	Thr 130	Leu	Glu	Ala	His	Val 135	Asp	His	Ala	Val	Ser 140	Leu	Val	Gln	Gly
Gln 145	Val	Ala	Thr	Asp	Val 150										

<210> 194

<211> 310

<212> PRT

<213> homo sapiens

<400> 194

Glu 1	Ala	Pro	Ala	Ala 5	Ala	Arg	Thr	Gln	Ser 10	Pro	Ala	Ala	Ala 15	Ala	Gln
Arg	Gly	Asp	Asn 20	Val	Tyr	Val	Val	Thr 25	Glu	Val	Leu	Gln	Thr 30	Gln	Lys
Glu	Val	Glu 35	Val	Thr	Arg	Thr	His 40	Lys	Arg	Glu	Gly	Ser 45	Gly	Arg	Phe
Ser	Leu 50	Pro	Gly	Ala	Thr	Cys 55	Leu	Gln	Gly	Glu	Gly 60	Gln	Gly	His	Leu
Ser 65	Gln	Lys	Lys	Thr	Val 70	Thr	Ile	Pro	Ser	Gly 75	Ser	Thr	Leu	Ala	Phe 80
Arg	Val	Ala	Gln	Leu 85	Val	Ile	Asp	Ser	Asp 90	Leu	Asp	Val	Leu	Leu 95	Phe
Pro	Asp	Lys	Lys 100	Gln	Arg	Thr	Phe	Gln 105	Pro	Pro	Ala	Thr	Gly 110	His	Lys
Arg	Ser	Thr 115	Ser	Glu	Gly	Ala	Trp 120	Pro	Gln	Leu	Pro	Ser 125	Gly	Leu	Ser
Met	Met 130	Arg	Cys	Leu	His	Asn 135	Phe	Leu	Thr	Asp	Gly 140	Val	Pro	Ala	Glu
Gly 145	Ala	Phe	Thr	Glu	Asp 150	Phe	Gln	Gly	Leu	Arg 155	Ala	Glu	Val	Glu	Thr 160
Ile	Ser	Lys	Glu	Leu 165	Glu	Leu	Leu	Asp	Arg 170	Glu	Leu	Cys	Gln	Leu 175	Leu
Leu	Glu	Gly	Leu 180	Glu	Gly	Val	Leu	Arg 185	Asp	Gln	Leu	Ala	Leu 190	Arg	Ala
Leu	Glu	Glu 195	Ala	Leu	Glu	Gln	Gly 200	Gln	Ser	Leu	Gly	Pro 205	Val	Glu	Pro
Leu	Asp 210	Gly	Pro	Ala	Gly	Ala 215	Val	Leu	Glu	Cys	Leu 220	Val	Leu	Ser	Ser

Gly 225	Met	Leu	Val	Pro	Glu 230	Leu	Ala	Ile	Pro	Val 235	Val	Tyr	Leu	Leu	Gly 240
Ala	Leu	Thr	Met	Leu 245	Ser	Glu	Thr	Gln	His 250	Lys	Leu	Leu	Ala	Glu 255	Ala
Leu	Glu	Ser	Gln 260	Thr	Leu	Leu	Gly	Pro 265	Leu	Glu	Leu	Val	Gly 270	Ser	Leu
Leu	Glu	Gln 275	Ser	Ala	Pro	Trp	Gln 280	Glu	Arg	Arg	Pro	Cys 285	Pro	Cys	Pro
Pro	Gly 290	Ser	Trp	Gly	Thr	Ala 295	Gly	Ala	Lys	Glu	His 300	Arg	Pro	Gly	Ser
Cys 305	Trp	Thr	Ser	Val	Ala 310										

<210> 195

<211> 244

<212> PRT

<213> homo sapiens

<400> 195

Thr 1	Thr	Gly	Ile	Ala 5	Ser	Ser	Gly	Thr	Ser 10	Ile	Pro	Glu	Asp	Asn 15	Thr
Arg	His	Ser	Arg 20	Thr	Ala	Pro	Ala	Gly 25	Pro	Ser	Arg	Gly	Ser 30	Thr	Gly
Pro	Arg	Leu 35	Trp	Pro	Cys	Ser	Ser 40	Ala	Ser	Ser	Lys	Ala 45	Arg	Arg	Ala
Ser	Trp 50	Ser	Arg	Ser	Thr	Pro 55	Ser	Arg	Pro	Ser	Ser 60	Ser	Ser	Trp	His
Ser 65	Ser	Leu	Ser	Lys	Ser 70	Ser	Ser	Ser	Leu	Glu 75	Met	Val	Ser	Thr	Ser 80
Ala	Arg	Arg	Pro	Trp 85	Lys	Ser	Ser	Val	Asn 90	Ala	Pro	Ser	Ala	Gly 95	Thr
Pro	Ser	Val 100	Arg	Lys	Leu	Trp	Arg	His 105	Leu	Ile	Met	Glu	Arg 110	Pro	Glu
Gly	Ser	Cys 115	Gly	Gln	Ala	Pro	Ser 120	Leu	Val	Glu	Arg	Leu 125	Trp	Pro	Val
Ala	Gly 130	Gly	Trp	Lys	Val	Leu 135	Cys	Phe	Leu	Ser	Gly 140	Lys	Arg	Arg	Thr
Ser 145	Lys	Ser	Glu	Ser	Ile 150	Thr	Ser	Trp	Ala	Thr 155	Arg	Asn	Ala	Arg	Val 160
Leu	Pro	Glu	Gly	Met 165	Val	Thr	Val	Phe	Phe 170	Trp	Leu	Arg	Trp	Pro 175	Trp
Pro	Ser	Pro	Cys 180	Lys	His	Val	Ala	Pro 185	Gly	Arg	Glu	Asn	Arg 190	Pro	Glu
Pro	Ser	Arg	Leu	Trp	Val	Arg	Val	Thr	Ser	Thr	Ser	Phe	Cys	Val	Cys

			195				200					205			
Ser	Thr	Ser	Val	Thr	Thr	Tyr	Thr	Leu	Ser	Pro	Arg	Cys	Ala	Ala	Ala
	210					215					220				
Ala	Gly	Leu	Cys	Val	Leu	Ala	Ala	Ala	Gly	Ala	Ser	His	Gly	Ala	Glu
225					230					235					240
Ser	Ala	Arg	Cys												

<210> 196  
 <211> 229  
 <212> PRT  
 <213> homo sapiens

<400> 196

Thr	Gly	His	Met	Ala	Thr	Gly	Leu	Leu	Ala	Phe	Leu	Gly	Leu	Ala	Ala
1				5					10					15	
Gly	Gly	Gln	Thr	Leu	Cys	Pro	Ala	Gly	Glu	Leu	Pro	Gly	His	Ala	Arg
			20					25					30		
Ala	Gln	Ala	Ser	Gly	Ala	Pro	Gly	Ser	Val	Leu	Ile	Ala	Val	Pro	Gly
		35					40					45			
Arg	Arg	Arg	Val	His	Thr	Cys	Gly	Pro	Gly	Pro	Ala	Ala	Pro	Ser	Thr
	50					55					60				
Arg	Gly	Glu	Cys	Pro	Pro	Pro	Ala	Leu	Gly	His	Thr	Arg	Pro	Ala	Arg
65					70					75					80
Pro	Arg	Pro	Val	Leu	Leu	Arg	Pro	Ser	Cys	Ser	Pro	Gly	Ala	Arg	Gly
				85					90					95	
Ala	Gly	Thr	Trp	Ser	Ala	Leu	Leu	Pro	Arg	Gly	Thr	Leu	Leu	Gln	Glu
			100					105					110		
Ala	Ala	His	Gln	Leu	Glu	Arg	Pro	Gln	Gln	Gly	Leu	Arg	Leu	Gln	Arg
		115					120					125			
Leu	Arg	Gln	Gln	Leu	Val	Leu	Arg	Phe	Thr	Gln	His	Gly	Gln	Cys	Pro
	130					135					140				
Gln	Gln	Val	Asp	Asn	Arg	Asp	Ser	Glu	Phe	Arg	His	Gln	His	Ser	Gly
145					150					155					160
Gly	Gln	His	Gln	Ala	Leu	Gln	Asp	Ser	Thr	Cys	Trp	Thr	Val	Gln	Gly
				165					170					175	
Leu	His	Arg	Pro	Lys	Ala	Leu	Ala	Leu	Leu	Gln	Arg	Leu	Leu	Gln	Gly
			180					185					190		
Ser	Gln	Gly	Gln	Leu	Val	Pro	Gln	His	Pro	Leu	Gln	Ala	Leu	Gln	Gln
		195					200					205			
Gln	Leu	Ala	Gln	Leu	Ser	Val	Gln	Lys	Leu	Gln	Phe	Leu	Gly	Asp	Gly
	210					215					220				
Leu	His	Leu	Cys	Pro											
225															

<210> 197

<211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 197

Thr 1	Glu	Ile	Leu	Pro 5	Val	Phe	Val	Arg	Leu 10	Ala	Gly	Val	Pro	Ile 15	Cys
Ser	Thr	Gly	Asn 20	Ala	Ser	Ala	Met	Leu 25	Gln	Pro	Gln	Lys	Pro 30	Gly	Leu
Ser	Leu	Gln 35	Gln	Gln	Ala	Glu	Pro 40	Cys	Leu	Trp	Ser	Gly 45	Ala	Val	His
Ser	Ser 50	Val	Cys	Leu	Val	Leu 55	Gly	Leu	Glu	Leu	Asp 60	Arg	Gly	Gly	Val
Ser 65	Ser	Pro	Ser	Leu	Asn 70	Ser	Glu	Gln	Thr	Leu 75	Cys	Leu	Ala	Pro	Val 80
Cys	Pro	Gly	Asn	Ser 85	Pro	Gly	Pro	His	Trp 90	Glu	Pro	Leu	Val	Phe 95	

<210> 198  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 198

Ala 1	Val	Pro	Arg	Gly 5	Ser	Leu	Arg	Glu	Asp 10	Gly	Lys	Val	Arg	Cys 15	Met
Ser	Asn	Leu	Leu 20	Met	Ala	Gly	Ser	Pro 25	Leu	Cys	Pro	Leu	Ser 30	Leu	Ala
Leu	Val	Ile 35	Ala	Glu	Leu	Cys	Ala 40	Gln	Cys	Cys	Gly	Leu 45	Ala	Val	Ala
Arg	Leu 50	Phe	Leu	Trp	Gly	Ala 55	Arg	Ala	Gly	Cys	Gly 60	Asn	Gln	Ser	Ser
Gln 65	Thr	Asp	Val	Ser	Gln 70	Ala	Glu	Asp	Ser	Phe 75	Leu	Ala	Glu	Val	Ser 80
Pro	His	Leu	Gln	Val 85	Ser	Gly	Trp	Gly	Gly 90	Ala	Arg	Arg	Gly	Arg 95	His
Thr	Pro	Cys	Leu 100	Thr											

<210> 199  
 <211> 155  
 <212> PRT  
 <213> homo sapiens

<400> 199

Val 1	Arg	His	Thr	Ser 5	His	Leu	Ala	Val	Leu 10	Thr	Gln	Gly	Ala	Pro 15	Gly
His	Cys	Ser	Cys	Ala	Ala	Trp	Ala	Leu	Leu	Leu	Arg	Thr	Pro	Arg	Ala



1000  
 900  
 800  
 700  
 600  
 500  
 400  
 300  
 200  
 100  
 0

20							25					30				
Pro	Asn	Glu	Gly	Leu	Gly	Asn	Cys	Leu	Gly	Thr	Leu	Gly	Pro	Gly	Thr	
		35					40					45				
Gly	Ser	Val	Leu	Asn	Ser	Gly	Lys	Val	Lys	Arg	Pro	His	Leu	Tyr	Pro	
	50					55					60					
Ala	Gln	Ala	Gln	Glu	Gln	Gly	Arg	Gln	Ser	Cys	Gly	Gln	His	Pro	Thr	
65					70					75					80	
Thr	Asp	Thr	Val	Leu	Pro	Ala	Ala	Gly	Val	Arg	Gly	Leu	Val	Ser	Glu	
				85					90					95		
Ala	Ala	Ala	Trp	His	Trp	His	Cys	Leu	Cys	Tyr	Arg	Trp	Gly	Leu	Leu	
			100					105				110				
Arg	Val	Ser	Gln	Ile	Gln	Gly	Glu	Phe	Gln	Phe	Thr	Gln	Pro	Lys	Gly	
		115					120					125				
Pro	Val	Cys	Arg	Ala	Ala	Leu	Thr	Arg	Ala	Gln	Gln	His	Ser	Thr	Glu	
	130					135					140					
Leu	Gly	Lys	Gly	Arg	Gly	Glu	Arg	Val	Lys	Asp						
145					150					155						

<210> 200  
 <211> 138  
 <212> PRT  
 <213> homo sapiens

<400> 200

Arg	Met	Lys	Cys	Ser	Gln	Pro	Pro	Arg	Cys	His	Phe	Gln	Ser	Asp	Phe
1				5					10					15	
Gln	Lys	Cys	Ala	Pro	Cys	Pro	Arg	Ala	Gln	Thr	His	Trp	Leu	Glu	Pro
			20					25					30		
Pro	Gly	Arg	Val	Gln	Thr	Ile	Ser	Ser	Met	Arg	Asn	Ala	Gln	Lys	Gly
		35					40					45			
Phe	Ala	Asp	Ser	Ile	Arg	Leu	Trp	Arg	Leu	Pro	Ala	Ser	Gly	Val	Gly
	50					55					60				
Trp	Val	Val	Ser	Pro	Pro	Ile	Gln	Thr	Gln	Glu	Val	Ala	Pro	Glu	Gly
65				70						75					80
Met	Tyr	Leu	Val	Gly	Ser	Ser	Ser	Gly	Thr	Leu	Gly	Gly	Cys	Arg	Ala
				85					90					95	
Leu	Thr	Gln	Val	Phe	Leu	Ser	Leu	Ser	Ser	Leu	Gly	Cys	Val	Cys	Ala
			100					105					110		
Cys	Ala	Cys	Ala	Cys	Leu	Cys	Phe	Ser	Leu	Trp	Ala	His	Gln	Asp	Ala
		115					120					125			
Pro	Arg	Arg	Ala	Cys	Ala	Arg	Val	Pro	Thr						
	130					135									

<210> 201  
 <211> 132  
 <212> PRT



130

<210> 203  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 203

Leu	Ala	Ala	Ile	Lys	Asp	Gln	Leu	Glu	Gly	Val	Gln	Gln	Ala	Leu	Ser
1				5					10					15	
Gln	Ala	Ala	Pro	Ile	Pro	Glu	Glu	Asp	Thr	Asp	Thr	Glu	Glu	Gly	Asp
			20					25					30		
Asp	Phe	Glu	Leu	Leu	Asp	Gln	Ser	Glu	Leu	Asp	Gln	Ile	Glu	Ser	Glu
		35					40					45			
Leu	Gly	Leu	Thr	Gln	Asp	Gln	Glu	Ala	Glu	Ala	Gln	Gln	Asn	Lys	Lys
	50					55					60				
Ser	Ser	Gly	Phe	Leu	Ser	Asn	Leu	Leu	Gly	Gly	His				
65					70					75					

<210> 204  
 <211> 102  
 <212> PRT  
 <213> homo sapiens

<400> 204

Arg	Val	Cys	Ser	Lys	His	Phe	Leu	Arg	Leu	Pro	Pro	Ser	Gln	Lys	Arg
1				5					10					15	
Thr	Gln	Thr	Leu	Lys	Lys	Val	Met	Thr	Leu	Asn	Tyr	Leu	Thr	Ser	Gln
			20					25					30		
Ser	Trp	Ile	Lys	Leu	Arg	Val	Asn	Trp	Asp	Leu	His	Lys	Thr	Arg	Lys
		35					40					45			
Gln	Lys	His	Ser	Lys	Ile	Arg	Ser	Leu	Gln	Val	Ser	Phe	Gln	Ile	Cys
	50					55					60				
Trp	Glu	Ala	Ile	Asn	Leu	Gly	Ile	Ser	Leu	Gln	Gln	Ser	Thr	Lys	Asn
65					70					75					80
Thr	Lys	Lys	Ile	Ser	Asn	Lys	Lys	Lys	Lys	Lys	Lys	Arg	Lys	Arg	Lys
				85					90					95	
Lys	Leu	Asn	Cys	Lys	Leu										
			100												

<210> 205  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 205

Ile	Cys	Leu	His	His	Asn	His	Cys	Leu	Cys	Asp	Thr	Gln	Leu	Leu	Ala
1				5					10					15	
Phe	Tyr	Gly	Leu	Ile	Pro	Pro	Thr	Ala	Arg	Leu	Glu	Met	Ala	Val	Asn

			20					25					30			
Gly	Ala	Cys	Phe	Phe	Thr	Asn	Lys	Pro	Lys	Ser	Thr	Thr	Ala	Glu	Ile	
		35					40					45				
Thr	Trp	Lys	Arg	Phe	Ser	Leu	Ser	Arg	Val	Leu	Lys	Tyr	Thr	Phe	Lys	
	50					55					60					
Phe	Phe	Pro	Lys	Lys	Leu	Ile	Leu	Ile	Val	Phe	Pro	Lys	Ser	Phe	Asn	
65					70					75					80	

<210> 206  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

Gly	Lys	Pro	Ala	Ala	Leu	Glu	Ala	His	Gln	Gly	Ser	Arg	Leu	Gln	Gly	
1				5					10					15		
Arg	Ser	Arg	Glu	Gln	Ala	Ala	Ile	Pro	Pro	Leu	Leu	Ser	Ser	Arg	Thr	
			20					25					30			
Gln	Leu	Cys	Gly	Leu	Gly	Phe	Leu	Phe	Ala	Gly	Leu	Ala	Pro	Cys	Arg	
		35					40					45				
Thr	Leu	Val	Leu	Glu	Leu	Glu	Gly	Pro	Ile	Leu	Pro	Arg	Gly	Asp	Ser	
	50					55					60					
Gln	Gly	Cys	Arg	Gly	Ile	Gly	Trp	Arg	Arg	Val	Leu					
65					70					75						

<210> 207  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

Asn	Leu	Arg	Val	Ser	Gln	Leu	Pro	Trp	Lys	Pro	Thr	Arg	Ala	Pro	Asp	
1				5					10					15		
Cys	Arg	Glu	Glu	Ala	Gly	Ser	Arg	Gln	Pro	Tyr	Leu	His	Ser	Cys	Pro	
			20					25					30			
Gln	Gly	Leu	Ser	Cys	Val	Ala	Leu	Asp	Phe	Phe	Leu	Arg	Asp	Leu	Arg	
		35					40					45				
Pro	Ala	Gly	His	Trp	Cys	Trp	Ser	Trp	Arg	Val	Leu	Ser	Cys	Pro	Gly	
	50					55					60					
Val	Thr	Pro	Arg	Val	Ala	Gly	Gly									
65					70											

<210> 208  
 <211> 73  
 <212> PRT  
 <213> homo sapiens

<400> 208  
 Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp Phe

1					5					10					15		
Gln	Val	Gly	Pro	Tyr	Cys	Ser	His	Arg	Gln	Arg	Pro	Gln	Glu	Ala	Asp		
			20					25					30				
Gly	Trp	Lys	Arg	Gly	Val	Thr	Ile	Thr	Gly	Val	Val	Met	Leu	Arg	Val		
		35					40					45					
Cys	Leu	Asp	Pro	Pro	Arg	Thr	Thr	Leu	Phe	Leu	Arg	Val	Thr	Pro	Leu		
	50					55					60						
Pro	Ser	His	Ala	Ser	Gln	Gly	Cys	Ser									
65					70												

<210> 209  
 <211> 182  
 <212> PRT  
 <213> homo sapiens  
 <400> 209

Gln	Arg	Trp	Leu	Trp	Thr	Ser	Ser	Thr	Ser	Pro	Cys	Trp	Ile	Arg	Ala		
1				5					10					15			
Phe	Leu	Pro	Pro	Ala	Gly	Gln	Val	Trp	Pro	Cys	Ser	Leu	Gly	Arg	Ala		
			20					25					30				
Pro	Ala	Pro	Leu	Thr	Thr	Leu	Gln	Leu	Thr	Met	Gln	Leu	Met	Pro	Lys		
		35					40					45					
Leu	Trp	Cys	Pro	Val	Cys	Ser	Ser	Pro	Gly	Ser	His	Cys	His	Leu	Gln		
	50					55					60						
Arg	Gly	Ser	Leu	Leu	Arg	Pro	Thr	Leu	Leu	His	Leu	Ala	Pro	Pro	Trp		
65					70					75					80		
Leu	Leu	Ala	Trp	Pro	Asn	Leu	Ala	Phe	Cys	Ala	Met	Leu	Glu	Leu	Glu		
				85					90					95			
Leu	Leu	Leu	Phe	Phe	Arg	Gly	Gly	Asn	Arg	Val	Glu	Ser	Gly	Lys	Gly		
			100					105					110				
Leu	Ala	Pro	Lys	Cys	Cys	Cys	Cys	Gly	Phe	Phe	Ala	Phe	Ser	Lys	Asp		
		115					120					125					
Ala	Leu	Pro	Gly	Pro	Lys	Leu	Gln	Thr	Ala	Val	Leu	Ser	Lys	Gln	Val		
	130					135					140						
Arg	Ser	Leu	Gly	Phe	Gly	Ala	His	Leu	Leu	Ser	Gly	Ser	Ile	Ser	Ile		
145					150					155					160		
Leu	Leu	Leu	Ala	Thr	Ser	Gly	Gln	Arg	Pro	Pro	Gln	Pro	His	Ile	Ala		
				165					170					175			
Arg	Cys	Trp	Gln	Lys	Gly												
			180														

<210> 210  
 <211> 130  
 <212> PRT  
 <213> homo sapiens  
 <400> 210

Val 1	Gly	Pro	Gly	Lys 5	Gln	Pro	Trp	Trp	Gly 10	Gln	Val	Lys	Gln	Cys 15	Gly	
Ser	Gln	Gln	Gly 20	Thr	Pro	Leu	Lys	Val 25	Ala	Val	Ala	Pro	Arg 30	Ala	Ala	
Ala	His	Trp 35	Thr	Pro	Gln	Leu	Trp 40	His	Gln	Leu	His	Gly 45	Glu	Leu	Gln	
Ser	Gly 50	Gln	Arg	Gly	Trp	Gly 55	Pro	Ala	Lys	Arg	Ala 60	Arg	Pro	Asp	Leu	
Pro 65	Ser	Gly	Arg	Gln	Glu 70	Gly	Pro	Asp	Pro	Ala 75	Arg	Arg	Ser	Arg	Gly 80	
Ser	Pro	Gln	Pro	Pro 85	Leu	Leu	Leu	Ile	Ala 90	Thr	Gly	Thr	Ser	Gly 95	Asp	
Arg	Leu	Cys	Ser 100	Trp	Glu	Ser	Arg	Ser 105	Pro	Gly	Phe	Val	Gly 110	Leu	Pro	
Ala	Gly	Asp 115	Arg	His	Val	Ser	His 120	Arg	Glu	Arg	Pro	Gly 125	Ser	Arg	Pro	
Gln	Leu 130															

<210> 211  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 211

Val 1	Thr	Gly	Lys	Gly 5	Arg	Asp	Pro	Gly	Leu 10	Ser	Cys	Ser	Ser	Ser 15	Trp	
Lys	Arg	Trp	Ser 20	Arg	Thr	Val	Thr	Ile 25	His	Ala	Asp	Thr	Glu 30	Gln	Gln	
Tyr	Glu	Thr 35	Glu	Gln	Leu	Arg	Ala 40	Val	Ser	Ser	Ser	Ala 45	Glu	Ala	Ala	
Trp	Ala 50	Ala	Thr	Pro	Pro	Phe 55	Cys	Asn	His	Pro	Met 60	Met	Ser	Pro	Pro	
His 65	Leu	Thr	Ser	Arg	Trp 70	Gly	Trp	Met	Ala	Glu 75	Gln	Met	Lys	Pro	Ala 80	
Leu	Trp	Arg	Gly	Ser 85	Leu	Thr	Glu	Met	His 90	Thr	Phe	Met	Gly	Glu 95	Val	
Asp	Gly	His	Leu 100	Thr	Ser	Leu	Met	Phe 105	His	Thr	Val	Asp	Cys 110	Thr		

<210> 212  
 <211> 243  
 <212> PRT  
 <213> homo sapiens

<400> 212

Asp 1	Val	Gln	Val	Ala 5	Gly	Pro	Glu	Pro	Asp 10	Cys	Arg	Val	His	Ser 15	His
Val	Leu	Pro	Gly 20	Gln	Ala	His	Arg	Leu 25	Ala	Pro	Gly	Pro	Tyr 30	Ser	Val
Gly	Glu	Ser 35	Leu	Gln	Pro	Arg	Glu 40	Gly	Cys	Glu	Asp	Cys 45	Asp	Arg	Gln
Lys	Ala 50	Asn	Leu	Arg	Ile	Arg 55	Phe	Lys	Pro	Ser	Leu 60	Phe	Gln	His	Val
Gly 65	Thr	His	Ser	Ser	Leu 70	Ala	Gly	Lys	Ile	Gln 75	Lys	Leu	Lys	Asp	Lys 80
Asp	Phe	Gly	Lys	Gln 85	Ala	Leu	Arg	Lys	Glu 90	His	Val	Asn	Pro	Pro 95	Ala
Glu	Val	Ser	Thr 100	Ser	Leu	Lys	Thr	Tyr 105	Gln	His	Phe	Thr	Leu 110	Glu	Lys
Ala	Tyr	Leu 115	Arg	Glu	Asp	Phe	Phe 120	Trp	Ala	Phe	Thr	Pro 125	Ala	Ala	Gly
Asp	Phe 130	Ile	Arg	Phe	Arg	Phe 135	Phe	Gln	Pro	Leu	Arg 140	Leu	Glu	Arg	Phe
Phe 145	Phe	Arg	Ser	Gly	Asn 150	Ile	Glu	His	Pro	Glu 155	Asp	Lys	Leu	Phe	Asn 160
Thr	Ser	Val	Glu	Val 165	Leu	Pro	Phe	Asp	Asn 170	Pro	Gln	Ser	Asp	Lys 175	Glu
Ala	Leu	Gln	Glu 180	Gly	Arg	Thr	Ala	Thr 185	Leu	Arg	Tyr	Pro	Arg 190	Ser	Pro
Asp	Gly	Tyr 195	Leu	Gln	Ile	Gly	Ser 200	Phe	Tyr	Lys	Gly	Val 205	Ala	Glu	Gly
Glu 210	Val	Asp	Pro	Ala	Phe	Gly 215	Pro	Leu	Glu	Ala	Leu 220	Arg	Leu	Ser	Ile
Gln 225	Thr	Asp	Ser	Pro	Val 230	Trp	Val	Ile	Leu	Ser 235	Glu	Ile	Phe	Leu	Lys 240
Lys	Ala	Asp													

<210> 213

<211> 244

<212> PRT

<213> homo sapiens

<400> 213

Gly 1	Arg	Thr	Gly	Val 5	Ser	Val	Val	Met	Gly 10	Ile	Pro	Ser	Val	Arg 15	Arg
Glu	Val	His	Ser 20	Tyr	Leu	Thr	Asp	Thr 25	Leu	His	Ser	Leu	Ile 30	Ser	Glu
Leu	Ser	Pro 35	Gln	Glu	Lys	Glu	Asp 40	Ser	Val	Ile	Val	Val 45	Leu	Ile	Ala

Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Ala	Val	Thr	Glu	Asn	Ile	Lys	Ala
	50					55					60				
Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	Gly	Leu	Leu	Glu	Val	Ile	Ser	Pro
65					70					75					80
Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe	Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly
				85					90					95	
Asp	Pro	Lys	Glu	Arg	Val	Arg	Trp	Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr
			100					105					110		
Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln	Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln
		115					120					125			
Leu	Glu	Asp	Asp	Ile	Val	Ala	Lys	Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys
	130					135					140				
Asn	Phe	Ala	Leu	Gln	Gln	Pro	Ser	Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe
145					150					155					160
Ser	Gln	Leu	Gly	Phe	Ile	Gly	Lys	Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser
				165					170					175	
Leu	Ile	Val	Glu	Phe	Ile	Leu	Met	Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp
			180					185					190		
Trp	Leu	Leu	Asp	His	Ile	Leu	Trp	Val	Lys	Val	Cys	Asn	Pro	Glu	Lys
		195					200					205			
Asp	Ala	Lys	Thr	Val	Thr	Gly	Arg	Lys	Pro	Thr	Cys	Gly	Ser	Ala	Ser
	210					215					220				
Asn	Arg	Pro	Ser	Ser	Ser	Thr	Trp	Ala	Leu	Thr	Pro	Arg	Trp	Leu	Ala
225					230					235					240

Arg Ser Arg Asn

<210> 214

<211> 210

<212> PRT

<213> homo sapiens

<400> 214

Pro	Ala	Glu	Ser	Gln	Pro	Ala	Asp	Pro	Leu	Gln	Thr	Val	Pro	Leu	Pro
1				5					10					15	
Ala	Arg	Gly	His	Ser	Leu	Leu	Ala	Gly	Trp	Gln	Asp	Pro	Glu	Thr	Glu
			20					25					30		
Gly	Gln	Arg	Leu	Trp	Lys	Ala	Gly	Ala	Ala	Glu	Gly	Ala	Cys	Glu	Pro
		35					40					45			
Ala	Ser	Arg	Gly	Glu	His	Glu	Pro	Glu	Asp	Ile	Pro	Ala	Leu	His	Pro
	50					55					60				
Gly	Glu	Ser	Leu	Pro	Ala	Arg	Gly	Leu	Leu	Leu	Gly	Leu	His	Pro	Cys
65					70					75					80
Arg	Gly	Gly	Leu	His	Pro	Leu	Pro	Leu	Leu	Pro	Thr	Ser	Lys	Thr	Gly
				85					90					95	



Ala	Val	Leu	Leu	Pro	Gln	Trp	Glu	His	Arg	Ala	Pro	Gly	Gly	Gln	Ala	
			100					105					110			
Leu	Gln	His	Val	Cys	Gly	Gly	Ala	Ala	Leu	Arg	Gln	Pro	Ser	Val	Arg	
		115					120					125				
Gln	Gly	Gly	Pro	Ala	Gly	Gly	Pro	His	Arg	His	Pro	Pro	Val	Pro	Ser	
	130					135					140					
Glu	Pro	Arg	Arg	Leu	Pro	Pro	Asp	Arg	Leu	Leu	Leu	Gln	Gly	Ser	Gly	
145					150					155					160	
Arg	Gly	Arg	Gly	Gly	Pro	Ser	Leu	Arg	Pro	Ser	Gly	Ser	Thr	Ala	Pro	
				165					170					175		
Leu	Asp	Pro	Asp	Gly	Leu	Pro	Cys	Val	Gly	Asp	Ser	Glu	Arg	Asp	Leu	
			180					185					190			
Pro	Glu	Lys	Gly	Arg	Leu	Ser	Cys	Gly	Leu	Leu	Arg	Val	Pro	Cys	Gly	
		195					200					205				
Gln	Pro															
	210															

<210> 215  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 215

Gly	Gly	Ala	Gly	Leu	Val	His	Gly	Ser	Ala	Asp	Trp	Pro	Cys	Leu	Ala	
1				5					10					15		
Pro	Trp	Arg	Val	Ser	Ser	Cys	Phe	Leu	Pro	Gly	Thr	Glu	Leu	Arg	Gly	
			20					25					30			
Leu	Gly	Ala	Pro	Gly	Ala	Lys	Ser	Arg	Leu	Trp	Cys	Arg	Gly	Gly	Gly	
		35					40					45				
Leu	Ser	Leu	Asn	Arg	His	Pro	Glu	Val	Leu	Leu	Arg	Cys	Trp	Val	His	
	50					55					60					
Pro	Glu	Trp	His	Gly	Glu	Gln	Leu	Trp	Pro	Val	Leu	Leu	Pro	Arg	Pro	
65				70						75						
Val	Leu	Gly	Lys	Leu	Ser	Ser	Gly	Pro	Ser	Leu	Gln	Arg	Pro	Arg	Met	
				85					90					95		
Gly	Trp	Val	Trp	Gly	Thr	His	Gly	Glu	Trp	Pro	Glu	Glu	Leu	Arg	Val	
			100					105					110			
Lys	Arg	Ala	Pro	Val	Cys	Trp	Leu	Gln	Arg	Pro	Gly	Ala	Pro	Leu	Ser	
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<210> 216  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 216

Phe	Pro	Gln	Asp	Trp	Pro	Arg	Lys	Glu	His	Arg	Pro	Gln	Leu	Leu	Pro	
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1				5				10				15			
Val	Pro	Leu	Arg 20	Val	Asp	Pro	Ala	Ser 25	Gln	Glu	His	Leu	Arg 30	Val	Ser
Val	Lys	Arg 35	Gln	Ala	Ser	Thr	Pro 40	Ala	Pro	Glu	Pro	Ala 45	Leu	Ser	Ser
Arg	Cys 50	Pro	Gln	Thr	Pro	Gln 55	Leu	Cys	Ala	Arg	Gln 60	Glu	Ala	Ala	Arg
His 65	Thr	Pro	Gly	Arg	Gln 70	Ala	Arg	Pro	Val	Arg 75	Gly	Pro	Met	Asp	Lys 80
Pro	Ser	Pro	Ala	Ser 85	Gly	Lys	Thr	Gly	Pro 90	Phe	Pro	Thr	Gly	His 95	Ala
Pro	Glu	Leu	Trp 100	Gln	Ile	Ala	Gly	Ala 105	Ile	Val	Trp	Gly	Glu 110	Phe	Asn
Lys	Ser	Pro 115	Phe	Glu	Asn	Glu	Lys 120	Lys	Lys	Lys	Lys	Lys			

<210> 217

<211> 142

<212> PRT

<213> homo sapiens

<400> 217

Val 1	Pro	His	Thr	His 5	Pro	Ile	Leu	Gly	Leu 10	Cys	Lys	Glu	Gly	Pro 15	Glu
Leu	Ser	Phe	Pro 20	Arg	Thr	Gly	Leu	Gly 25	Arg	Ser	Thr	Gly	His 30	Ser	Cys
Ser	Pro	Cys 35	His	Ser	Gly	Trp	Thr 40	Gln	His	Leu	Arg	Ser 45	Thr	Ser	Gly
Cys 50	Arg	Leu	Arg	Asp	Arg	Pro 55	Pro	Pro	Leu	His	Gln 60	Ser	Leu	Leu	Leu
Ala 65	Pro	Gly	Ala	Pro	Arg 70	Pro	Arg	Ser	Ser	Val 75	Pro	Gly	Lys	Lys	Gln 80
Leu	Asp	Thr	Arg	Gln 85	Gly	Ala	Lys	His	Gly 90	Gln	Ser	Ala	Asp	Pro 95	Trp
Thr	Ser	Pro	Ala 100	Pro	Pro	Gln	Gly	Lys 105	Gln	Gly	Leu	Ser	Leu 110	Gln	Asp
Thr	Pro	Gln 115	Ser	Cys	Gly	Arg	Leu 120	Gln	Glu	Pro	Ser	Cys 125	Gly	Glu	Asn
Leu	Ile 130	Lys	Ala	Leu	Leu	Lys 135	Met	Lys	Lys	Lys	Lys 140	Lys	Lys		

<210> 218

<211> 379

<212> PRT

<213> homo sapiens

<400> 218

Arg 1	Arg	Gly	Leu	Glu 5	Gly	Phe	Asn	Gly	Gly 10	Trp	Thr	Glu	Met	Pro 15	Gly
Ile	Leu	Trp	Met 20	Glu	Pro	Thr	Gln	Pro 25	Pro	Asp	Phe	Ala	Leu 30	Ala	Tyr
Arg	Pro	Ser 35	Phe	Pro	Glu	Asp	Arg 40	Glu	Pro	Gln	Ile	Pro 45	Tyr	Pro	Glu
Pro	Thr 50	Trp	Pro	Pro	Pro	Leu 55	Ser	Ala	Pro	Arg	Val 60	Pro	Tyr	His	Ser
Ser 65	Val	Leu	Ser	Val	Thr 70	Arg	Pro	Val	Val	Val 75	Ser	Ala	Thr	His	Pro 80
Thr	Leu	Pro	Ser	Ala 85	His	Gln	Pro	Pro	Val 90	Ile	Pro	Ala	Thr	His 95	Pro
Ala	Leu	Ser	Arg 100	Asp	His	Gln	Ile	Pro 105	Val	Ile	Ala	Ala	Asn 110	Tyr	Pro
Asp	Leu	Pro 115	Ser	Ala	Tyr	Gln	Pro 120	Gly	Ile	Leu	Ser	Val 125	Ser	His	Ser
Ala	Gln 130	Pro	Pro	Ala	His	Gln 135	Pro	Pro	Met	Ile	Ser 140	Thr	Lys	Tyr	Pro
Glu 145	Leu	Phe	Pro	Ala	His 150	Gln	Ser	Pro	Met	Phe 155	Pro	Asp	Thr	Arg	Val 160
Ala	Gly	Thr	Gln	Thr 165	Thr	Thr	His	Leu	Pro 170	Gly	Ile	Pro	Pro	Asn 175	His
Ala	Pro	Leu	Val 180	Thr	Thr	Leu	Gly	Ala 185	Gln	Arg	Pro	Pro	Gln 190	Ala	Pro
Asp	Ala	Leu 195	Val	Leu	Arg	Thr	Gln 200	Ala	Thr	Gln	Leu	Pro 205	Ile	Ile	Pro
Thr	Ala 210	Gln	Pro	Ser	Leu	Thr 215	Thr	Thr	Ser	Arg	Ser 220	Pro	Val	Ser	Pro
Ala 225	His	Gln	Ile	Ser	Val 230	Pro	Ala	Ala	Thr	Gln 235	Pro	Ala	Ala	Leu	Pro 240
Thr	Leu	Leu	Pro	Ser 245	Gln	Ser	Pro	Thr	Asn 250	Gln	Thr	Ser	Pro	Ile 255	Ser
Pro	Thr	His	Pro 260	His	Ser	Lys	Ala	Pro 265	Gln	Ile	Pro	Arg	Glu 270	Asp	Gly
Pro	Ser	Pro 275	Lys	Leu	Ala	Leu	Trp 280	Leu	Pro	Ser	Pro	Ala 285	Pro	Thr	Ala
Ala	Pro 290	Thr	Ala	Leu	Gly	Glu 295	Ala	Gly	Leu	Ala	Glu 300	His	Ser	Gln	Arg
Asp 305	Asp	Arg	Trp	Leu	Leu 310	Val	Ala	Leu	Leu	Val 315	Pro	Thr	Cys	Val	Phe 320
Leu	Val	Val	Leu	Leu 325	Ala	Leu	Gly	Ile	Val 330	Tyr	Cys	Thr	Arg	Cys 335	Gly

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Pro	His	Ala	Pro	Asn	Lys	Arg	Ile	Thr	Asp	Cys	Tyr	Arg	Trp	Val	Ile
			340					345					350		
His	Ala	Gly	Ser	Lys	Ser	Pro	Thr	Glu	Pro	Met	Pro	Pro	Arg	Gly	Ser
		355					360					365			
Leu	Thr	Gly	Val	Gln	Thr	Cys	Arg	Thr	Ser	Val					
	370					375									

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 <213> homo sapiens

<400> 219

Val	Asp	Thr	Asp	Glu	Cys	Gln	Ile	Ala	Gly	Val	Cys	Gln	Gln	Met	Cys
1				5					10					15	
Val	Asn	Tyr	Val	Gly	Gly	Phe	Glu	Cys	Tyr	Cys	Ser	Glu	Gly	His	Glu
			20					25					30		
Leu	Glu	Ala	Asp	Gly	Ile	Ser	Cys	Ser	Pro	Ala	Gly	Ala	Met	Gly	Ala
		35					40					45			
Gln	Gly	Ser	Gln	Asp	Leu	Gly	Asp	Glu	Leu	Leu	Asp	Asp	Gly	Glu	Asp
	50					55					60				
Glu	Glu	Asp	Glu	Asp	Glu	Ala	Trp	Lys	Ala	Ser	Thr	Val	Ala	Gly	Arg
	65				70					75					80
Arg	Cys	Leu	Gly	Ser	Cys	Gly	Trp	Ser	Leu	Arg	Ser	Arg	Leu	Thr	Leu
				85					90					95	
Pro	Trp	Pro	Ile	Asp	Arg	Ala	Ser	Gln	Arg	Thr	Glu	Ser	His	Arg	Tyr
			100					105					110		
Pro	Thr	Arg	Ser	Pro	Pro	Gly	His	Pro	Arg	Ser	Val	Pro	Pro	Gly	Ser
		115					120					125			
Pro	Thr	Thr	Pro	Gln	Cys	Ser	Pro	Ser	Pro	Gly	Leu	Trp	Trp	Ser	Leu
	130					135					140				
Pro	Arg	Ile	Pro	His	Cys	Leu	Leu	Pro	Thr	Ser	Leu	Leu			
	145				150					155					

<210> 220  
 <211> 211  
 <212> PRT  
 <213> homo sapiens

<400> 220

Pro	Pro	Pro	Pro	Gly	Pro	Leu	Cys	Leu	Leu	Pro	Ile	Lys	Ser	Leu	Cys
1				5					10					15	
Leu	Leu	Pro	Pro	Ser	Pro	Gln	Pro	Ser	Pro	Pro	Ser	Cys	Pro	Leu	Arg
			20					25					30		
Ala	Pro	Leu	Thr	Arg	Pro	His	Pro	Ser	Ala	Leu	His	Ile	Pro	Ile	Pro
		35					40					45			



<210> 222  
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 <213> homo sapiens

<400> 222

Asn 1	Lys	Glu	Leu	Ser 5	Ser	Leu	Lys	Ser	Ser 10	Asp	Val	Val	Met	Thr 15	His	
Thr	Glu	Ser	Cys 20	Ile	Thr	Val	Ala	Ser 25	Arg	Ala	Thr	His	Leu 30	Phe	Gly	
Leu	Ser	Asp 35	Gly	His	Ser	Phe	Thr 40	Thr	Gln	Gln	Gln	Thr 45	Pro	His	Thr	
Gly	Thr 50	Arg	Met	Ser	Ala	Ser 55	Thr	Trp	Glu	Ala	Val 60	Ala	Glu	Pro	Gly	
Arg 65	Trp	Pro	Gly	Pro	Asp 70	His	Gly	Leu	Ser	Gly 75	Ala	Gly	His	Gln	Gly 80	
Val	Arg	Val	Pro	Met 85	Leu	Pro	Gln	Gly	Val 90	Gly	Met	Thr	Gly	Arg 95	Ser	
Leu	Val	Thr	Arg 100	Gln	Trp	Thr	Ser	Leu 105	Gly	Glu	Gly	Trp	Arg 110	Glu	Arg	
Ala	Gly	Gln 115	Ala	Pro	Ala	Ala	His 120	Arg	Leu	Ala	His	Ala 125	Asn	Thr	Leu	
Lys	Ala 130	Leu	Leu	Gly	Gly	Phe 135	Ser	Glu	Asn	Gln	Gly 140	Glu	Ala	Leu	Val	
Ser 145	Phe	Pro	Arg	Lys	Val 150	Pro	Ile	Leu	Pro	Pro 155	Ala	Pro	Leu	Ser	Pro 160	
Glu	Pro	Arg	Asp	Pro 165	Gln	Gly	Val	Leu	Ala 170	Gly	Gly	Ala	Lys	Gln 175	Arg	
Cys	Leu	Arg	Pro 180	Pro	Glu	Pro	Ser	Leu 185	Pro	Met	Ile	Pro	Arg 190	His	Ala	
Arg	Gln	Gly 195	Val	Gly	Leu											

<210> 223  
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 <212> PRT  
 <213> homo sapiens

<400> 223

Ser 1	His	Gly	Met	Pro 5	Gly	Arg	Gly	Trp	Ala 10	Cys	Glu	Val	Asp	Trp 15	His	
Ser	Cys	Pro	His 20	Thr	Leu	Pro	Gly	Trp 25	Ala	Pro	Glu	Ile	Trp 30	Gly	Ser	
Pro	Ser	Gln 35	His	Gly	Val	Leu	Gly 40	Ala	Cys	Pro	Gly	Pro 45	Phe	Thr	Arg	

Thr	Glu	Ala	Pro	His	Pro	Leu	Ser	His	Phe	Ser	Arg	Trp	Lys	Thr	Gln
	50					55					60				
Arg	Arg	Lys	Arg	Pro	Trp	Gly	Gly	Val	Pro	Ser	Cys	Leu	Gln	Leu	Ala
65					70					75					80
Pro	Trp	Val	Pro	Leu	Cys	Gly	Gly	Ser	Pro	Asp	Ser	Ile	Ser	Ser	Ala
				85					90					95	

Ser Glu

<210> 224  
 <211> 298  
 <212> PRT  
 <213> homo sapiens

<400> 224

Ala	Thr	Arg	Arg	Arg	Ala	Ala	Glu	Ala	Gly	Met	Ala	Ala	Val	Leu	Gln
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Arg	Val	Glu	Arg	Leu	Ser	Asn	Arg	Val	Val	Arg	Val	Leu	Gly	Cys	Asn
			20					25					30		
Pro	Gly	Pro	Met	Thr	Leu	Gln	Gly	Thr	Asn	Thr	Tyr	Leu	Val	Gly	Thr
		35					40					45			
Gly	Pro	Arg	Arg	Ile	Leu	Ile	Asp	Thr	Gly	Glu	Pro	Ala	Ile	Pro	Glu
	50					55					60				
Tyr	Ile	Ser	Cys	Leu	Lys	Gln	Ala	Leu	Thr	Glu	Phe	Asn	Thr	Ala	Ile
65					70					75					80
Gln	Glu	Ile	Val	Val	Thr	His	Trp	His	Arg	Asp	His	Ser	Gly	Gly	Ile
				85					90					95	
Gly	Asp	Ile	Cys	Lys	Ser	Ile	Asn	Asn	Asp	Thr	Thr	Tyr	Cys	Ile	Lys
			100					105					110		
Lys	Leu	Pro	Arg	Asn	Pro	Gln	Arg	Glu	Glu	Ile	Ile	Gly	Asn	Gly	Glu
		115					120					125			
Gln	Gln	Tyr	Val	Tyr	Leu	Lys	Asp	Gly	Asp	Val	Ile	Lys	Thr	Glu	Gly
	130					135					140				
Ala	Thr	Leu	Arg	Val	Leu	Tyr	Thr	Pro	Gly	His	Thr	Asp	Asp	His	Met
145					150					155					160
Ala	Leu	Leu	Leu	Glu	Glu	Glu	Asn	Ala	Ile	Phe	Ser	Gly	Asp	Cys	Ile
				165					170					175	
Leu	Gly	Glu	Gly	Thr	Thr	Val	Phe	Glu	Asp	Leu	Tyr	Asp	Tyr	Met	Asn
			180					185					190		
Ser	Leu	Lys	Glu	Leu	Leu	Lys	Ile	Lys	Ala	Asp	Ile	Ile	Tyr	Pro	Gly
		195					200					205			
His	Gly	Pro	Val	Ile	His	Asn	Ala	Glu	Ala	Lys	Ile	Gln	Gln	Tyr	Ile
	210					215					220				
Ser	His	Arg	Asn	Ile	Arg	Glu	Gln	Gln	Ile	Leu	Thr	Leu	Phe	Arg	Glu
225					230					235					240

Asn	Phe	Glu	Lys	Ser	Phe	Thr	Val	Met	Glu	Leu	Val	Lys	Ile	Ile	Tyr
				245					250					255	
Lys	Asn	Thr	Pro	Glu	Asn	Leu	His	Glu	Met	Ala	Lys	His	Asn	Leu	Leu
			260					265					270		
Leu	His	Leu	Lys	Lys	Leu	Glu	Lys	Glu	Gly	Lys	Ile	Phe	Ser	Asn	Thr
		275					280					285			
Asp	Pro	Asp	Lys	Lys	Trp	Lys	Ala	His	Leu						
	290					295									

<210> 225  
 <211> 58  
 <212> PRT  
 <213> homo sapiens

<400> 225

Gly	Phe	Ser	Trp	Gly	Arg	Ser	Pro	Leu	Gly	Arg	Cys	Trp	Cys	Leu	Gly
1				5					10					15	
Gly	Ser	Trp	Asp	Pro	Gly	Tyr	Ser	Pro	Thr	His	Ala	Arg	Leu	Asp	Trp
			20					25					30		
Thr	Ala	Ala	Arg	Arg	Ala	Ala	Val	Gln	Gln	Pro	Phe	Pro	Pro	Gln	Pro
		35					40					45			
Pro	Ala	Gly	Val	Ser	Pro	Ile	Trp	Ile	Leu						
	50					55									

<210> 226  
 <211> 73  
 <212> PRT  
 <213> homo sapiens

<400> 226

Ser	Gly	Ser	Leu	Ser	Leu	Asn	His	Ile	Ser	Ile	Phe	Gln	Ile	Asn	Ile
1				5					10					15	
Leu	Leu	Leu	Ser	Ile	Ser	Tyr	Asn	Phe	Phe	Ser	Leu	Arg	Ile	Pro	Trp
			20					25					30		
Glu	Phe	Phe	Asn	Ala	Ile	Gly	Ser	Val	Ile	Ile	Asp	Ala	Phe	Thr	Asn
		35				40						45			
Ile	Ser	Tyr	Ala	Ser	Arg	Met	Ile	Ser	Val	Pro	Val	Ser	His	Tyr	Asn
	50					55					60				
Phe	Leu	Asp	Cys	Cys	Val	Lys	Phe	Ser							
65					70										

<210> 227  
 <211> 141  
 <212> PRT  
 <213> homo sapiens

<400> 227

Ala	Phe	Leu	Leu	Arg	Pro	Ser	Val	Thr	Ala	Ser	Thr	Arg	Leu	Leu	Pro
1				5					10					15	



Val	Cys	Ala	Ser 20	Pro	Arg	Ser	Ser	Pro 25	Gly	Pro	Ser	Pro	Ala 30	Gln	Gln	
Gln	Gln	Ala 35	Trp	Gln	Gln	Ala	Trp 40	Ser	Ser	Ala	Arg	Ala 45	Pro	Ser	Arg	
Cys	Arg 50	Ala	Arg	Pro	Ser	Ser 55	Ser	Glu	Arg	Pro	Cys 60	Pro	Ala	Val	Gly	
Arg 65	Leu	Ala	Ser	Leu	Tyr 70	Cys	Cys	Cys	Met	Val 75	Phe	Ala	Ser	Pro	Pro 80	
Arg	Pro	Gly	Arg	Thr 85	Trp	Val	His	Cys	Thr 90	Gly	Trp	Pro	Arg	Leu 95	Ala	
Thr	Gly	Leu	Trp 100	Pro	Leu	Thr	Cys	Gln 105	Val	Trp	Gly	Thr	Pro 110	Arg	Lys	
Gln	Gln	Pro 115	Leu	Pro	Leu	Leu	Gly 120	Ser	Trp	Pro	Leu	Ala 125	Ala	Ser	Trp	
Arg	Leu 130	Trp	Trp	Met	Pro	Trp 135	Ser	Trp	Ala	Pro	Arg 140	Leu				

<210> 228

<211> 244

<212> PRT

<213> homo sapiens

<400> 228

Val 1	Pro	Pro	Pro	Ala 5	Leu	Gly	His	Arg	Gln 10	His	Ala	Pro	Ala	Ser 15	Arg	
Leu	Arg	Glu	Ser 20	Thr	Gln	Leu	Pro	Arg 25	Pro	Phe	Thr	Ser	Thr 30	Ala	Ala	
Ala	Gly	Met 35	Ala	Ala	Ser	Val	Glu 40	Gln	Arg	Glu	Gly	Thr 45	Ile	Gln	Val	
Gln	Gly 50	Gln	Ala	Leu	Phe	Phe 55	Arg	Glu	Ala	Leu	Pro 60	Gly	Ser	Gly	Gln	
Ala 65	Arg	Phe	Ser	Val	Leu 70	Leu	Leu	His	Gly	Ile 75	Arg	Phe	Ser	Ser	Glu 80	
Thr	Trp	Gln	Asn	Leu 85	Gly	Thr	Leu	His	Arg 90	Leu	Ala	Gln	Ala	Gly 95	Tyr	
Arg	Ala	Val	Ala 100	Ile	Asp	Leu	Pro	Gly 105	Leu	Gly	His	Ser	Lys 110	Glu	Ala	
Ala	Ala	Pro 115	Ala	Pro	Ile	Gly	Glu 120	Leu	Ala	Pro	Gly	Ser 125	Phe	Leu	Ala	
Ala	Val 130	Val	Asp	Ala	Leu	Glu 135	Leu	Gly	Pro	Pro	Val 140	Val	Ile	Ser	Pro	
Ser 145	Leu	Ser	Gly	Met	Tyr 150	Ser	Leu	Pro	Phe	Leu 155	Thr	Ala	Pro	Gly	Ser 160	
Gln	Leu	Pro	Gly	Phe 165	Val	Pro	Val	Ala	Pro 170	Ile	Cys	Thr	Asp	Lys 175	Ile	

Asn	Ala	Ala	Asn	Tyr	Ala	Ser	Val	Lys	Thr	Pro	Ala	Leu	Ile	Val	Tyr
			180					185					190		
Gly	Asp	Gln	Asp	Pro	Met	Gly	Gln	Thr	Ser	Phe	Glu	His	Leu	Lys	Gln
		195					200					205			
Leu	Pro	Asn	His	Arg	Val	Leu	Ile	Met	Lys	Gly	Ala	Gly	His	Pro	Cys
	210					215					220				
Tyr	Leu	Asp	Lys	Pro	Glu	Glu	Trp	His	Thr	Gly	Leu	Leu	Asp	Phe	Leu
225					230					235					240
Gln	Gly	Leu	Gln												

<210> 229  
 <211> 144  
 <212> PRT  
 <213> homo sapiens

<400> 229

Trp	Thr	Asp	His	Asn	Arg	Gly	Ala	Gln	Leu	Gln	Gly	Ile	His	His	Ser
1				5					10					15	
Arg	Gln	Glu	Ala	Ala	Arg	Gly	Gln	Leu	Pro	Asn	Arg	Gly	Arg	Gly	Cys
			20					25					30		
Cys	Phe	Leu	Gly	Val	Pro	Gln	Thr	Trp	Gln	Val	Asn	Gly	His	Ser	Pro
		35					40					45			
Val	Ala	Ser	Leu	Gly	Gln	Pro	Val	Gln	Cys	Thr	Gln	Val	Leu	Pro	Gly
	50					55					60				
Leu	Gly	Gly	Glu	Ala	Asn	Thr	Met	Gln	Gln	Gln	Tyr	Arg	Glu	Ala	Ser
65					70					75					80
Leu	Pro	Thr	Ala	Gly	Gln	Gly	Leu	Ser	Glu	Glu	Glu	Gly	Leu	Ala	Leu
				85					90					95	
His	Leu	Asp	Gly	Ala	Leu	Ala	Leu	Leu	His	Ala	Cys	Cys	His	Ala	Cys
			100					105					110		
Cys	Cys	Cys	Ala	Gly	Glu	Gly	Pro	Gly	Glu	Leu	Arg	Gly	Leu	Ala	Gln
		115					120					125			
Thr	Gly	Ser	Arg	Arg	Val	Leu	Ala	Val	Thr	Glu	Gly	Arg	Arg	Arg	Asn
	130					135					140				

<210> 230  
 <211> 135  
 <212> PRT  
 <213> homo sapiens

<400> 230

Leu	Glu	Phe	Phe	Ile	Pro	Cys	Leu	Gly	Ser	Val	Asn	Glu	Ala	Cys	Leu
1				5					10					15	
Phe	Pro	Gly	Val	Ser	Phe	His	Gly	Leu	Tyr	Phe	Ser	Ser	Ser	Ser	Gly
			20					25					30		
Ser	Phe	Ala	Gly	Ser	Ser	Leu	Trp	Lys	Leu	His	Glu	Arg	Trp	Leu	Gly

				35				40					45			
Leu	Gly	Phe	Ala	Gly	Val	Tyr	Ser	Arg	Val	Lys	Ala	Glu	Trp	Asp	Leu	
	50					55					60					
Arg	Pro	Arg	Leu	Gly	Thr	Thr	Gln	Ala	Glu	Lys	Gly	Arg	Phe	His	His	
65					70					75					80	
Ser	Gln	Cys	Pro	Pro	His	Ser	Thr	Thr	Ser	Ala	Arg	Ala	Pro	Pro	Ser	
				85					90					95		
Leu	Leu	Pro	His	Pro	Ala	Ile	Val	Arg	Gly	Ala	Thr	Val	Gly	Arg	Arg	
			100					105					110			
Val	Pro	Arg	Arg	Gly	Leu	Phe	Leu	Leu	Pro	Val	Pro	Glu	Lys	Ala	Phe	
		115					120					125				
Pro	Leu	Leu	Lys	Phe	Lys	His										
	130					135										

<210> 231  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 231

Gly	Gly	Pro	Val	Cys	Trp	Glu	Pro	Gln	Val	Thr	Pro	Phe	Ser	Ser	Tyr	
1				5					10					15		
Ser	Val	Pro	Gly	Ala	Ser	Cys	Pro	Pro	Leu	Gln	Ile	Leu	Gly	Lys	Glu	
			20					25					30			
Asn	Val	Tyr	Val	Ala	Gly	Tyr	Cys	Met	Val	Thr	Ser	Glu	Gly	Arg	Pro	
		35					40					45				
Leu	Gly	Thr	His	Leu	Pro	Thr	Ala	Ala	Gln	Ala	Arg	Ala	Gln	Ala	His	
	50					55					60					
Leu	Leu	Val	Leu	Arg	Pro	Gln	Ile	Lys	Pro	Ser	Pro	His	His	Met	Ala	
65					70					75					80	
Ser	Asp	Arg	Phe	Leu	Pro	Ser	Arg	Lys	Phe	Cys	Gly	Cys	Ala	Val	Leu	
				85					90					95		

<210> 232  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 232

Cys	Cys	Gly	Glu	Gly	Thr	Val	Asn	Asp	Gly	Asn	Val	Pro	Ser	Gln	Pro	
1				5					10					15		
Gly	Ser	Cys	Leu	Thr	Trp	Val	Ser	Asn	Pro	Thr	Leu	Pro	Ser	Pro	Trp	
			20					25					30			
Ser	Thr	Leu	Gln	Arg	Ser	Arg	Gly	Pro	Ala	Asn	Ala	Arg	Glu	Val	Ser	
		35					40					45				
Thr	Glu	Lys	Ser	Leu	Gln	Asn	Ser	His	Trp	Lys	Arg	Arg	Asn	Lys	Gly	
	50					55					60					

His	Gly	Lys	Lys	Pro	Gln	Gly	Arg	Asp	Arg	Pro	Arg	Ser	Gln	Thr	Leu
65					70					75					80

Gly Arg Glu

<210> 233

<211> 52

<212> PRT

<213> homo sapiens

<400> 233

Ala	Ser	Pro	Ala	Ser	Leu	Ala	Gln	Ala	Thr	Ser	Arg	Gln	Pro	Ala	Pro
1				5					10					15	

Ser	Pro	Arg	Ala	Arg	Ser	His	Leu	Ala	Thr	Ser	Thr	Ser	Trp	Thr	Ser
			20					25					30		

Ser	Ala	Arg	Ser	Asp	Ala	Gly	Cys	Gly	Glu	Cys	Arg	Arg	Asp	Pro	Gly
		35					40					45			

Ala	Pro	Pro	Arg
	50		

<210> 234

<211> 94

<212> PRT

<213> homo sapiens

<400> 234

Leu	Gly	Ser	Ala	Trp	Gln	Gln	Leu	Arg	Arg	Pro	Glu	Ala	Ser	Glu	Thr
1				5					10					15	

Leu	Arg	Leu	Val	Gly	Thr	His	Arg	Pro	Arg	Gln	Arg	Ala	Leu	Pro	Arg
			20					25					30		

Gln	Arg	Val	Ala	Ser	Pro	Pro	Pro	Arg	Arg	Gly	Leu	Gly	Leu	Thr	Ser
		35					40					45			

Pro	Pro	Val	Arg	Leu	Gly	Gln	Val	Val	Pro	Gly	Leu	Met	Pro	Gly	Val
	50					55					60				

Val	Ser	Ala	Ala	Gly	Thr	Gln	Val	Arg	Arg	Leu	Asp	Glu	Val	Pro	Ala
65					70					75					80

Ser	Leu	Arg	Leu	Gln	His	His	Leu	Gln	Leu	Arg	Glu	Gly	Leu
				85					90				

<210> 235

<211> 95

<212> PRT

<213> homo sapiens

<400> 235

Ala	Arg	Pro	Ser	Arg	Ser	Trp	Arg	Trp	Cys	Cys	Ser	Arg	Ser	Asp	Ala
1				5					10					15	

Gly	Thr	Ser	Ser	Arg	Arg	Arg	Thr	Trp	Val	Pro	Ala	Ala	Leu	Thr	Thr
			20					25					30		

Pro	Gly	Ile	Arg	Pro	Gly	Thr	Thr	Cys	Pro	Arg	Arg	Thr	Gly	Gly	Glu
		35					40					45			
Val	Arg	Pro	Ser	Pro	Arg	Arg	Gly	Gly	Gly	Leu	Ala	Thr	Arg	Cys	Leu
	50					55					60				
Gly	Lys	Ala	Arg	Trp	Arg	Gly	Leu	Cys	Val	Pro	Thr	Ser	Arg	Arg	Val
	65				70					75					80
Ser	Asp	Ala	Ser	Gly	Arg	Arg	Ser	Cys	Cys	Gln	Ala	Glu	Pro	Arg	
				85					90					95	

<210> 236

<211> 174

<212> PRT

<213> homo sapiens

<400> 236

Ala	Pro	Thr	Asn	Thr	Arg	Ser	Ser	Ser	Lys	Phe	Ala	Thr	Ser	Gly	Ser
1				5					10					15	
Pro	Gly	Tyr	Pro	Ile	Ala	Ser	Ser	Gly	Ala	Ser	Pro	Glu	Val	Arg	Gln
			20					25					30		
Arg	Arg	Thr	Thr	Phe	Phe	Arg	Phe	Arg	Pro	Gly	Glu	Ser	Leu	Cys	Gly
		35					40					45			
Asp	Met	Lys	Leu	Leu	Thr	His	Asn	Leu	Leu	Ser	Ser	His	Val	Arg	Gly
	50					55					60				
Val	Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Val	Arg
	65				70					75					80
Ile	Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala	Arg	Met	Ile	Pro
				85					90					95	
Lys	Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp	Asn	Leu	Arg	Leu
			100					105					110		
Ile	Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu	Glu	Asn	Glu	Glu
		115					120					125			
Phe	Leu	Arg	Thr	Met	His	His	Leu	Leu	Leu	Glu	Val	Glu	Val	Ile	Glu
	130					135					140				
Gly	Thr	Leu	Gln	Cys	Pro	Glu	Ser	Gly	Arg	Met	Phe	Pro	Ile	Ser	Arg
	145				150					155					160
Gly	Ile	Pro	Asn	Met	Leu	Leu	Ser	Glu	Glu	Glu	Thr	Glu	Ser		
				165					170						

<210> 237

<211> 225

<212> PRT

<213> homo sapiens

<400> 237

Tyr	Arg	Ala	Gln	Lys	His	Cys	Val	Trp	Cys	His	Trp	Val	Lys	Gly	Trp
1				5					10					15	
Gly	Tyr	Thr	Arg	Gln	Asn	Ser	Glu	Thr	Gly	Tyr	Arg	Ser	Thr	Lys	Ile

20							25					30				
His	Ser	His 35	Asn	Lys	Lys	Asn	Trp 40	Arg	Leu	Ala	Gln	Ser 45	Thr	Leu	Ser	
Phe	Leu 50	Phe	Thr	Gln	Gln	His 55	Val	Gly	Asp	Pro	Ala 60	Ala	Asp	Gly	Glu	
His 65	Thr	Ser	Arg	Phe	Arg 70	Ala	Leu	Gln	Gly	Ala 75	Leu	Tyr	His	Phe	His 80	
Leu	Gln	Gln	Gln	Val 85	Val	His	Gly	Pro	Gln 90	Lys	Leu	Leu	Ile	Leu 95	Leu	
Ile	Ser	Leu	Asn 100	Arg	Pro	Phe	Arg	His 105	Leu	Asp	Gln	Thr	Gln 110	Val	Ile	
Gly	Arg	Leu 115	Gln	Glu	Arg	Arg	Pro 120	Leu	His	Phe	Arg	Tyr 125	His	Thr	Arg	
His 130	Glu	Val	Gly	Val	Glu	Phe 135	His	Arg	Ala	Asp	Thr 140	Asp	Leu	Gly	Gly	
Leu 145	Glu	Ala	Gln	Gly	Glu 150	Ala	Thr	Gly	Pro	His 155	Pro	Pro	His	Met	Arg 160	
Ala	Gln	Gln	Ile	Val 165	Gly	Lys	Gln	Phe	His 170	Val	Ala	Ala	Gln	Thr 175	Leu	
Ala	Arg	Pro	Glu 180	Pro	Glu	Lys	Gly	Arg 185	Pro	Pro	Leu	Pro	His 190	Phe	Arg	
Gly	Cys	Ser 195	Thr	Arg	Cys	Tyr	Trp 200	Ile	Ala	Arg	Arg	Thr 205	Gly	Ser	Gly	
Glu	Leu 210	Ala	Gly	Thr	Ser	Arg 215	Val	Cys	Gly	Ser	Ser 220	Phe	Leu	Tyr	Ala	

Asn  
225

<210> 238

<211> 209

<212> PRT

<213> homo sapiens

<400> 238

Thr 1	Phe	Asn	Glu	Lys 5	Lys	Ile	Tyr	Asn	Thr 10	Glu	Leu	Lys	Asn	Thr 15	Val
Phe	Gly	Val	Ile 20	Gly	Ser	Arg	Val	Gly 25	Asp	Thr	His	Gly	Arg 30	Ile	Arg
Lys	Gln	Gly 35	Ile	Asp	Gln	Gln	Lys 40	Tyr	Thr	Val	Ile	Thr 45	Arg	Lys	Thr
Gly	Ala 50	Trp	His	Asn	Gln	Leu 55	Ser	Val	Ser	Ser	Ser 60	Leu	Ser	Ser	Met
Leu 65	Gly	Ile	Pro	Arg	Leu 70	Met	Gly	Asn	Ile	Arg 75	Pro	Asp	Ser	Gly	His 80



<210> 240  
 <211> 134  
 <212> PRT  
 <213> homo sapiens

<400> 240

Ser 1	Arg	Thr	Phe	Ser 5	Phe	Leu	Ser	Phe	Leu 10	His	Cys	Ala	Asn	Ile 15	Leu
Thr	Leu	Phe	Val 20	Ser	Phe	Gln	Glu	Pro 25	His	Arg	His	Ile	Gln 30	Val	Lys
Arg	Ser	Leu 35	Asn	Lys	Cys	Leu	Gln 40	Pro	Ser	Gln	Cys	Lys 45	Asn	Lys	Tyr
Gln	Ser 50	Ser	Arg	Arg	Ser	Ser 55	Ser	Arg	Ala	Ala	Pro 60	Lys	Val	Pro	Thr
Ala 65	Thr	Pro	Asn	Asn	Tyr 70	Lys	Ser	Val	Gln	Arg 75	Glu	Cys	Trp	Arg	Glu 80
Cys	Glu	Trp	Val	Cys 85	Ala	Gly	Gly	His	Gly 90	Gly	Ala	Val	Cys	Lys 95	Ile
Gly	Val	Ala	Asn 100	His	Arg	Thr	Arg	Ala 105	Trp	Ser	Gly	Tyr	Pro 110	Pro	Pro
Thr	Gln	Arg 115	Gly	Arg	Ala	Ser	Pro 120	His	Thr	Leu	Thr	Ala 125	Glu	Phe	Ala
Leu	Gly 130	Arg	Val	Lys	Lys										

<210> 241  
 <211> 147  
 <212> PRT  
 <213> homo sapiens

<400> 241

Pro 1	Ala	Arg	Thr	Arg 5	Asp	Arg	Pro	Leu	Leu 10	Ala	Arg	Phe	Gly	Leu 15	Pro
Pro	Arg	Cys	Glu 20	Pro	Val	Gly	Ala	Pro 25	Leu	Ala	Ala	Leu	Ala 30	Leu	Ala
Arg	Glu	Arg 35	Arg	Glu	Arg	Gly	Arg 40	Phe	Pro	Arg	Pro	Cys 45	Lys	Cys	Leu
Phe	Phe 50	Asn	Ser	Ser	Gln	Cys 55	Glu	Leu	Cys	Cys	Glu 60	Cys	Val	Arg	Gly
Gly 65	Ala	Pro	Ala	Leu	Ser 70	Arg	Arg	Arg	Val	Ala 75	Thr	Pro	Cys	Pro	Cys 80
Pro	Met	Val	Cys	Asn 85	Ser	Asp	Phe	Ala	His 90	Arg	Ser	Thr	Val	Pro 95	Pro
Ser	Ala	His	Pro 100	Phe	Thr	Leu	Thr	Pro 105	Thr	Leu	Ser	Leu	Asn 110	Thr	Phe
Ile	Ile	Val	Arg	Arg	Gly	Arg	Trp	Asp	Phe	Gly	Arg	Ser	Ala	Ala	Ala



		115				120						125				
Thr	Ala	Ser	Gly	Gly	Leu	Ile	Phe	Ile	Phe	Ala	Leu	Arg	Trp	Leu	Lys	
	130					135					140					
Ala	Phe	Ile														
145																

<210> 242  
 <211> 88  
 <212> PRT  
 <213> homo sapiens

<400> 242

Pro	Val	Leu	Cys	Arg	Gly	Asn	Ser	Gly	Ser	Leu	Ser	Arg	Lys	Phe	Pro
1				5					10					15	
Pro	Lys	Pro	Gln	Lys	Pro	Ala	Asp	Lys	Asp	His	Pro	Arg	Thr	Cys	Val
			20					25					30		
Tyr	Leu	Glu	Asn	Arg	Ser	Pro	Gly	Lys	Ser	Asp	Leu	Ser	Ala	Thr	Pro
		35					40					45			
Gly	Arg	Ser	Gly	Leu	Glu	Ser	Gly	Tyr	Gln	Asn	Leu	Leu	Arg	Gln	His
	50					55					60				
Gln	Pro	His	Gly	Arg	Cys	Pro	Thr	Trp	Pro	Gly	Ser	Arg	Trp	Lys	Val
65					70					75					80
Pro	Arg	Arg	Phe	Pro	Gly	Tyr	Gly								
				85											

<210> 243  
 <211> 164  
 <212> PRT  
 <213> homo sapiens

<400> 243

Gln	Asp	Gly	Cys	Pro	Asp	Ser	Gly	Asp	Phe	Ala	Ala	Leu	Gln	Ser	Leu
1				5					10					15	
Leu	Lys	Ala	Ser	Ser	Lys	Asp	Val	Val	Arg	Gln	Leu	Cys	Gln	Glu	Ser
			20					25					30		
Phe	Ser	Ser	Ser	Ala	Leu	Gly	Leu	Lys	Lys	Leu	Leu	Asp	Val	Thr	Cys
		35					40					45			
Ser	Ser	Leu	Ser	Val	Thr	Gln	Glu	Glu	Ala	Glu	Glu	Leu	Leu	Gln	Ala
	50					55					60				
Leu	His	Arg	Leu	Thr	Arg	Leu	Val	Ala	Phe	Arg	Asp	Leu	Ser	Ser	Ala
65					70					75					80
Glu	Ala	Ile	Leu	Ala	Leu	Phe	Pro	Glu	Asn	Phe	His	Gln	Asn	Leu	Lys
				85					90					95	
Asn	Leu	Leu	Thr	Lys	Ile	Ile	Leu	Glu	His	Val	Ser	Thr	Trp	Arg	Thr
			100					105					110		
Glu	Ala	Gln	Ala	Asn	Gln	Ile	Ser	Leu	Pro	Arg	Leu	Val	Asp	Leu	Asp
		115					120					125			

Trp	Arg	Val	Asp	Ile	Lys	Thr	Ser	Ser	Asp	Ser	Ile	Ser	Arg	Met	Ala
	130					135					140				
Val	Ala	Pro	Pro	Gly	Leu	Val	Pro	Asp	Gly	Arg	Phe	Gln	Gly	Gly	Ser
145					150					155					160
Gln	Ala	Met	Gly												

<210> 244

<211> 87

<212> PRT

<213> homo sapiens

<400> 244

Phe	Ala	Trp	Ala	Ser	Val	Leu	Gln	Val	Asp	Thr	Cys	Ser	Arg	Met	Ile
1				5					10					15	
Phe	Val	Ser	Arg	Phe	Leu	Arg	Phe	Trp	Trp	Lys	Phe	Ser	Gly	Lys	Arg
			20					25					30		
Ala	Arg	Ile	Ala	Ser	Ala	Glu	Asp	Arg	Ser	Arg	Asn	Ala	Thr	Ser	Leu
		35					40					45			
Val	Arg	Arg	Cys	Arg	Ala	Trp	Ser	Ser	Ser	Ser	Ala	Ser	Ser	Trp	Val
	50					55					60				
Thr	Asp	Lys	Leu	Glu	His	Val	Thr	Ser	Lys	Ser	Phe	Phe	Lys	Pro	Arg
65					70					75					80
Ala	Glu	Leu	Glu	Lys	Leu	Ser									
				85											

<210> 245

<211> 129

<212> PRT

<213> homo sapiens

<400> 245

Asp	Gly	Pro	Gly	Gly	Pro	Thr	Ala	His	Pro	His	Arg	Cys	Ala	His	Pro
1				5					10					15	
Pro	Gly	Val	Cys	Pro	Gly	Gln	Ala	Pro	Ala	His	Leu	Leu	Leu	Cys	Ala
			20					25					30		
Ala	Ala	Pro	Gly	His	Pro	Gly	Gln	Gly	Gln	Gln	Pro	Ala	Ala	Gly	Gly
		35					40					45			
Leu	Val	Gly	Asp	Ala	Asp	Arg	Ala	Gly	Asp	Leu	Glu	Cys	Ser	Pro	Arg
	50					55					60				
Arg	Ile	Phe	Leu	His	Pro	Arg	Leu	His	Pro	Pro	Arg	His	Leu	Gly	Ser
65					70					75					80
Cys	His	Leu	Asp	Arg	Gly	Cys	Gly	Cys	Ala	Gly	Trp	Ser	Cys	Cys	Leu
				85					90					95	
His	Leu	Arg	Glu	Thr	Gly	Trp	Tyr	Ile	Leu	Gly	Pro	Ala	Glu	Asp	Ser
			100					105					110		
Ala	Ser	Ala	Gly	Ser	Phe	Leu	His	Ser	His	Arg	Cys	Pro	Gln	Thr	Leu

115

120

125

Glu

&lt;210&gt; 246

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 246

Ala 1	Ser	Pro	Ser	Asn 5	Ser	Gln	Pro	Thr	Ser 10	Pro	Ala	Ser	Ala	Pro 15	Ala
Leu	Pro	Pro	Pro 20	Ala	Arg	Arg	Ser	Arg 25	Gly	Ala	Gln	Thr	Val 30	Ser	Leu
Thr	Met	Gly 35	Thr	Ala	Asp	Ser	Asp 40	Glu	Met	Ala	Pro	Glu 45	Ala	Pro	Gln
His	Thr 50	His	Ile	Asp	Val	His 55	Ile	His	Gln	Glu	Ser 60	Ala	Leu	Ala	Lys
Leu 65	Leu	Leu	Thr	Cys	Cys 70	Ser	Ala	Leu	Arg	Pro 75	Arg	Ala	Thr	Gln	Ala 80
Arg	Gly	Ser	Ser	Arg 85	Leu	Leu	Val	Ala	Ser 90	Trp	Val	Met	Gln	Ile 95	Val
Leu	Gly	Ile	Leu 100	Ser	Ala	Val	Leu	Gly 105	Gly	Phe	Phe	Tyr	Ile 110	Arg	Asp
Tyr	Thr	Leu 115	Leu	Val	Thr	Ser	Gly 120	Ala	Ala	Ile	Trp	Thr 125	Gly	Ala	Val
Ala	Val 130	Leu	Ala	Gly	Ala	Ala 135	Ala	Phe	Ile	Tyr	Glu 140	Lys	Arg	Gly	Gly
Thr 145	Tyr	Trp	Ala	Leu	Leu 150	Arg	Thr	Leu	Leu	Ala 155	Leu	Ala	Ala	Phe	Ser 160
Thr	Ala	Ile	Ala	Ala 165	Leu	Lys	Leu	Trp	Asn 170	Glu	Asp	Phe	Arg	Tyr 175	Gly
Tyr	Ser	Tyr	Tyr 180	Asn	Ser	Ala	Cys	Arg 185	Ile	Ser	Ser	Ser	Ser 190	Asp	Trp
Asn	Thr	Pro 195	Ala	Pro	Thr	Gln	Ser 200	Pro	Glu	Glu	Val	Arg 205	Arg	Leu	His
Leu	Cys 210	Thr	Ser	Phe	Met	Asp 215	Met	Leu	Lys	Ala	Leu 220	Phe	Arg	Thr	Leu
Gln 225	Ala	Met	Leu	Leu	Gly 230	Val	Trp	Ile	Leu	Leu 235	Leu	Leu	Ala	Ser	Leu 240
Ala	Pro	Leu	Trp	Leu 245	Tyr	Cys	Trp	Arg	Met 250	Phe	Pro	Thr	Lys	Gly 255	Lys
Arg	Asp	Gln	Lys 260	Glu	Met	Leu	Glu	Val 265	Ser	Gly	Ile				

&lt;210&gt; 247

<211> 103  
<212> PRT  
<213> homo sapiens

<400> 247

Asp 1	Cys	Thr	Gln	Asp 5	Pro	Gln	His	Asp	Leu 10	His	His	Pro	Arg	Gly 15	His
Gln	Gln	Pro	Ala 20	Ala	Ala	Pro	Gly	Leu 25	Gly	Gly	Pro	Gly	Pro 30	Gln	Arg
Arg	Ala	Ala 35	Gly	Glu	Gln	Glu	Leu 40	Gly	Gln	Gly	Arg	Leu 45	Leu	Val	Asp
Val	His 50	Ile	Asp	Val	Gly	Val 55	Leu	Trp	Gly	Leu	Arg 60	Gly	His	Leu	Ile
Thr 65	Val	Gly	Cys	Ser	His 70	Cys	Gln	Gly	His	Ser 75	Leu	Arg	Ser	Ser	Gly 80
Pro	Ala	Ser	Gly	Arg 85	Arg	Glu	Gly	Trp	Gly 90	Ala	Gly	Trp	Arg	Ser 95	Gly
Leu	Arg	Val	Gly 100	Gly	Gly	Gly									

<210> 248  
<211> 86  
<212> PRT  
<213> homo sapiens

<400> 248

Gly 1	Ser	Arg	Arg	Arg 5	Asp	Gly	Gly	Gly	Ala 10	Gly	Ala	Ala	Pro	Val 15	Ala
Pro	Arg	Ala	Leu 20	Gly	Arg	Arg	Ala	Arg 25	Ala	Gly	Arg	Cys	Ser 30	Glu	Asp
Glu	Gly	Gly 35	Gly	Gly	Ala	Gln	Arg 40	Val	Trp	Gly	Glu	Gln 45	Pro	Val	Leu
Ala	Ser 50	Gly	Gln	Ser	Pro	Pro 55	Gly	Gln	Glu	Gly	Ser 60	Phe	Thr	Arg	Val
Trp 65	Thr	Arg	Ala	Ser	Leu 70	Pro	Thr	Leu	Gly	Gln 75	Val	Leu	Gln	Pro	Gly 80
Gly	Val	His	Val	Gln 85	Val										

<210> 249  
<211> 154  
<212> PRT  
<213> homo sapiens

<400> 249

Ala 1	Arg	Gly	Gly	Ala 5	Met	Ala	Ala	Gly	Leu 10	Ala	Arg	Leu	Leu	Leu 15	Leu
Leu	Gly	Leu	Ser	Ala	Gly	Gly	Pro	Ala	Pro	Ala	Gly	Ala	Ala	Lys	Met

	20						25				30					
Lys	Val	Val	Glu	Glu	Pro	Asn	Ala	Phe	Gly	Val	Asn	Asn	Pro	Phe	Leu	
		35					40					45				
Pro	Gln	Ala	Ser	Arg	Leu	Gln	Ala	Lys	Arg	Asp	Pro	Ser	Pro	Val	Ser	
	50					55					60					
Gly	Pro	Val	His	Leu	Phe	Arg	Leu	Ser	Gly	Lys	Cys	Phe	Ser	Leu	Val	80
	65				70					75						
Glu	Ser	Thr	Tyr	Lys	Tyr	Glu	Phe	Cys	Pro	Phe	His	Asn	Val	Thr	Gln	
				85					90					95		
His	Glu	Gln	Thr	Phe	Arg	Trp	Asn	Ala	Tyr	Ser	Gly	Ile	Leu	Gly	Ile	
			100					105					110			
Trp	His	Glu	Trp	Glu	Ile	Ala	Asn	Asn	Thr	Phe	Thr	Gly	Met	Trp	Met	
		115					120					125				
Arg	Asp	Gly	Asp	Asp	Cys	Arg	Ser	Arg	Ser	Arg	Gln	Ser	Lys	Val	Glu	
	130					135					140					
Leu	Ala	Cys	Ala	Ser	Pro	Ser	Asn	Cys	Val							
	145				150											

<210> 250  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 250

Pro	Leu	Asp	Ala	Val	Ala	Arg	Ala	Arg	Thr	Arg	Gln	Leu	His	Leu	Ala
1				5					10					15	
Leu	Pro	Ala	Pro	Gly	Thr	Ala	Val	Val	Thr	Val	Pro	His	Pro	His	Ala
			20					25					30		
Arg	Glu	Gly	Val	Val	Gly	Asp	Leu	Pro	Leu	Val	Pro	Asp	Ala	Glu	Asp
		35					40					45			
Pro	Thr	Val	Gly	Val	Pro	Ala	Glu	Gly	Leu	Leu	Val	Leu	Gly	His	Val
	50					55					60				
Val	Glu	Arg	Ala	Glu	Leu	Ile	Leu	Val	Arg	Gly	Leu	His	Gln	Ala	Glu
	65				70					75					80
Ala	Leu	Ala	Arg	Glu	Ser	Glu	Glu	Met	His	Gly	Ser	Arg	His	Gly	
				85					90					95	

<210> 251  
 <211> 240  
 <212> PRT  
 <213> homo sapiens

<400> 251

Lys	Val	Thr	Asp	Gly	His	Thr	Arg	Thr	Pro	Arg	Ser	Gly	Val	Pro	Arg
1				5					10					15	
Gln	His	Glu	Ala	Gly	Ser	Pro	Gly	Leu	Thr	Ala	Ser	His	Ala	Met	Ser
			20					25					30		

Ile	His	Leu	Ala	Gly	Ser	Leu	Thr	Ala	Met	Asp	Ser	Ile	Cys	Ala	Ser
		35					40					45			
Glu	Arg	Ser	Gln	Gly	Val	Trp	Arg	Ala	Pro	Thr	Pro	Gly	Cys	Gln	Gly
	50					55					60				
Leu	Ser	Pro	Gly	Pro	Arg	Pro	Gly	Glu	Leu	Pro	Gly	Gly	Ser	Ser	Pro
65					70					75					80
Glu	Glu	Arg	Leu	Gly	Arg	Leu	Ala	Val	Ala	Gly	Pro	Pro	Arg	Gly	Ala
				85					90					95	
Gln	Asn	Val	Ser	Gln	Ala	Gly	Pro	Glu	Ala	Glu	Ala	Pro	Pro	Leu	Arg
			100					105					110		
Phe	Gly	His	Ala	Trp	Gly	Ala	Gln	Thr	Pro	Arg	Leu	Gly	Ala	Pro	Gly
		115					120					125			
Pro	Trp	Thr	Pro	Leu	Pro	Thr	Leu	Pro	Ser	His	Ile	Pro	Pro	Phe	Trp
	130					135					140				
Ser	Gln	Thr	Pro	Ala	Gln	Arg	Lys	Glu	Gly	Phe	Thr	Glu	Glu	Gly	Gln
145					150					155					160
Gly	Arg	Ala	Trp	Pro	Gln	Gly	Gly	Asp	Glu	Asp	Ile	Ser	Gly	Pro	Gly
				165					170					175	
Ser	Cys	Arg	Leu	Leu	Trp	Glu	Glu	Glu	Pro	Cys	Val	Cys	Lys	Leu	Leu
			180					185					190		
Gly	Leu	Ala	Ala	Arg	Pro	Thr	Ala	Gly	Pro	Ser	Leu	Asp	Pro	Cys	Thr
		195					200					205			
Trp	Pro	Ser	Ser	Cys	Pro	Leu	Ala	Ala	Pro	Gly	Leu	Gly	Thr	Gly	Ile
	210					215					220				
Glu	Pro	Arg	Gly	Leu	Gly	Trp	Leu	Gly	Gln	Gly	Arg	Asp	Arg	Glu	Gly
225					230					235					240

<210> 252

<211> 216

<212> PRT

<213> homo sapiens

<400> 252

Gly	Leu	Val	Met	Pro	Gly	Glu	Leu	Arg	Arg	Pro	Gly	Leu	Gly	Pro	Gln
1				5					10					15	
Ala	His	Gly	Leu	Pro	Ser	Pro	Leu	Cys	Pro	Pro	Ile	Phe	Pro	Leu	Phe
			20					25					30		
Gly	Pro	Arg	His	Gln	His	Lys	Glu	Arg	Arg	Gly	Ser	Gln	Arg	Lys	Ala
		35					40					45			
Arg	Ala	Glu	Pro	Gly	Pro	Arg	Glu	Gly	Met	Arg	Thr	Phe	Pro	Val	Gln
	50					55					60				
Val	Ala	Ala	Gly	Cys	Ser	Gly	Arg	Lys	Ser	His	Ala	Ser	Val	Asn	Cys
65					70					75					80
Trp	Gly	Trp	Arg	Pro	Ala	Pro	Leu	Gln	Gly	Pro	Ala	Leu	Thr	Pro	Ala

85								90				95			
Arg	Gly	His	Pro 100	Ala	Ala	Leu	Trp	Leu 105	Pro	Leu	Ala	Leu	Ala 110	Gln	Ala
Ser	Ser	Leu 115	Glu	Gly	Trp	Ala	Gly 120	Trp	Ala	Arg	Ala	Gly 125	Thr	Gly	Arg
Gly	Ser 130	Thr	Ser	Asp	Pro	Asp 135	Val	Gly	Trp	Leu	Cys 140	Pro	Pro	Arg	Arg
Glu 145	Ala	Gln	Gln	Thr	Ser 150	Tyr	Thr	Lys	Ala	Lys 155	Ser	Thr	Ile	Gly	Glu 160
Pro	Arg	Ser	His	Phe 165	Met	Gly	Arg	Arg	Pro 170	Arg	Pro	Gln	Gly	Pro 175	Gln
Ser	Lys	Ala	Arg 180	Gly	Arg	Phe	Ile	Pro 185	Glu	Asp	Ser	Pro	Pro 190	Gly	Ala
Ala	Pro	Ala 195	Trp	Gly	Gly	Val	Ser 200	Arg	Pro	Leu	Gly	Cys 205	Leu	Ser	Val
Cys	Gly 210	Thr	Pro	Trp	Ser	Thr 215	Pro								

<210> 253

<211> 218

<212> PRT

<213> homo sapiens

<400> 253

Val 1	Leu	Arg	Arg	Leu 5	Tyr	Ile	Tyr	Ile	Leu 10	Tyr	Ile	Thr	Asn	Met 15	Lys
Trp	Phe	Ser	Thr 20	Gln	Pro	Leu	Trp	Leu 25	Asn	Thr	Lys	Gln	Arg 30	Ser	His
Arg	Arg	Gly 35	Pro	Gly	Pro	Pro	Pro 40	Ala	Pro	Leu	Ser	Gly 45	Val	Leu	Gly
Ser	Arg 50	Gly	Leu	Pro	His	His 55	Pro	Ser	Gln	Gly	Trp 60	Gly	Arg	Ala	Gly
Pro 65	Arg	Ala	Gly	Ala	Asn 70	Val	Ala	Trp	Asn	Ser 75	Asn	Cys	Ile	Val	Arg 80
Trp	Val	Gly	Gly	Gln 85	Trp	Ala	Arg	Gly	Cys 90	Ser	Gln	Pro	Gly	Pro 95	Phe
Thr	Thr	Asn	Leu 100	Ala	Met	Thr	Cys	Gly 105	Gly	Pro	Trp	Gly	Ser 110	Gly	Cys
Leu	Leu	Gly 115	Ser	Thr	Leu	Ser	Glu 120	Val	Ser	Pro	Trp	Ala 125	Pro	Pro	Ser
Cys	Pro 130	Gln	Gly	His	Pro	Val 135	Leu	Pro	Thr	Arg	Leu 140	Trp	Ala	Trp	Gly
Leu 145	Gln	Asp	Pro	Leu	Cys 150	Arg	Val	Arg	Val	Gly 155	Ala	Gly	His	Gly	Ser 160

Arg	His	Gln	Pro	Asp 165	Ala	Pro	Val	Gly	Val 170	Ala	Arg	Ser	Trp	Asp 175	Gly
Val	Val	Arg	Asn 180	Thr	Ala	Pro	Lys	Thr 185	Gln	Asn	Lys	Asn	Thr 190	Thr	Asn
Gly	Arg	Arg 195	Ser	Pro	Pro	Pro	Thr 200	Glu	Val	Gly	Phe	Glu 205	Pro	Leu	Leu
Ile	Phe 210	Pro	Val	Ser	Phe	Leu 215	Gln	Pro	Trp						

<210> 254  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 254

Arg 1	Asp	Gly	Gly	Gly 5	Ala	Gly	Ala	Ala	Pro 10	Val	Ala	Pro	Arg	Ala 15	Leu
Gly	Arg	Arg	Ala 20	Arg	Ala	Gly	Arg	Cys 25	Ser	Glu	Asp	Glu	Gly 30	Gly	Gly
Gly	Ala	Gln 35	Arg	Val	Trp	Val	Ser 40	Ser	Leu	Ala	Gly	Trp 45	Arg	Leu	Glu
Arg	Gly 50	Thr	Ala	Arg	Ala	Arg 55	Ser	Pro	Leu	Thr	Leu 60	Pro	Leu	Pro	Val
Gly 65	Gly	Thr	Thr	Arg	Ser 70	Cys	Leu	Arg	Pro	Val 75	Ala	Ser	Arg	Pro	

<210> 255  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 255

Leu 1	Gly	Leu	Glu	Ala 5	Thr	Gly	Leu	Arg	Gln 10	Glu	Arg	Val	Val	Pro 15	Pro
Thr	Gly	Ser	Gly 20	Lys	Val	Ser	Gly	Glu 25	Arg	Ala	Arg	Ala	Val 30	Pro	Arg
Ser	Ser	Arg 35	Gln	Pro	Ala	Arg	Leu 40	Leu	Thr	Gln	Thr	Arg 45	Trp	Ala	Pro
Pro	Pro 50	Pro	Ser	Ser	Ser	Leu 55	His	Leu	Pro	Ala	Arg 60	Ala	Arg	Arg	Pro
Arg 65	Ala	Arg	Gly	Ala	Thr 70	Gly	Ala	Ala	Pro	Ala 75	Pro	Pro	Pro	Ser	

<210> 256  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 256



Trp 1	Pro	Gly	Gly	Asp 5	Trp	Pro	Glu	Ala	Arg 10	Thr	Gly	Cys	Ser	Thr 15	Tyr
Gly	Lys	Arg	Gln 20	Gly	Gln	Arg	Gly	Thr 25	Gly	Pro	Gly	Arg	Pro 30	Pro	Leu
Glu	Pro	Pro 35	Ala	Arg	Glu	Ala	Ala 40	His	Pro	Asn	Ala	Leu 45	Gly	Ser	Ser
Thr	Thr 50	Phe	Ile	Phe	Ala	Ala 55	Pro	Ala	Gly	Ala	Gly 60	Pro	Pro	Ala	Glu
Ser 65	Pro	Arg	Ser	Asn	Arg 70	Ser	Arg	Ala	Ser	Pro 75	Ala	Ala	Ile	Ala	

<210> 257  
 <211> 51  
 <212> PRT  
 <213> homo sapiens

<400> 257

Gly 1	His	Leu	Gly	Gly 5	Pro	Thr	Gly	Ser	Val 10	Cys	Ser	Arg	Ile	Leu 15	Leu
Ala	Ser	Ser	Pro 20	Phe	Tyr	Met	Asn	Cys 25	Cys	Ile	Asn	Lys	His 30	Arg	Val
Pro	Glu	Thr 35	Thr	Glu	Val	Ile	Ile 40	Leu	Pro	Thr	Glu	Cys 45	Trp	Pro	Gly
Gln	Ala 50	Trp													

<210> 258  
 <211> 49  
 <212> PRT  
 <213> homo sapiens

<400> 258

Gly 1	Gly	Gly	Phe	Leu 5	Gly	Gln	Ile	Asp	Lys 10	Ser	Lys	Asp	Asn	Ile 15	Ser
Leu	Val	Thr	Val 20	Ile	Gln	Leu	His	Ser 25	Tyr	Thr	Val	Ala	Leu 30	Phe	Gly
Leu	Ser	His 35	Glu	Glu	Val	Leu	Val 40	Thr	Asn	Tyr	Val	Phe 45	Val	Gly	Cys
Phe															

<210> 259  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 259

Ala 1	Phe	Thr	Arg	Asn 5	Thr	Thr	Asn	Lys	Val 10	Ser	Asp	Met	Leu	Ala 15	Asn
Gln	Ala	Arg	Leu	Arg	Ser	Leu	Arg	Arg	Pro	Asn	Trp	Leu	Cys	Leu	Leu

			20					25					30			
Lys	Asp	Ser	Ser	Gly	Leu	Val	Ser	Ile	Leu	His	Glu	Leu	Leu	His	Lys	
		35					40					45				

<210> 260  
 <211> 179  
 <212> PRT  
 <213> homo sapiens

<400> 260

Pro	Gly	Ile	Ser	Val	Ser	Val	Asp	Lys	Met	Glu	Ser	Ser	Pro	Phe	Asn	
1				5					10					15		
Arg	Arg	Gln	Trp	Thr	Ser	Leu	Ser	Leu	Arg	Val	Thr	Ala	Lys	Glu	Leu	
			20					25					30			
Ser	Leu	Val	Asn	Lys	Asn	Lys	Ser	Ser	Ala	Ile	Val	Glu	Ile	Phe	Ser	
		35					40					45				
Lys	Tyr	Gln	Lys	Ala	Ala	Glu	Glu	Thr	Asn	Met	Glu	Lys	Lys	Arg	Ser	
	50					55					60					
Asn	Thr	Glu	Asn	Leu	Ser	Gln	His	Phe	Arg	Lys	Gly	Thr	Leu	Thr	Val	
65					70					75					80	
Leu	Lys	Lys	Lys	Trp	Glu	Asn	Pro	Gly	Leu	Gly	Ala	Glu	Ser	His	Thr	
				85					90					95		
Asp	Ser	Leu	Arg	Asn	Ser	Ser	Thr	Glu	Ile	Arg	His	Arg	Ala	Asp	His	
			100					105					110			
Pro	Pro	Ala	Glu	Val	Thr	Ser	His	Ala	Ala	Ser	Gly	Ala	Lys	Ala	Asp	
		115					120					125				
Gln	Glu	Glu	Gln	Ile	His	Pro	Arg	Ser	Arg	Leu	Arg	Ser	Pro	Pro	Glu	
	130					135					140					
Ala	Leu	Val	Gln	Gly	Arg	Tyr	Pro	His	Ile	Lys	Asp	Gly	Glu	Asp	Leu	
145					150					155					160	
Lys	Asp	His	Ser	Thr	Glu	Ser	Lys	Lys	Met	Glu	Asn	Cys	Leu	Gly	Glu	
				165					170					175		
Ser	Arg	His														

<210> 261  
 <211> 56  
 <212> PRT  
 <213> homo sapiens

<400> 261

Gln	Ala	Thr	Leu	Leu	Leu	Glu	Pro	Lys	Leu	Thr	Lys	Lys	Asn	Lys	Ser	
1				5					10					15		
Thr	Pro	Asp	Leu	Asp	Ser	Gly	His	Leu	Leu	Lys	Pro	Ser	Phe	Arg	Val	
			20					25					30			
Asp	Ile	Pro	Thr	Ser	Arg	Thr	Val	Arg	Ile	Leu	Lys	Thr	Thr	Gln	Gln	
		35					40					45				

Lys Val Lys Lys Trp Lys Ile Val  
50 55

<210> 262  
<211> 94  
<212> PRT  
<213> homo sapiens

<400> 262

Asp 1	Ser	Ala	Pro	Ser 5	Pro	Gly	Phe	Ser	His 10	Phe	Phe	Phe	Asn	Thr 15	Val
Arg	Val	Pro	Phe 20	Leu	Lys	Cys	Trp	Glu 25	Arg	Phe	Ser	Val	Leu 30	Leu	Leu
Phe	Phe	Ser 35	Met	Phe	Val	Ser	Ser 40	Ala	Ala	Phe	Trp	Tyr 45	Leu	Glu	Asn
Ile	Ser 50	Thr	Ile	Ala	Asp	Asp 55	Leu	Phe	Leu	Leu	Thr 60	Arg	Glu	Ser	Ser
Leu 65	Ala	Val	Thr	Leu	Asn 70	Asp	Ser	Glu	Val	His 75	Cys	Arg	Leu	Leu	Asn 80
Gly	Asp	Asp	Ser	Ile 85	Leu	Ser	Thr	Asp	Thr 90	Glu	Ile	Pro	Gly		

<210> 263  
<211> 75  
<212> PRT  
<213> homo sapiens

<400> 263

Val 1	Met	Ser	Asp	Pro 5	Ala	Asp	Lys	Ala	Ala 10	Arg	Ala	Asp	Ser	Ala 15	Arg
Ala	Ala	Arg	Gly 20	Lys	Arg	Lys	Lys	Asn 25	Val	Glu	Glu	Asn	Met 30	Ala	Tyr
Ser	Ala	Leu 35	Met	Glu	Val	Ala	Gly 40	Tyr	Cys	Leu	Ile	Glu 45	Arg	Met	Leu
Trp	Asn 50	Pro	Met	Leu	Lys	Ile 55	Lys	Ser	Val	Trp	Leu 60	Cys	Ser	Tyr	Ala
Val 65	Met	Val	Ile	Pro	Arg 70	Gln	Leu	Ala	Lys	Val 75					

<210> 264  
<211> 74  
<212> PRT  
<213> homo sapiens

<400> 264

Ala 1	Met	Phe	Ser	Ser 5	Thr	Phe	Phe	Phe	Leu 10	Leu	Pro	Arg	Ala	Ala 15	Arg
Ala	Glu	Ser	Ala 20	Arg	Ala	Ala	Leu	Ser 25	Ala	Gly	Ser	Leu	Ile 30	Thr	Tyr

Ala	Phe	Tyr	Lys	Arg	Leu	Pro	Lys	Lys	Lys	Leu	Leu	Thr	Arg	Asn	Val
		35					40					45			
Asp	Lys	Pro	Leu	Lys	Ala	Asn	Lys	Gln	Gln	Thr	Val	Val	Phe	Ala	Phe
	50					55					60				
Ser	Tyr	Ser	Trp	Gln	Ala	Glu	Val	Arg	Ala						
65					70										

<210> 265

<211> 63

<212> PRT

<213> homo sapiens

<400> 265

Asp	Ser	Lys	Ala	Phe	Ser	Leu	Leu	Ser	Ser	Asn	Gln	Pro	Leu	Pro	Ser
1				5					10					15	
Lys	Leu	Ser	Arg	Pro	Cys	Phe	Pro	Pro	His	Phe	Phe	Phe	Phe	Tyr	Leu
			20					25					30		
Glu	Pro	Leu	Glu	Pro	Asn	Arg	Leu	Glu	Pro	Pro	Cys	Leu	Leu	Asp	His
		35					40					45			
Ser	Ser	Pro	Thr	His	Phe	Ile	Lys	Gly	Tyr	Pro	Lys	Arg	Asn	Cys	
	50					55					60				

<210> 266

<211> 94

<212> PRT

<213> homo sapiens

<400> 266

Arg	Arg	Gly	Ser	Gly	Ser	Arg	Ser	Ser	Met	Ala	Pro	Val	Leu	Ala	Ser
1				5					10					15	
Met	Leu	Trp	Met	Ser	Thr	Arg	Gly	Thr	Ala	Met	Thr	Ser	Thr	Ser	Leu
			20					25					30		
Cys	Thr	Ser	Arg	Ala	Arg	Ser	Arg	Pro	Met	Pro	Ser	Ser	Ser	Ser	Pro
		35					40					45			
Thr	Pro	Thr	Ala	Trp	Arg	Cys	Cys	Cys	Ala	Thr	Arg	Thr	Arg	Val	Ser
	50					55					60				
Thr	Ser	Thr	Arg	Thr	Gly	Ala	Ser	Leu	Arg	Met	Trp	Cys	Cys	Ser	Gly
65					70					75					80
Gly	Arg	Cys	Leu	Leu	Leu	Trp	Pro	Thr	Ser	Ala	Pro	Thr	Arg		
				85					90						

<210> 267

<211> 254

<212> PRT

<213> homo sapiens

<400> 267

Gly	Asp	Arg	Lys	Pro	Leu	Tyr	His	Tyr	Gly	Arg	Gly	Met	Asn	Pro	Ala
1				5					10					15	

Asp	Lys	Pro	Ala 20	Trp	Ala	Arg	Glu	Val 25	Lys	Glu	Arg	Thr	Arg 30	Met	Asn
Lys	Gln	Gln 35	Asn	Ser	Pro	Leu	Ala 40	Lys	Ser	Lys	Pro	Gly 45	Ser	Thr	Gly
Pro	Glu 50	Pro	Pro	Ser	Pro	Gln 55	Ala	Ser	Pro	Gly	Pro 60	Pro	Gly	Leu	Pro
Trp 65	Ala	Pro	Lys	Pro	Tyr 70	His	Lys	Phe	Met	Ala 75	Phe	Lys	Ser	Phe	Ala 80
Asp	Leu	Pro	His	Arg 85	Pro	Leu	Leu	Val	Asp 90	Leu	Thr	Val	Glu	Glu 95	Gly
Gln	Arg	Leu	Lys 100	Val	Ile	Tyr	Gly	Ser 105	Ser	Ala	Gly	Phe	His 110	Ala	Val
Asp	Val	Asp 115	Ser	Gly	Asn	Ser	Tyr 120	Asp	Ile	Tyr	Ile	Pro 125	Val	His	Ile
Gln	Ser 130	Gln	Ile	Thr	Pro	His 135	Ala	Ile	Ile	Phe	Leu 140	Pro	Asn	Thr	Asp
Gly 145	Met	Glu	Met	Leu	Leu 150	Cys	Tyr	Glu	Asp	Glu 155	Gly	Val	Tyr	Val	Asn 160
Thr	Tyr	Gly	Arg	Ile 165	Ile	Lys	Asp	Val	Val 170	Leu	Gln	Trp	Gly	Glu 175	Met
Pro	Thr	Ser	Val 180	Ala	Tyr	Ile	Cys	Ser 185	Asn	Gln	Ile	Met	Gly 190	Trp	Gly
Glu	Lys	Ala 195	Ile	Glu	Ile	Arg	Ser 200	Val	Glu	Thr	Gly	His 205	Leu	Asp	Gly
Val	Phe 210	Met	His	Lys	Arg	Ala 215	Gln	Arg	Leu	Lys	Phe 220	Leu	Cys	Glu	Arg
Asn 225	Asp	Lys	Val	Phe	Phe 230	Ala	Ser	Val	Arg	Ser 235	Gly	Gly	Ser	Ser	Gln 240
Val	Tyr	Phe	Met	Thr 245	Leu	Asn	Arg	Asn	Cys 250	Ile	Met	Asn	Trp		

<210> 268

<211> 231

<212> PRT

<213> homo sapiens

<400> 268

Gly 1	Lys	Lys	His	Leu 5	Val	Ile	Pro	Leu	Thr 10	Gln	Glu	Leu	Glu	Pro 15	Leu
Ser	Ser	Phe	Val 20	His	Glu	Asp	Pro	Val 25	Glu	Val	Ala	Arg	Leu 30	His	Arg
Ala	Asp	Leu 35	Asn	Gly	Phe	Leu	Thr 40	Pro	Ala	His	Tyr	Leu 45	Val	Gly	Ala
Asp	Val 50	Gly	His	Arg	Ser	Arg 55	His	Leu	Pro	Pro	Leu 60	Gln	His	His	Ile

Leu 65	Asn	Asp	Ala	Pro	Val 70	Arg	Val	Asp	Val	Asp 75	Thr	Leu	Val	Leu	Val 80
Ala	Gln	Gln	His	Leu 85	His	Ala	Val	Gly	Val 90	Gly	Glu	Glu	Asp	Asp 95	Gly
Met	Gly	Arg	Asp 100	Leu	Ala	Leu	Asp	Val 105	His	Arg	Asp	Val	Asp 110	Val	Ile
Ala	Val	Pro 115	Arg	Val	Asp	Ile	His 120	Ser	Met	Glu	Ala	Ser 125	Thr	Gly	Ala
Ile	Asp 130	Asp	Leu	Glu	Pro	Leu 135	Pro	Leu	Leu	Tyr	Cys 140	Gln	Val	Asp	Gln
Gln 145	Arg	Ala	Val	Gly	Glu 150	Val	Gly	Lys	Gly	Leu 155	Glu	Gly	His	Glu	Phe 160
Val	Val	Gly	Phe	Gly 165	Gly	Pro	Gly	Glu	Ala 170	Trp	Gly	Pro	Trp	Gly 175	Gly
Leu	Gly	Ala	Gly 180	Gly	Leu	Arg	Pro	Arg 185	Ala	Ala	Trp	Leu	Ala 190	Leu	Gly
Gln	Gly	Arg 195	Val	Leu	Leu	Leu	Val 200	His	Pro	Cys	Ser	Leu 205	Phe	Tyr	Leu
Ser	Gly 210	Pro	Gly	Trp	Phe	Val 215	Ser	Gly	Ile	His	Ala 220	Pro	Thr	Ile	Met
Val 225	Gln	Gly	Leu	Pro	Val 230	Pro									

<210> 269

<211> 454

<212> PRT

<213> homo sapiens

<400> 269

Gly 1	Ala	Gly	Cys	Thr 5	Ser	Pro	Gly	Leu	Trp 10	Ala	Arg	Lys	Ala	Ala 15	Ala
Arg	Cys	Leu	Pro 20	Thr	Tyr	Pro	Ser	Arg 25	Ala	Gln	Pro	Ser	Asn 30	Val	Gly
Arg	Arg	Arg 35	Arg	Arg	Arg	Pro	Gly 40	Leu	Gly	Ala	Leu	Ala 45	Ala	Gly	Val
Pro	Ala 50	Met	Ala	Glu	Ser	Val 55	Glu	Arg	Leu	Gln	Gln 60	Arg	Val	Gln	Glu
Leu 65	Glu	Arg	Glu	Leu	Ala 70	Gln	Glu	Arg	Ser	Leu 75	Gln	Val	Pro	Arg	Ser 80
Gly	Asp	Gly	Gly	Gly 85	Gly	Arg	Val	Arg	Ile 90	Glu	Lys	Met	Ser	Ser 95	Glu
Val	Val	Asp	Ser 100	Asn	Pro	Tyr	Ser	Arg 105	Leu	Met	Ala	Leu	Lys 110	Arg	Met
Gly	Ile	Val	Ser	Asp	Tyr	Glu	Lys	Ile	Arg	Thr	Phe	Ala	Val	Ala	Ile

[illegible]

450

<210> 270  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 270

Lys 1	Leu	Thr	Val	Pro 5	Lys	Phe	Asn	Arg	Asn 10	Phe	Asn	Thr	Phe	Cys 15	Thr
Lys	Ile	Pro	Ala 20	Thr	Thr	Pro	Ile	Val 25	Val	Gly	Arg	Leu	Ala 30	Ala	Gln
Thr	Pro	Ser 35	Arg	Phe	Arg	Val	Phe 40	Ser	Ser	Ile	Phe	Ala 45	Ala	Thr	Thr
Ser	Gly 50	Gly	Ala	His	Ala	Lys 55	Gln	Ala	Asp	Ser	Pro 60	Gly	Ile	Ile	Ser
Cys 65	Ile	Cys	Pro	Glu	Thr 70	Ala	Phe	Ser	Leu	Thr 75	Pro	Asp	Ser	Ile	His 80
Val	Cys	Pro	Ser	Ser 85	Leu	Gln	Ala	Val	Phe 90	Ile	Val	Ile	Arg	Ala 95	Ser
Lys	Leu	Ser	Thr 100	Gln	Leu	Arg	Thr	Arg 105	Ser	Thr	Gly	Phe	Pro 110	Ser	Ser
Asn	Pro	Pro 115	Leu	Leu	Ile	Leu	Ser 120	Met	Lys	Cys					

<210> 271  
 <211> 176  
 <212> PRT  
 <213> homo sapiens

<400> 271

Cys 1	Ser	Ser	Glu	Tyr 5	Val	Leu	Leu	Leu	Glu 10	Leu	Tyr	Leu	Ile	Leu 15	Leu
Asp	Glu	Val	Gly 20	Arg	Lys	Val	Tyr	Ser 25	Tyr	Trp	Leu	Val	Pro 30	Pro	Cys
His	Asn	Gln 35	Arg	Val	Ala	Thr	Tyr 40	Gln	Cys	His	Ile	Leu 45	Ser	Ala	Phe
Gln	Gln 50	Ser	His	Tyr	Leu	Leu 55	His	Gln	His	Leu	Leu 60	Leu	Leu	Arg	Gln
Arg 65	Tyr	Gly	Phe	Ser	His 70	Ser	Arg	Leu	Gln	Phe 75	Pro	Phe	Val	Ser	Met 80
Pro	Ser	Ser	Gly	Cys 85	Arg	Asp	Ser	Asn	Pro 90	Pro	Pro	Leu	Ser	Ser 95	Ser
Ser	Arg	Cys	Gly 100	Pro	Gly	Arg	Pro	Leu 105	Arg	Arg	Arg	Ser	Ser 110	Gly	Pro
Ala	Asp	Ser 115	Ser	Pro	Gly	Gln	Val 120	Pro	Ala	Pro	Ala	Pro 125	Gly	Pro	Ala



Ala	Ala	Gly	Ala	Pro	Gln	Thr	Pro	Pro	Trp	Leu	Gly	Leu	Arg	Pro	Pro
	130					135					140				
Thr	Leu	Pro	Ala	Arg	Ala	Phe	Ala	Ala	Ala	Phe	Ala	Pro	Arg	Cys	Ser
145					150					155					160
Ala	Gly	Pro	Ala	Arg	Gly	Thr	Trp	Gly	Gly	Thr	Ser	Pro	Leu	Pro	Ser
				165					170					175	

<210> 272  
 <211> 117  
 <212> PRT  
 <213> homo sapiens

<400> 272

Glu	Ala	Arg	Gln	Ala	Trp	Thr	Gly	Ala	Lys	Gly	Ala	Gly	Ser	Leu	Thr
1				5					10					15	
Phe	Ser	Ser	Leu	Gln	Ser	Gly	His	Leu	Ala	Ser	Gly	Ser	Gln	Ser	Pro
			20					25					30		
Glu	Ser	Thr	Lys	Ala	Pro	Gly	Thr	Pro	Pro	Thr	Pro	Ser	Tyr	Pro	Gly
		35					40					45			
Thr	Pro	Ser	Arg	Gln	Leu	Leu	Trp	Gln	Trp	Val	Gln	Pro	Arg	Pro	Ala
	50					55					60				
Leu	Pro	Ala	Ser	Ser	Pro	Cys	Ser	Arg	His	Gln	Leu	Tyr	Leu	Pro	Arg
65					70					75					80
Gln	Ala	Met	Ser	Trp	Leu	Leu	Ser	Pro	Ala	Pro	Ser	Val	Pro	Leu	Asp
				85					90					95	
Phe	Ser	Gly	Ala	Ser	Pro	Val	Trp	Ala	Thr	Leu	Cys	Phe	Pro	His	Pro
			100					105					110		
Arg	Leu	Pro	His	Arg											
		115													

<210> 273  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 273

Ala	Pro	Ala	Leu	Pro	Pro	Pro	Ala	Gly	Asn	Val	Leu	Ala	Ser	Gln	Pro
1				5					10					15	
Ser	Thr	Ile	Cys	Ser	Pro	Arg	Leu	Leu	Arg	Gly	Gln	Pro	Ser	Leu	Gly
			20					25					30		
His	Pro	Leu	Phe	Pro	Ser	Ser	Ser	Ala	Pro	Thr	Gln	Val	Thr	Asp	Pro
		35					40					45			
Ala	Asp	Ser	Phe	Ser	Leu	Gly	Lys	Val	Gly	Cys	Cys	Leu	Thr	Ser	Pro
	50					55					60				
Ser	Ser	Pro	Pro	Pro	Ile	His	Thr	His	Arg	His	Pro	Pro	Thr	Pro	Gly
65					70					75					80

Arg Leu Val Ser His Met  
85

<210> 274  
<211> 177  
<212> PRT  
<213> homo sapiens

<400> 274

Glu 1	Ala	Arg	Thr	Leu 5	Pro	Ala	Gly	Gly	Gly 10	Arg	Ala	Gly	Ala	Tyr 15	Cys
Arg	Glu	Arg	Arg 20	Leu	Ala	Val	Leu	Ala 25	Trp	Ala	Gly	Pro	Thr 30	Ala	Ile
Thr	Val	Ala 35	Tyr	Leu	Gly	Ser	Leu 40	Gly	Arg	Met	Glu	Trp 45	Val	Gly	Cys
Gln	Gly 50	Leu	Trp	Cys	Phe	Leu 55	Val	Ile	Gly	Thr	Leu 60	Met	Pro	Ser	Ala
His 65	Phe	Ala	Lys	Lys	Lys 70	Lys	Leu	Met	Thr	Leu 75	Leu	Pro	Trp	Leu	Leu 80
Ser	Met	Leu	Ala	Trp 85	Pro	Pro	Arg	Val	Gly 90	Gly	Thr	Ser	Pro	Leu 95	Leu
Ala	Glu	Ala	Gly 100	Glu	Gln	Val	Leu	Ser 105	Tyr	Asp	Pro	Ile	His 110	Gln	Ala
Gly	Val	Leu 115	Ser	Pro	Ser	Gly	His 120	His	Ser	Ser	Gln	His 125	Gln	Gly	Pro
Val	Gly 130	Leu	Gly	Gln	Gly	Ser 135	Glu	Lys	Gly	Trp	Gln 140	Glu	Val	Pro	Arg
Ser 145	Ser	Gln	Pro	Gly	Arg 150	Gly	Thr	Asn	Ala	Leu 155	Asn	Thr	Ser	Lys	Leu 160
Arg	Asp	Pro	Lys	Val 165	Ser	Thr	Pro	Gly	Ser 170	Gly	Leu	Pro	Pro	His 175	Arg

His

<210> 275  
<211> 71  
<212> PRT  
<213> homo sapiens

<400> 275

Gln 1	Phe	Pro	Gly	Pro 5	Ser	Val	Pro	Glu	Gln 10	Ser	Thr	Ser	Val	Ser 15	Val
Thr	Thr	Ser	Cys 20	Leu	Phe	Pro	Ser	Leu 25	His	Leu	Leu	Gln	Phe 30	Ile	Tyr
Met	Leu	Leu 35	Leu	Leu	Val	His	Phe 40	Cys	Leu	Pro	Tyr	Gln 45	Ala	Val	Asn
Glu	Gly 50	Arg	Asn	Leu	Val	Cys 55	Phe	Ile	His	His	His 60	Val	Pro	Ser	Ala

Trp His Ile Val Gly Leu His  
65 70

<210> 276  
<211> 102  
<212> PRT  
<213> homo sapiens

<400> 276

Phe 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Phe	Phe	Phe 10	Phe	Phe	Phe	Cys	Leu 15	Ile
Asn	Met	Ser	Ile 20	Tyr	Leu	Ala	Pro	Asp 25	Gly	Asn	Thr	Lys	Ser 30	Trp	Gln
Trp	Glu	Trp 35	Lys	Gly	Ser	Leu	Ser 40	Gln	Ile	Leu	Pro	Tyr 45	Tyr	Val	Asp
Pro	Lys 50	Ala	Gly	Leu	Gly	Ser 55	Lys	Ala	His	Lys	Pro 60	Pro	Lys	Gln	Ile
Phe 65	Ile	Glu	His	Leu	Asp 70	Tyr	Tyr	Arg	Pro	Ser 75	Ile	Leu	Leu	Gly	Thr 80
Met	Gly	Asp	Val	Lys 85	Glu	Val	Ile	Ser	His 90	Met	Ile	Cys	Leu	Gln 95	Gly
Ala	Lys	Asn	Ala 100	Ser	Gly										

<210> 277  
<211> 65  
<212> PRT  
<213> homo sapiens

<400> 277

Gly 1	Val	Ile	Glu	Ser 5	Arg	Arg	Val	Leu	Ser 10	Arg	Gly	Val	Ile	Arg 15	Phe
Ile	Phe	Lys	Gln 20	Pro	Asn	Pro	Gly	Arg 25	Cys	Gly	Pro	Ile	Leu 30	Ser	Ala
Leu	Lys	Lys 35	Ile	Pro	Phe	Pro	Tyr 40	Leu	Pro	Ala	Ser	Ile 45	Met	Ser	Val
Glu	Glu 50	Ser	Asn	Cys	Gly	Ser 55	Phe	Glu	Gly	Asp	Gly 60	Pro	Phe	Phe	Pro
Val 65															

<210> 278  
<211> 65  
<212> PRT  
<213> homo sapiens

<400> 278

Phe 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Phe	Phe	Phe 10	Phe	Phe	Phe	Leu	Phe	Asn 15	Lys
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----	-----------	-----

Tyr	Glu	His	Leu 20	Phe	Gly	Thr	Arg	Trp 25	Gln	Tyr	Lys	Ile	Leu 30	Ala	Val
Gly	Val	Glu 35	Arg	Phe	Ser	Leu	Ser 40	Asn	Thr	Ser	Ile	Leu 45	Cys	Arg	Pro
Lys	Gly 50	Arg	Thr	Trp	Gln	Gln 55	Gly	Ser	Gln	Thr	Thr 60	Gln	Thr	Asn	Ile

Tyr  
65

<210> 279  
 <211> 489  
 <212> PRT  
 <213> homo sapiens

<400> 279

Leu 1	Ala	Asp	Ser	Phe 5	Pro	Gly	Ser	Ser	Pro 10	Tyr	Glu	Gly	Tyr	Asn 15	Tyr
Gly	Ser	Phe	Glu 20	Asn	Val	Ser	Gly	Ser 25	Thr	Asp	Gly	Leu	Val 30	Asp	Ser
Ala	Gly	Thr 35	Gly	Asp	Leu	Ser	Asp 40	Gly	Tyr	Gln	Gly	Arg 45	Ser	Phe	Glu
Pro	Val 50	Gly	Thr	Arg	Pro	Arg 55	Val	Asp	Ser	Met	Ser 60	Ser	Val	Glu	Glu
Asp 65	Asp	Tyr	Asp	Thr	Leu 70	Thr	Asp	Ile	Asp	Ser 75	Asp	Lys	Asn	Val	Ile 80
Arg	Thr	Lys	Gln	Tyr 85	Leu	Tyr	Val	Ala	Asp 90	Leu	Ala	Arg	Lys	Asp 95	Lys
Arg	Val	Leu	Arg 100	Lys	Lys	Tyr	Gln	Ile 105	Tyr	Phe	Trp	Asn	Ile 110	Ala	Thr
Ile	Ala	Val 115	Phe	Tyr	Ala	Leu	Pro 120	Val	Val	Gln	Leu	Val 125	Ile	Thr	Tyr
Gln	Thr 130	Val	Val	Asn	Val	Thr 135	Gly	Asn	Gln	Asp	Ile 140	Cys	Tyr	Tyr	Asn
Phe 145	Leu	Cys	Ala	His	Pro 150	Leu	Gly	Asn	Leu	Ser 155	Ala	Phe	Asn	Asn	Ile 160
Leu	Ser	Asn	Leu	Gly 165	Tyr	Ile	Leu	Leu	Gly 170	Leu	Leu	Phe	Leu	Leu 175	Ile
Ile	Leu	Gln	Arg 180	Glu	Ile	Asn	His	Asn 185	Arg	Ala	Leu	Leu	Arg 190	Asn	Asp
Leu	Cys	Ala 195	Leu	Glu	Cys	Gly	Ile 200	Pro	Lys	His	Phe	Gly 205	Leu	Phe	Tyr
Ala	Met 210	Gly	Thr	Ala	Leu	Met 215	Met	Glu	Gly	Leu	Leu 220	Ser	Ala	Cys	Asp
His	Val	Cys	Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met

225					230					235					240
Tyr	Met	Ile	Ala	Gly 245	Leu	Cys	Met	Leu	Lys 250	Leu	Tyr	Gln	Lys	Arg 255	His
Pro	Asp	Ile	Asn 260	Ala	Ser	Ala	Tyr	Ser 265	Ala	Tyr	Ala	Cys	Leu 270	Ala	Ile
Val	Ile	Phe 275	Phe	Ser	Val	Leu	Gly 280	Val	Val	Phe	Gly	Lys 285	Gly	Asn	Thr
Ala	Phe 290	Trp	Ile	Val	Phe	Ser 295	Ile	Ile	His	Ile	Ile 300	Ala	Thr	Leu	Leu
Leu 305	Ser	Thr	Gln	Leu	Tyr 310	Tyr	Met	Gly	Arg	Trp 315	Lys	Leu	Asp	Ser	Gly 320
Ile	Phe	Arg	Arg	Ile 325	Leu	His	Val	Leu	Tyr 330	Thr	Asp	Cys	Ile	Arg 335	Gln
Cys	Ser	Gly	Pro 340	Leu	Tyr	Val	Asp	Arg 345	Met	Val	Leu	Leu	Val 350	Met	Gly
Asn	Val	Ile 355	Asn	Trp	Ser	Leu	Ala 360	Ala	Tyr	Gly	Leu	Ile 365	Met	Arg	Pro
Asn	Asp 370	Phe	Ala	Ser	Tyr	Leu 375	Leu	Ala	Ile	Gly	Ile 380	Cys	Asn	Leu	Leu
Leu 385	Tyr	Phe	Ala	Phe	Tyr 390	Ile	Ile	Met	Lys	Leu 395	Arg	Ser	Gly	Glu	Arg 400
Ile	Lys	Leu	Ile	Pro 405	Leu	Leu	Cys	Ile	Val 410	Cys	Thr	Ser	Val	Val 415	Trp
Gly	Phe	Ala	Leu 420	Phe	Phe	Phe	Phe	Gln 425	Gly	Leu	Ser	Thr	Trp 430	Gln	Lys
Thr	Pro	Ala 435	Glu	Ser	Arg	Glu	His 440	Asn	Arg	Asp	Cys	Ile 445	Leu	Leu	Asp
Phe	Phe 450	Asp	Asp	His	Asp	Ile 455	Trp	His	Phe	Leu	Ser 460	Ser	Ile	Ala	Met
Phe 465	Gly	Ser	Phe	Leu	Val 470	Leu	Leu	Thr	Leu	Asp 475	Asp	Asp	Leu	Asp	Thr 480
Val	Gln	Arg	Asp	Lys 485	Ile	Tyr	Val	Phe							

<210> 280  
 <211> 182  
 <212> PRT  
 <213> homo sapiens

<400> 280

Ala 1	Pro	Leu	Cys	His 5	Arg	Pro	Val	Thr	Leu 10	Ser	Cys	Cys	Gly	Asp 15	Glu
Ser	Gln	His	Arg 20	Cys	Pro	Ala	Leu	Asp 25	Gly	Ser	Arg	Thr	Ala 30	Arg	Ser

Ser	Leu	Gly	Leu	Ala	Trp	Asp	Ser	His	Gly	Val	Ala	Trp	Asn	Leu	Ala
		35					40					45			
Ala	Ala	Leu	Cys	Arg	Gly	Ala	Gly	Leu	Leu	Pro	Trp	Asp	Pro	Gln	Met
	50					55					60				
Leu	Ala	Lys	Leu	Leu	Leu	Ser	Ser	Gln	Cys	Trp	Gly	Leu	Pro	Trp	Ala
65					70					75					80
Pro	Val	Leu	Trp	Leu	Ser	Ile	Cys	Pro	Phe	Ala	Arg	Gly	Arg	Met	Glu
				85					90					95	
Gly	Thr	Pro	Ser	Pro	Phe	His	Ala	Leu	His	Phe	Ala	Arg	Pro	Pro	Pro
			100					105					110		
His	Asn	Ala	Pro	Ala	Trp	Asp	Leu	Arg	Pro	Leu	Phe	Pro	Pro	Ile	Leu
		115					120					125			
Pro	Leu	Gln	Gly	Leu	Val	Trp	Gly	Leu	Asn	Leu	Cys	Pro	Val	Ser	Gly
	130					135					140				
Pro	Gln	Phe	Ser	Leu	Gly	Cys	Pro	Trp	Leu	Pro	Ser	Leu	Pro	Ile	Pro
145					150					155					160
Val	Ser	Gln	Asp	Gly	Trp	Gly	Tyr	Glu	Ile	Leu	Gly	Val	Gly	Gln	Leu
				165					170					175	
Val	Pro	Asp	Phe	Trp	Cys										
			180												

<210> 281

<211> 536

<212> PRT

<213> homo sapiens

<400> 281

Ala	Arg	Pro	Gly	Cys	Pro	Ala	Ala	Ile	Gln	Cys	Trp	Ala	Ala	Val	Leu
1				5					10					15	
Gly	Leu	Ile	Pro	Thr	Ala	Arg	Gln	Ser	Asp	Arg	Ser	Met	Thr	Gln	Arg
			20					25					30		
Ser	Ser	Gly	Pro	Leu	Glu	Val	Lys	Arg	Arg	Ala	Gln	Leu	Leu	Leu	Glu
		35					40					45			
Asp	Ile	Asp	Leu	Val	Pro	Leu	His	Ser	Ile	Gln	Val	Val	Ile	Gln	Cys
	50					55					60				
Gln	Gln	His	Gln	Glu	Gly	Pro	Glu	His	Gly	Asp	Gly	Gly	Glu	Glu	Val
65					70					75					80
Pro	Asp	Val	Val	Val	Val	Lys	Glu	Val	Glu	Glu	Asp	Ala	Val	Pro	Val
				85					90					95	
Val	Leu	Pro	Arg	Leu	Cys	Arg	Gly	Phe	Leu	Pro	Gly	Ala	Glu	Ser	Leu
			100					105					110		
Glu	Glu	Glu	Glu	Glu	Arg	Glu	Ala	Pro	Asp	His	Gly	Gly	Ala	Asn	Asp
		115					120					125			
Ala	Glu	Gln	Gly	Asp	Glu	Leu	Asp	Pro	Leu	Pro	Thr	Pro	Glu	Leu	His
	130					135					140				

Asp 145	Asp	Val	Glu	Gly	Glu 150	Val	Lys	Glu	Gln	Val 155	Ala	Asp	Ala	Asn	Gly 160
Gln	Gln	Val	Gly	Ser 165	Glu	Ile	Ile	Gly	Ala 170	His	Asp	Lys	Pro	Ile 175	Gly
Ser	Gln	Arg	Pro 180	Val	Asp	Asp	Val	Ala 185	His	Asp	Gln	Gln	His 190	His	Ala
Val	His	Val 195	Glu	Arg	Pro	Ala	Ala 200	Leu	Pro	Asp	Ala	Val 205	Cys	Val	Glu
His	Val 210	Glu	Asp	Ala	Ala	Glu 215	Asp	Pro	Arg	Val	Gln 220	Phe	Pro	Pro	Ala
His 225	Val	Ile	Glu	Leu	Arg 230	Ala	Glu	Glu	Gln	Gly 235	Gly	Asp	Asp	Val	Asn 240
Asp	Gly	Glu	Asp	Asp 245	Pro	Glu	Arg	Arg	Val 250	Pro	Phe	Ala	Lys	Asp 255	His
Ala	Gln	His	Arg 260	Glu	Glu	Asp	Asp	Asn 265	Gly	Gln	Ala	Gly	Val 270	Gly	Thr
Val	Gly	Ala 275	Gly	Val	Asp	Val	Arg 280	Val	Pro	Leu	Leu	Val 285	Glu	Leu	Gln
His	Ala 290	Glu	Ser	Gly	Asp	His 295	Val	His	Glu	Arg	Cys 300	Val	Lys	Leu	Glu
Ile 305	Gly	Ile	Val	Gly	Ala 310	His	Met	Ile	Ala	Ser 315	Thr	Glu	Gln	Pro	Leu 320
His	His	Gln	Gly	Cys 325	Ala	His	Gly	Val	Glu 330	Lys	Pro	Lys	Val	Phe 335	Gly
Asp	Pro	Thr	Phe 340	Gln	Gly	Thr	Glu	Val 345	Ile	Ala	Gln	Gln	Gly 350	Pro	Val
Val	Val	Asp 355	Leu	Pro	Leu	Gln	Asp 360	Asp	Glu	Gln	Glu	Lys 365	Gln	Pro	Gln
Gln	Asp 370	Val	Pro	Gln	Val	Ala 375	Glu	Asp	Val	Val	Glu 380	Gly	Ala	Glu	Ile
Ala 385	Gln	Trp	Val	Gly	Ala 390	Glu	Glu	Val	Val	Val 395	Ala	Asp	Val	Leu	Ile 400
Pro	Cys	Asp	Ile	His 405	His	Arg	Leu	Val	Gly 410	Asp	His	Gln	Leu	His 415	His
Arg	Lys	Gly	Ile 420	Glu	Asp	Ser	Asn	Gly 425	Gly	Asn	Val	Pro	Glu 430	Val	Asp
Leu	Val	Leu 435	Phe	Pro	Gln	Asn	Thr 440	Leu	Val	Leu	Pro	Cys 445	Gln	Val	Ser
His	Ile 450	Glu	Val	Leu	Leu	Gly 455	Ala	Asn	Asp	Ile	Leu 460	Val	Gly	Ile	Asp
Val 465	Gly	Gln	Cys	Val	Val 470	Val	Ile	Leu	Leu	His 475	Arg	Ala	His	Gly	Val 480

His	Ser	Gly	Pro	Ser 485	Thr	Tyr	Arg	Phe	Lys 490	Gly	Ala	Ala	Leu	Val 495	Thr
Val	Arg	Glu	Val 500	Pro	Ser	Ala	Ser	Ala 505	Val	Asn	Gln	Thr	Ile 510	Gly	Arg
Ser	Arg	Asn 515	Ile	Leu	Lys	Gly	Ala 520	Ile	Val	Val	Thr	Leu 525	Ile	Arg	Gly
Thr	Ala 530	Arg	Lys	Arg	Ile	Ser 535	Gln								

<210> 282

<211> 551

<212> PRT

<213> homo sapiens

<400> 282

Pro 1	Leu	Ser	Ser	Pro 5	Ser	Cys	Cys	Arg	Tyr 10	Arg	Arg	Cys	Cys	Arg 15	Arg
Leu	Arg	Pro	Pro 20	Leu	Arg	Ser	Val	Val 25	Gln	Pro	Gly	Pro	Arg 30	Thr	Met
Ser	Leu	Ser 35	Arg	Ser	Glu	Glu	Met 40	His	Arg	Leu	Thr	Glu 45	Asn	Val	Tyr
Lys	Thr 50	Ile	Met	Glu	Gln	Phe 55	Asn	Pro	Ser	Leu	Arg 60	Asn	Phe	Ile	Ala
Met 65	Gly	Lys	Asn	Tyr	Glu 70	Lys	Ala	Leu	Ala	Gly 75	Val	Thr	Tyr	Ala	Ala 80
Lys	Gly	Tyr	Phe	Asp 85	Ala	Leu	Val	Lys	Met 90	Gly	Glu	Leu	Ala	Ser 95	Glu
Ser	Gln	Gly	Ser 100	Lys	Glu	Leu	Gly	Asp 105	Val	Leu	Phe	Gln	Met 110	Ala	Glu
Val	His	Arg 115	Gln	Ile	Gln	Asn	Gln 120	Leu	Glu	Glu	Met	Leu 125	Lys	Ser	Phe
His	Asn 130	Glu	Leu	Leu	Thr	Gln 135	Leu	Glu	Gln	Lys	Val 140	Glu	Leu	Asp	Ser
Arg 145	Tyr	Leu	Ser	Ala	Ala 150	Leu	Lys	Lys	Tyr	Gln 155	Thr	Glu	Gln	Arg	Ser 160
Lys	Gly	Asp	Ala	Leu 165	Asp	Lys	Cys	Gln	Ala 170	Glu	Leu	Lys	Lys	Leu 175	Arg
Lys	Lys	Ser	Gln 180	Gly	Ser	Lys	Asn	Pro 185	Gln	Lys	Tyr	Ser	Asp 190	Lys	Glu
Leu	Gln	Tyr 195	Ile	Asp	Ala	Ile	Ser 200	Asn	Lys	Gln	Gly	Glu 205	Leu	Glu	Asn
Tyr	Val 210	Ser	Asp	Gly	Tyr	Lys 215	Thr	Ala	Leu	Thr	Glu 220	Glu	Arg	Arg	Arg
Phe	Cys	Phe	Leu	Val	Glu	Lys	Gln	Cys	Ala	Val	Ala	Lys	Asn	Ser	Ala



225					230					235					240				
Ala	Tyr	His	Ser	Lys 245	Gly	Lys	Glu	Leu	Leu 250	Ala	Gln	Lys	Leu	Pro 255	Leu				
Trp	Gln	Gln	Ala 260	Cys	Ala	Asp	Pro	Ser 265	Lys	Ile	Pro	Glu	Arg 270	Ala	Val				
Gln	Leu	Met 275	Gln	Gln	Val	Ala	Ser 280	Asn	Gly	Ala	Thr	Leu 285	Pro	Ser	Ala				
Leu	Ser 290	Ala	Ser	Lys	Ser	Asn 295	Leu	Val	Ile	Ser	Asp 300	Pro	Ile	Pro	Gly				
Ala 305	Lys	Pro	Leu	Pro	Val 310	Pro	Pro	Glu	Leu	Ala 315	Pro	Phe	Val	Gly	Arg 320				
Met	Ser	Ala	Gln	Glu 325	Ser	Thr	Pro	Ile	Met 330	Asn	Gly	Val	Thr	Gly 335	Pro				
Asp	Gly	Glu	Asp 340	Tyr	Ser	Pro	Trp	Ala 345	Asp	Arg	Lys	Ala	Ala 350	Gln	Pro				
Lys	Ser	Leu 355	Ser	Pro	Pro	Gln	Ser 360	Gln	Ser	Lys	Leu	Ser 365	Asp	Ser	Tyr				
Ser	Asn 370	Thr	Leu	Pro	Val	Arg 375	Lys	Ser	Val	Thr	Pro 380	Lys	Asn	Ser	Tyr				
Ala 385	Thr	Thr	Glu	Asn	Lys 390	Thr	Leu	Pro	Arg	Ser 395	Ser	Ser	Met	Ala	Ala 400				
Gly	Leu	Glu	Arg	Asn 405	Gly	Arg	Met	Arg	Val 410	Lys	Ala	Ile	Phe	Ser 415	His				
Ala	Ala	Gly	Asp 420	Asn	Ser	Thr	Leu	Leu 425	Ser	Phe	Lys	Glu	Gly 430	Asp	Leu				
Ile	Thr	Leu 435	Leu	Val	Pro	Glu	Ala 440	Arg	Asp	Gly	Trp	His 445	Tyr	Gly	Glu				
Ser	Glu 450	Lys	Thr	Lys	Met	Arg 455	Gly	Trp	Phe	Pro	Phe 460	Ser	Tyr	Thr	Arg				
Val 465	Leu	Asp	Ser	Asp	Gly 470	Ser	Asp	Arg	Leu	His 475	Met	Ser	Leu	Gln	Gln 480				
Gly	Lys	Ser	Ser	Ser 485	Thr	Gly	Asn	Leu	Leu 490	Asp	Lys	Asp	Asp	Leu 495	Ala				
Ile	Pro	Pro	Pro 500	Asp	Tyr	Gly	Ala	Ala 505	Ser	Arg	Ala	Phe	Pro 510	Ala	Gln				
Thr	Ala	Ser 515	Gly	Phe	Lys	Gln	Arg 520	Pro	Tyr	Ser	Val	Ala 525	Val	Pro	Ala				
Phe	Ser 530	Gln	Gly	Leu	Asp	Asp 535	Tyr	Gly	Ala	Arg	Ser 540	Met	Ser	Ser	Ala				
Asp 545	Val	Glu	Val	Ala	Arg 550	Phe													

<211> 185  
 <212> PRT  
 <213> homo sapiens

<400> 283

Ala 1	Gly	Glu	Ala	Ala 5	Gly	Gln	Pro	Gly	Ser 10	Pro	Pro	Ser	His	Gln 15	Leu
Ala	Lys	Cys	Pro 20	Pro	Leu	Thr	Gln	Gly 25	Tyr	Pro	Arg	Leu	His 30	Gly	His
Val	Thr	Arg 35	Gly	Val	Tyr	Pro	Gln 40	Glu	Ala	Ala	Pro	Gln 45	Pro	Trp	Ala
Ala	Gln 50	Pro	Leu	Gly	Leu	Ala 55	Leu	Gln	Gly	Pro	Ala 60	Pro	His	Ser	Ala
Arg 65	Pro	Cys	Leu	Glu	Gln 70	Leu	Gly	Ser	Ser	Pro 75	Gly	Gln	Thr	Gln	Val 80
Gly	Gln	Asp	Gln	Ala 85	Ala	Gly	Ala	Trp	Met 90	Phe	Ser	Thr	Gln	Glu 95	Arg
Thr	Asp	Asp	Asp 100	Arg	Thr	Gly	Tyr	Met 105	Gly	Arg	Ala	Gly	Glu 110	Ala	Thr
Arg	Trp	Ala 115	Ala	Leu	Gln	Met	Trp 120	Pro	Ser	Ala	Glu	Glu 125	Gly	Gly	Arg
Pro	Val 130	Val	Gly	His	Cys	Arg 135	Leu	Gln	Leu	Asp	Val 140	Gly	Lys	Gly	Ile
Leu 145	Thr	Leu	Val	Arg	Arg 150	Leu	Arg	Ile	Trp	Pro 155	Leu	Pro	His	Arg	Arg 160
Cys	Ser	Trp	Thr	Ala 165	Leu	His	Ser	His	Pro 170	Gly	Pro	Gly	Arg	Arg 175	Arg
Ala	Arg	Pro	His 180	Cys	Arg	Ala	Ser	Ala 185							

<210> 284  
 <211> 518  
 <212> PRT  
 <213> homo sapiens

<400> 284

Ser 1	Gly	Gly	Ser	Glu 5	Ser	Gly	His	Phe	His 10	Ile	Gly	Ala	Ala	His 15	Gly
Pro	Arg	Ser	Ile 20	Val	Ile	Gln	Ala	Leu 25	Gly	Glu	Gly	Gly	His 30	Gly	His
Thr	Val	Gly 35	Pro	Leu	Leu	Glu	Ala 40	Ala	Gly	Arg	Leu	Gly 45	Gly	Glu	Gly
Pro	Gly 50	Gly	Gly	Ala	Val	Ile 55	Gly	Gly	Trp	Asp	Gly 60	Gln	Val	Val	Leu
Val 65	Gln	Glu	Val	Ala	Arg 70	Ala	Ala	Ala	Leu	Pro 75	Leu	Leu	Gln	Ala	His 80

Val	Gln	Pro	Val	Thr 85	Ala	Ile	Ala	Val	Gln 90	Asp	Pro	Gly	Val	Gly 95	Glu
Gly	Lys	Pro	Ala 100	Pro	His	Leu	Gly	Leu 105	Leu	Thr	Leu	Ser	Val 110	Val	Pro
Ala	Ile	Ala 115	Gly	Leu	Arg	His	Gln 120	Gln	Gly	Asn	Glu	Val 125	Thr	Leu	Leu
Glu	Ala 130	Gln	Glu	Gly	Ala	Val 135	Val	Pro	Ser	Ser	Val 140	Gly	Glu	Asp	Gly
Leu 145	His	Pro	His	Thr	Ala 150	Ile	Ala	Leu	Gln	Ala 155	Gly	Cys	His	Gly	Ala 160
Arg	Ala	Arg	Gln	Ser 165	Leu	Val	Leu	Gly	Gly 170	Gly	Ile	Ala	Val	Phe 175	Trp
Gly	His	Ala	Leu 180	Ala	His	Gly	Glu	Cys 185	Val	Gly	Val	Gly	Val 190	Ala	Glu
Leu	Ala	Leu 195	Arg	Leu	Arg	Arg	Arg 200	Gln	Gly	Phe	Gly	Leu 205	Gly	Ser	Leu
Ala	Val 210	Ser	Pro	Arg	Ala	Val 215	Val	Leu	Ala	Ile	Arg 220	Ala	Cys	Asp	Ala
Val 225	His	Asp	Gly	Cys	Ala 230	Leu	Leu	Gly	Arg	His 235	Pro	Pro	His	Glu	Arg 240
Cys	Gln	Leu	Gly	Gly 245	His	Arg	Gln	Gly	Leu 250	Gly	Pro	Arg	Asn	Gly 255	Val
Gly	Asn	Asp	Gln 260	Val	Gly	Leu	Gly	Gly 265	Arg	Gln	Gly	Ala	Gly 270	Glu	Gly
Gly	Ala	Val 275	Ala	Gly	His	Leu	Leu 280	His	Glu	Leu	His	Arg 285	Ala	Leu	Arg
Asp	Leu 290	Ala	Gly	Val	Gly	Thr 295	Gly	Leu	Leu	Pro	Gln 300	Arg	Gln	Leu	Leu
Arg 305	Gln	Gln	Leu	Leu	Ala 310	Leu	Gly	Val	Val	Gly 315	Arg	Gly	Val	Leu	Gly 320
His	Gly	Ala	Leu	Leu 325	Leu	His	Gln	Glu	Ala 330	Glu	Ala	Pro	Ala	Leu 335	Leu
Cys	Gln	Cys	Gly 340	Leu	Val	Ala	Val	Gly 345	His	Val	Ile	Leu	Gln 350	Leu	Ala
Leu	Leu	Val 355	Ala	Asp	Gly	Val	Asp 360	Val	Leu	Gln	Leu	Leu 365	Val	Arg	Val
Leu	Leu 370	Arg	Ile	Leu	Ala	Ala 375	Leu	Ala	Leu	Leu	Pro 380	Lys	Leu	Leu	Gln
Leu 385	Ser	Leu	Thr	Leu	Val 390	Gln	Gly	Val	Ala	Phe 395	Ala	Pro	Leu	Leu	Ser 400
Leu	Val	Phe	Leu	Gln 405	Arg	Ser	Thr	Gln	Ile 410	Pro	Gly	Val	Gln 415	Leu	His

Leu	Leu	Leu	Gln	Leu	Arg	Lys	Gln	Leu	Val	Val	Lys	Arg	Leu	Gln	His
			420					425					430		
Phe	Phe	Gln	Leu	Ile	Leu	Asp	Leu	Pro	Val	Asp	Phe	Ser	His	Leu	Glu
		435					440					445			
Glu	Asn	Val	Ser	Glu	Phe	Phe	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Gln	Leu
	450					455					460				
Pro	His	Leu	His	Gln	Gly	Val	Lys	Val	Ala	Phe	Gly	Cys	Ile	Arg	His
465					470					475				480	
Thr	Cys	Gln	Cys	Leu	Leu	Val	Ile	Leu	Pro	His	Gly	Asp	Glu	Val	Pro
				485					490					495	
Glu	Ala	Arg	Val	Glu	Leu	Leu	His	Asp	Gly	Leu	Ile	Asp	Ile	Phe	Arg
			500					505					510		
Glu	Pro	Val	His	Leu	Leu										
		515													

<210> 285  
 <211> 217  
 <212> PRT  
 <213> homo sapiens

<400> 285

Val	Arg	Glu	Ala	Ala	Arg	Arg	Glu	Gln	Arg	Tyr	Gln	Glu	Gln	Gly	Gly
1				5					10					15	
Glu	Ala	Ser	Pro	Gln	Arg	Thr	Trp	Glu	Gln	Gln	Gln	Glu	Val	Val	Ser
			20					25					30		
Arg	Asn	Arg	Asn	Glu	Gln	Glu	Ser	Ala	Val	His	Pro	Arg	Glu	Ile	Phe
		35					40					45			
Lys	Gln	Lys	Glu	Arg	Ala	Met	Ser	Thr	Thr	Ser	Ile	Ser	Ser	Pro	Gln
	50					55					60				
Pro	Gly	Lys	Leu	Arg	Ser	Pro	Phe	Leu	Gln	Lys	Gln	Leu	Thr	Gln	Pro
65					70					75					80
Glu	Thr	His	Phe	Gly	Arg	Glu	Pro	Ala	Ala	Ala	Ile	Ser	Arg	Pro	Arg
				85					90					95	
Ala	Asp	Leu	Pro	Ala	Glu	Glu	Pro	Ala	Pro	Ser	Thr	Pro	Pro	Cys	Leu
			100					105					110		
Val	Gln	Ala	Glu	Glu	Glu	Ala	Val	Tyr	Glu	Glu	Pro	Pro	Glu	Gln	Glu
		115					120					125			
Thr	Phe	Tyr	Glu	Gln	Pro	Pro	Leu	Val	Gln	Gln	Gln	Gly	Ala	Gly	Ser
	130					135					140				
Glu	His	Ile	Asp	His	His	Ile	Gln	Gly	Gln	Gly	Leu	Ser	Gly	Gln	Gly
145					150					155					160
Leu	Cys	Ala	Arg	Ala	Leu	Tyr	Asp	Tyr	Gln	Ala	Ala	Asp	Asp	Thr	Glu
				165					170					175	
Ile	Ser	Phe	Asp	Pro	Glu	Asn	Leu	Ile	Thr	Gly	Ile	Glu	Val	Ile	Asp

			180					185					190			
Glu	Gly	Trp	Trp	Arg	Gly	Tyr	Gly	Pro	Asp	Gly	His	Phe	Gly	Met	Phe	
		195					200					205				
Pro	Ala	Asn	Tyr	Val	Glu	Leu	Ile	Glu								
	210					215										

<210> 286  
 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 286

Ala	Gly	Ala	Ser	Gly	Arg	Leu	Trp	Leu	Pro	Ser	Ala	Phe	Ile	Cys	Leu	
1				5					10					15		
Phe	Ser	Phe	Ser	Leu	Ala	Ser	Lys	Gly	Trp	Trp	Pro	Pro	Leu	Phe	Arg	
			20					25					30			
Met	Thr	Leu	Gly	Asn	Ser	Glu	Arg	Arg	Glu	Leu	Phe	Leu	Ala	Glu	Phe	
		35					40					45				
Val	Thr	Lys	Val	Arg	Val	Asp	His	Gly	Gly	Leu	Ala	Ala	Gly	Asn	Leu	
	50					55					60					
Ser	Cys	Trp	Ser	Leu	Leu	Cys	Ala	Pro	His	Ser	Ile	Ser	Leu	Ser	Leu	
65				70						75					80	
Cys	Leu	Gly	Tyr	Gly	Lys	Trp	Gly	Cys	Arg	Trp	Pro	Ser	Ser	His	Pro	
				85					90					95		
Gly	Tyr	Ser	Lys	Thr	Ala	Asp	Thr	Thr	Cys	Ser	Ser	Thr	Arg	Leu	Thr	
			100					105					110			
Arg	Cys	Leu	Gln	Ala	Pro	Val	Cys	Ala	Ser	Thr	Asp	Ser	Asp	Phe	Arg	
		115					120					125				
Lys	Ser	Asn	Thr	Glu	Trp	Pro	Trp	Pro	Val	Val	Phe	Pro	Tyr	Phe	Leu	
	130					135					140					
Ser	Gln	Leu	Ile	Arg	Val	Ser	Glu	Glu	Gln	Ile	Cys	Phe	Trp	Thr	Lys	
145					150					155					160	
Lys	Lys															

<210> 287  
 <211> 173  
 <212> PRT  
 <213> homo sapiens

<400> 287

Leu	Leu	Ala	Cys	Arg	Gly	Trp	Pro	Gly	Arg	Arg	Trp	Trp	Glu	Glu	Leu	
1				5					10					15		
Asn	Ser	Gly	Lys	Val	Met	Tyr	Ala	Phe	Cys	Arg	Val	Lys	Asp	Pro	Asn	
			20					25					30			
Ser	Gly	Leu	Pro	Lys	Phe	Val	Leu	Ile	Asn	Trp	Thr	Gly	Glu	Gly	Val	
		35					40					45				

Asn	Asp	Val	Arg	Lys	Gly	Ala	Cys	Ala	Ser	His	Val	Ser	Thr	Met	Ala
	50					55					60				
Ser	Phe	Leu	Lys	Gly	Ala	His	Val	Thr	Ile	Asn	Ala	Arg	Ala	Glu	Glu
65				70						75					80
Asp	Val	Glu	Pro	Glu	Cys	Ile	Met	Glu	Lys	Val	Ala	Lys	Ala	Ser	Gly
				85					90					95	
Ala	Asn	Tyr	Ser	Phe	His	Lys	Glu	Ser	Gly	Arg	Phe	Gln	Asp	Val	Gly
			100					105					110		
Pro	Gln	Ala	Pro	Val	Gly	Ser	Val	Tyr	Gln	Lys	Thr	Asn	Ala	Val	Ser
		115					120					125			
Glu	Ile	Lys	Arg	Val	Gly	Lys	Asp	Ser	Phe	Trp	Ala	Lys	Ala	Glu	Lys
	130					135					140				
Glu	Glu	Glu	Asn	Arg	Arg	Leu	Glu	Glu	Lys	Arg	Arg	Ala	Glu	Glu	Ala
145					150					155					160
Gln	Arg	Gln	Trp	Ser	Arg	Ser	Ala	Gly	Ser	Val	Ser	Ala			
				165					170						

<210> 288

<211> 597

<212> PRT

<213> homo sapiens

<400> 288

Glu	Lys	Cys	Gly	Gln	Tyr	Ile	Gln	Lys	Gly	Tyr	Ser	Lys	Leu	Lys	Ile
1				5					10					15	
Tyr	Asn	Cys	Glu	Leu	Glu	Asn	Val	Ala	Glu	Phe	Glu	Gly	Leu	Thr	Asp
			20					25					30		
Phe	Ser	Asp	Thr	Phe	Lys	Leu	Tyr	Arg	Gly	Lys	Ser	Asp	Glu	Asn	Glu
		35					40					45			
Asp	Pro	Ser	Val	Val	Gly	Glu	Phe	Lys	Gly	Ser	Phe	Arg	Ile	Tyr	Pro
	50					55					60				
Leu	Pro	Asp	Asp	Pro	Ser	Val	Pro	Ala	Pro	Pro	Arg	Gln	Phe	Arg	Glu
65					70					75					80
Leu	Pro	Asp	Ser	Val	Pro	Gln	Glu	Cys	Thr	Val	Arg	Ile	Tyr	Ile	Val
				85					90					95	
Arg	Gly	Leu	Glu	Leu	Gln	Pro	Gln	Asp	Asn	Asn	Gly	Leu	Cys	Asp	Pro
			100					105					110		
Tyr	Ile	Lys	Ile	Thr	Leu	Gly	Lys	Lys	Val	Ile	Glu	Asp	Arg	Asp	His
		115					120					125			
Tyr	Ile	Pro	Asn	Thr	Leu	Asn	Pro	Val	Phe	Gly	Arg	Met	Tyr	Glu	Leu
	130					135					140				
Ser	Cys	Tyr	Leu	Pro	Gln	Glu	Lys	Asp	Leu	Lys	Ile	Ser	Val	Tyr	Asp
145					150					155					160
Tyr	Asp	Thr	Phe	Thr	Arg	Asp	Glu	Lys	Val	Gly	Glu	Thr	Ile	Ile	Asp
				165					170					175	

Leu	Glu	Asn	Arg 180	Phe	Leu	Ser	Arg	Phe 185	Gly	Ser	His	Cys	Gly 190	Ile	Pro
Glu	Glu	Tyr 195	Cys	Val	Ser	Gly	Val 200	Asn	Thr	Trp	Arg	Asp 205	Gln	Leu	Arg
Pro	Thr 210	Gln	Leu	Leu	Gln	Asn 215	Val	Ala	Arg	Phe	Lys 220	Gly	Phe	Pro	Gln
Pro 225	Ile	Leu	Ser	Glu	Asp 230	Gly	Ser	Arg	Ile	Arg 235	Tyr	Gly	Gly	Arg	Asp 240
Tyr	Ser	Leu	Asp	Glu 245	Phe	Glu	Ala	Asn	Lys 250	Ile	Leu	His	Gln	His 255	Leu
Gly	Ala	Pro	Glu 260	Glu	Arg	Leu	Ala	Leu 265	His	Ile	Leu	Arg	Thr 270	Gln	Gly
Leu	Val	Pro 275	Glu	His	Val	Glu	Thr 280	Arg	Thr	Leu	His	Ser 285	Thr	Phe	Gln
Pro	Asn 290	Ile	Ser	Gln	Gly	Lys 295	Leu	Gln	Met	Trp	Val 300	Asp	Val	Phe	Pro
Lys 305	Ser	Leu	Gly	Pro	Pro 310	Gly	Pro	Pro	Phe	Asn 315	Ile	Thr	Pro	Arg	Lys 320
Ala	Lys	Lys	Tyr	Tyr 325	Leu	Arg	Val	Ile	Ile 330	Trp	Asn	Thr	Lys	Asp 335	Val
Ile	Leu	Asp	Glu 340	Lys	Ser	Ile	Thr	Gly 345	Glu	Glu	Met	Ser	Asp 350	Ile	Tyr
Val	Lys	Gly 355	Trp	Ile	Pro	Gly	Asn 360	Glu	Glu	Asn	Lys	Gln 365	Lys	Thr	Asp
Val	His 370	Tyr	Arg	Ser	Leu	Asp 375	Gly	Glu	Gly	Asn	Phe 380	Asn	Trp	Arg	Phe
Val 385	Phe	Pro	Phe	Asp	Tyr 390	Leu	Pro	Ala	Glu	Gln 395	Leu	Cys	Ile	Val	Ala 400
Lys	Lys	Glu	His	Phe 405	Trp	Ser	Ile	Asp	Gln 410	Thr	Glu	Phe	Arg	Ile 415	Pro
Pro	Arg	Leu	Ile 420	Ile	Gln	Ile	Trp	Asp 425	Asn	Asp	Lys	Phe	Ser 430	Leu	Asp
Asp	Tyr	Leu 435	Gly	Phe	Leu	Glu	Leu 440	Asp	Leu	Arg	His	Thr 445	Ile	Ile	Pro
Ala	Lys 450	Ser	Pro	Glu	Lys	Cys 455	Arg	Leu	Asp	Met	Ile 460	Pro	Asp	Leu	Lys
Ala 465	Met	Asn	Pro	Leu	Lys 470	Ala	Lys	Thr	Ala	Ser 475	Leu	Phe	Glu	Gln	Lys 480
Ser	Met	Lys	Gly	Trp 485	Trp	Pro	Cys	Tyr	Ala 490	Glu	Lys	Asp	Gly	Ala 495	Arg
Val	Met	Ala	Gly 500	Lys	Val	Glu	Met	Thr 505	Leu	Glu	Ile	Leu	Asn 510	Glu	Lys

Glu	Ala	Asp	Glu	Arg	Pro	Ala	Gly	Lys	Gly	Arg	Asp	Glu	Pro	Asn	Met
		515					520					525			
Asn	Pro	Lys	Leu	Asp	Leu	Pro	Asn	Arg	Pro	Glu	Thr	Ser	Phe	Leu	Trp
	530					535					540				
Phe	Thr	Asn	Pro	Cys	Lys	Thr	Met	Lys	Phe	Ile	Val	Trp	Arg	Arg	Phe
545					550					555					560
Lys	Trp	Val	Ile	Ile	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Leu	Leu	Leu	Phe
				565					570					575	
Val	Ala	Val	Leu	Leu	Tyr	Ser	Leu	Pro	Asn	Tyr	Leu	Ser	Met	Lys	Ile
			580					585					590		
Val	Lys	Pro	Asn	Val											
		595													

<210> 289

<211> 120

<212> PRT

<213> homo sapiens

<400> 289

Asp	Gln	His	Ser	Cys	Phe	Lys	Met	Ser	Pro	Asp	Ser	Lys	Ala	Ser	His
1				5					10					15	
Asn	Pro	Ser	Phe	Pro	Lys	Met	Gly	Val	Glu	Ser	Asp	Met	Glu	Asp	Glu
			20					25					30		
Thr	Thr	Ala	Trp	Met	Asn	Leu	Lys	Pro	Thr	Lys	Ser	Cys	Thr	Ser	Thr
		35					40					45			
Ser	Gly	Pro	Leu	Lys	Ser	Gly	Leu	Leu	Phe	Thr	Ser	Ser	Gly	Leu	Arg
	50					55					60				
Gly	Trp	Ser	Leu	Ser	Thr	Trp	Lys	Gln	Gly	Leu	Cys	Thr	Ala	Pro	Ser
65					70					75					80
Ser	Pro	Thr	Phe	Pro	Arg	Glu	Asn	Phe	Arg	Cys	Gly	Trp	Met	Phe	Ser
				85					90					95	
Pro	Arg	Val	Trp	Gly	His	Gln	Ala	Leu	Leu	Ser	Thr	Ser	His	Pro	Gly
			100					105					110		
Lys	Pro	Arg	Asn	Thr	Thr	Cys	Val								
		115					120								

<210> 290

<211> 289

<212> PRT

<213> homo sapiens

<400> 290

Glu	Thr	Gln	Val	Val	Ile	Gln	Arg	Lys	Leu	Val	Ile	Val	Pro	Tyr	Leu
1				5					10					15	
Asn	Asp	Gln	Pro	Gly	Trp	Asp	Ser	Lys	Phe	Arg	Leu	Val	Asn	Thr	Pro
			20					25					30		



Glu	Met	Leu	Phe	Phe	Arg	Asn	Asp	Thr	Glu	Leu	Phe	Gly	Trp	Lys	Val	
		35					40					45				
Val	Lys	Arg	Glu	Asn	Lys	Ser	Pro	Val	Lys	Ile	Pro	Phe	Thr	Ile	Gln	
	50					55					60					
Arg	Ser	Val	Met	Asp	Ile	Cys	Phe	Leu	Phe	Val	Phe	Phe	Ile	Ala	Arg	
65					70					75					80	
Asn	Pro	Ala	Phe	Asp	Val	Asp	Val	Thr	His	Phe	Leu	Ser	Cys	Asp	Ala	
				85					90					95		
Phe	Leu	Val	Gln	Asp	Asn	Val	Leu	Gly	Val	Pro	Asp	Asp	His	Thr	Gln	
			100					105					110			
Val	Val	Phe	Leu	Gly	Phe	Pro	Gly	Cys	Asp	Val	Glu	Arg	Arg	Ala	Trp	
		115					120					125				
Trp	Pro	Gln	Thr	Leu	Gly	Glu	Asn	Ile	His	Pro	His	Leu	Lys	Phe	Ser	
	130					135					140					
Leu	Gly	Asn	Val	Gly	Leu	Glu	Gly	Ala	Val	Gln	Ser	Pro	Cys	Phe	His	
145					150					155					160	
Val	Leu	Arg	Asp	Gln	Pro	Leu	Ser	Pro	Glu	Asp	Val	Lys	Ser	Lys	Pro	
				165					170					175		
Leu	Phe	Arg	Gly	Pro	Glu	Val	Leu	Val	Gln	Asp	Phe	Val	Gly	Phe	Lys	
			180					185					190			
Phe	Ile	Gln	Ala	Val	Val	Ser	Ser	Ser	Ile	Ser	Asp	Ser	Thr	Pro	Ile	
		195					200					205				
Phe	Gly	Lys	Asp	Gly	Leu	Trp	Glu	Ala	Phe	Glu	Ser	Gly	Asp	Ile	Leu	
	210					215					220					
Lys	Gln	Leu	Cys	Trp	Ser	Gln	Leu	Ile	Ser	Pro	Gly	Ile	Asp	Ser	Arg	
225					230					235					240	
Asn	Thr	Val	Leu	Leu	Trp	Tyr	Ala	Ala	Val	Gly	Pro	Lys	Ala	Gly	Lys	
				245					250					255		
Glu	Ser	Val	Phe	Gln	Ile	Asn	Asn	Cys	Phe	Ser	Tyr	Phe	Phe	Ile	Pro	
			260					265					270			
Gly	Lys	Gly	Val	Ile	Ile	Ile	Asp	Arg	Asn	Phe	Gln	Val	Phe	Phe	Leu	
		275					280					285				

Arg

<210> 291

<211> 201

<212> PRT

<213> homo sapiens

<400> 291

Gly	Thr	Gly	Asp	Gly	Ser	Lys	Glu	Ile	Asn	Ile	Val	Trp	Gly	Ile	Gln	
1				5					10					15		
Val	Pro	Ile	Phe	His	Asn	Gly	Pro	Trp	Val	Ser	Thr	Asn	His	Pro	Val	
			20					25					30			

Ala	Arg	Phe 35	Pro	Arg	Ile	Thr	Ser 40	Leu	Ala	Ser	Glu	Gly 45	Ile	Ile	Val
Pro	Ser 50	Thr	Ser	Thr	Ile	Arg 55	Gly	Met	Gly	Val	Trp 60	Arg	Ala	Ser	Cys
Gly 65	Asp	Cys	Arg	Ala	Asp 70	Ser	Thr	Ser	Ser	Ile 75	Ala	Gln	Asp	Arg	Gly 80
Pro	Gly	Leu	Thr	Ile 85	Gly	His	Gln	Ala	Leu 90	Gly	Ser	Leu	Val	Trp 95	Val
Gly	Glu	Ser	Trp 100	Gly	Gln	Thr	Trp	Gly 105	Glu	Tyr	Leu	Gly	Gly 110	Pro	Arg
Trp	Leu	Gly 115	Trp	Leu	Asp	Leu	Arg 120	Gln	Ser	Trp	Ala	Leu 125	Ser	Ile	Ser
Glu	Glu 130	Val	Val	Lys	Lys	Arg 135	Asp	Phe	Leu	Phe	His 140	Phe	Leu	Asn	Phe
Leu 145	Cys	Met	Leu	Val	Glu 150	Asp	Met	Phe	Ala	His 155	Lys	Leu	Arg	Thr	Leu 160
Glu	Phe	Leu	Ala	Thr 165	Glu	Arg	Thr	Gln	Pro 170	Leu	Ile	Leu	Ala	Gln 175	Phe
Leu	Arg	Val	Gly 180	Gly	Asp	Glu	Leu	Leu 185	His	Phe	Leu	Leu	Trp 190	Val	Phe
Ala	Pro	His 195	Leu	Leu	Gly	Leu	Phe 200	Leu							

<210> 292

<211> 171

<212> PRT

<213> homo sapiens

<400> 292

Ser 1	Val	Ile	Phe	Phe 5	Lys	Ile	Gly	Phe	Cys 10	Glu	Gly	Arg	Leu	Val 15	Gly
Arg	Gly	Gly	Val 20	Pro	Gly	Ser	Glu	Ala 25	Gln	Ser	Cys	Val	Leu 30	Ser	Ser
Ser	Val	Trp 35	Ile	Ser	Leu	Ala	Ala 40	Ser	Leu	Met	Ser	Leu 45	Arg	Thr	Ile
Cys 50	Leu	Cys	Trp	Val	Met	Pro 55	Leu	Met	Leu	Arg	Thr 60	Arg	Arg	Val	Arg
Ser 65	Leu	Phe	Thr	Pro	Gly 70	Leu	Ser	Ser	His	Ser 75	Arg	Arg	Arg	Met	Phe 80
Cys	Arg	Phe	Gln	Gln 85	Ile	Ser	Leu	Met	Leu 90	Thr	Leu	Arg	Ser	Lys 95	Val
Thr	Gln	Pro	Arg 100	Arg	Lys	Asn	Leu	Leu 105	Ser	Gly	Trp	Gly	Ser 110	Glu	Ser
Ala	Thr	Arg 115	Ile	Lys	Pro	Gly	Tyr 120	Leu	Leu	Gln	Arg	Glu 125	Met	Ile	Ser

Ala	Arg	Glu	Met	Leu	Gly	Ala	Met	Leu	Arg	Met	Lys	Arg	Glu	Gln	Val
	130					135					140				
Leu	Cys	Ser	Gly	Arg	Gly	Leu	His	Ser	Ser	Pro	Ala	Ala	Ser	Leu	Gly
145					150					155					160
Phe	Ser	His	Ser	Ser	Ser	Leu	Gly	Phe	Ser	Phe					
				165					170						

<210> 293

<211> 485

<212> PRT

<213> homo sapiens

<400> 293

Glu	Lys	Glu	Lys	Pro	Lys	Glu	Glu	Glu	Trp	Glu	Lys	Pro	Lys	Asp	Ala
1				5					10					15	
Ala	Gly	Leu	Glu	Cys	Lys	Pro	Arg	Pro	Leu	His	Lys	Thr	Cys	Ser	Leu
			20					25					30		
Phe	Met	Arg	Asn	Ile	Ala	Pro	Asn	Ile	Ser	Arg	Ala	Glu	Ile	Ile	Ser
		35					40					45			
Leu	Cys	Lys	Arg	Tyr	Pro	Gly	Phe	Met	Arg	Val	Ala	Leu	Ser	Glu	Pro
	50					55					60				
Gln	Pro	Glu	Arg	Arg	Phe	Phe	Arg	Arg	Gly	Trp	Val	Thr	Phe	Asp	Arg
65					70					75					80
Ser	Val	Asn	Ile	Lys	Glu	Ile	Cys	Trp	Asn	Leu	Gln	Asn	Ile	Arg	Leu
				85					90					95	
Arg	Glu	Cys	Glu	Leu	Ser	Pro	Gly	Val	Asn	Arg	Asp	Leu	Thr	Arg	Arg
			100					105					110		
Val	Arg	Asn	Ile	Asn	Gly	Ile	Thr	Gln	His	Lys	Gln	Ile	Val	Arg	Asn
		115					120					125			
Asp	Ile	Lys	Leu	Ala	Ala	Lys	Leu	Ile	His	Thr	Leu	Asp	Asp	Arg	Thr
	130					135					140				
Gln	Leu	Trp	Ala	Ser	Glu	Pro	Gly	Thr	Pro	Pro	Leu	Pro	Thr	Ser	Leu
145					150					155					160
Pro	Ser	Gln	Asn	Pro	Ile	Leu	Lys	Asn	Ile	Thr	Asp	Tyr	Leu	Ile	Glu
				165					170					175	
Glu	Val	Ser	Ala	Glu	Glu	Glu	Glu	Leu	Leu	Gly	Ser	Ser	Gly	Gly	Ala
			180					185					190		
Pro	Pro	Glu	Glu	Pro	Pro	Lys	Glu	Gly	Asn	Pro	Ala	Glu	Ile	Asn	Val
		195					200					205			
Glu	Arg	Asp	Glu	Lys	Leu	Ile	Lys	Val	Leu	Asp	Lys	Leu	Leu	Leu	Tyr
	210					215					220				
Leu	Arg	Ile	Val	His	Ser	Leu	Asp	Tyr	Tyr	Asn	Thr	Cys	Glu	Tyr	Pro
225					230					235					240
Asn	Glu	Asp	Glu	Met	Pro	Asn	Arg	Cys	Gly	Ile	Ile	His	Val	Arg	Gly

				245					250					255		
Pro	Met	Pro	Pro	Asn	Arg	Ile	Ser	His	Gly	Glu	Val	Leu	Glu	Trp	Gln	
			260					265					270			
Lys	Thr	Phe	Glu	Glu	Lys	Leu	Thr	Pro	Leu	Leu	Ser	Val	Arg	Glu	Ser	
		275					280					285				
Leu	Ser	Glu	Glu	Glu	Ala	Gln	Lys	Met	Gly	Arg	Lys	Asp	Pro	Glu	Gln	
	290					295					300					
Glu	Val	Glu	Lys	Phe	Val	Thr	Ser	Asn	Thr	Gln	Glu	Leu	Gly	Lys	Asp	
305					310					315					320	
Lys	Trp	Leu	Cys	Pro	Leu	Ser	Gly	Lys	Lys	Phe	Lys	Gly	Pro	Glu	Phe	
				325				330					335			
Val	Arg	Lys	His	Ile	Phe	Asn	Lys	His	Ala	Glu	Lys	Ile	Glu	Glu	Val	
			340					345					350			
Lys	Lys	Glu	Val	Ala	Phe	Phe	Asn	Asn	Phe	Leu	Thr	Asp	Ala	Lys	Arg	
		355					360					365				
Pro	Ala	Leu	Pro	Glu	Ile	Lys	Pro	Ala	Gln	Pro	Pro	Gly	Pro	Ala	Gln	
	370					375					380					
Ile	Leu	Pro	Pro	Gly	Leu	Thr	Pro	Gly	Leu	Pro	Tyr	Pro	His	Gln	Thr	
385					390					395					400	
Pro	Gln	Gly	Leu	Met	Pro	Tyr	Gly	Gln	Pro	Arg	Pro	Pro	Ile	Leu	Gly	
				405				410					415			
Tyr	Gly	Ala	Gly	Ala	Val	Arg	Pro	Ala	Val	Pro	Thr	Gly	Gly	Pro	Pro	
			420					425					430			
Tyr	Pro	His	Ala	Pro	Tyr	Gly	Ala	Gly	Arg	Gly	Asn	Tyr	Asp	Ala	Phe	
		435					440					445				
Arg	Gly	Gln	Gly	Gly	Tyr	Pro	Gly	Lys	Pro	Arg	Asn	Arg	Met	Val	Arg	
	450					455					460					
Gly	Asp	Pro	Arg	Ala	Ile	Val	Glu	Tyr	Arg	Asp	Leu	Asp	Ala	Pro	Asp	
465					470					475					480	
Asp	Val	Asp	Phe	Phe												
				485												

<210> 294  
 <211> 368  
 <212> PRT  
 <213> homo sapiens

<400> 194

Glu	Ser	Ser	Gly	Phe	Gln	Ala	Ile	Gly	Arg	Ala	Glu	Asp	Asp	Ala	Arg
1				5					10					15	
Ser	Cys	Trp	Val	Lys	Thr	Ser	Glu	Ser	Thr	Arg	Pro	Tyr	Gln	Leu	Leu
			20					25					30		
Arg	Arg	Arg	Arg	Pro	Thr	Leu	Ile	Thr	Tyr	Arg	Ile	Phe	Arg	His	Arg
		35					40					45			

Arg	His 50	Lys	Asp	Thr	Ser	Ser 55	Gly	Asp	His	Leu	Thr 60	Cys	Arg	Leu	Asp
Pro 65	Gln	Ala	Lys	Asp	Leu 70	Lys	Asp	Gly	Thr	Gln 75	Glu	Glu	Ala	Thr	Lys 80
Arg	Gln	Glu	Ala	Pro 85	Val	Asp	Pro	Arg	Pro 90	Glu	Gly	Asp	Pro	Gln 95	Arg
Thr	Val	Ile	Ser 100	Trp	Arg	Gly	Ala	Val 105	Ile	Glu	Pro	Glu	Gln 110	Gly	Thr
Glu	Leu	Pro 115	Ser	Arg	Arg	Ala	Glu 120	Val	Pro	Thr	Lys	Pro 125	Pro	Leu	Pro
Pro	Ala 130	Arg	Thr	Gln	Gly	Thr 135	Pro	Val	His	Leu	Asn 140	Tyr	Arg	Gln	Lys
Gly 145	Val	Ile	Asp	Val	Phe 150	Leu	His	Ala	Trp	Lys 155	Gly	Tyr	Arg	Lys	Phe 160
Ala	Trp	Gly	His	Asp 165	Glu	Leu	Lys	Pro	Val 170	Ser	Arg	Ser	Phe	Ser 175	Glu
Trp	Phe	Gly	Leu 180	Gly	Leu	Thr	Leu	Ile 185	Asp	Ala	Leu	Asp	Thr 190	Met	Trp
Ile	Leu	Gly 195	Leu	Arg	Lys	Glu	Phe 200	Glu	Glu	Ala	Arg	Lys 205	Trp	Val	Ser
Lys	Lys 210	Leu	His	Phe	Glu	Lys 215	Asp	Val	Asp	Val	Asn 220	Leu	Phe	Glu	Ser
Thr 225	Ile	Arg	Ile	Leu	Gly 230	Gly	Leu	Leu	Ser	Ala 235	Tyr	His	Leu	Ser	Gly 240
Asp	Ser	Leu	Phe	Leu 245	Arg	Lys	Ala	Glu	Asp 250	Phe	Gly	Asn	Arg	Leu 255	Met
Pro	Ala	Phe	Arg 260	Thr	Pro	Ser	Lys	Ile 265	Pro	Tyr	Ser	Asp	Val 270	Asn	Ile
Gly	Thr	Gly 275	Val	Ala	His	Pro	Pro 280	Arg	Trp	Thr	Ser	Asp 285	Ser	Thr	Val
Ala	Glu 290	Val	Thr	Ser	Ile	Gln 295	Leu	Glu	Phe	Arg	Glu 300	Leu	Ser	Arg	Leu
Thr 305	Gly	Asp	Lys	Lys	Phe 310	Gln	Glu	Ala	Val	Glu 315	Lys	Val	Thr	Gln	His 320
Ile	His	Gly	Leu	Ser 325	Gly	Lys	Lys	Asp	Gly 330	Leu	Val	Pro	Met	Phe 335	Ile
Asn	Thr	His	Ser 340	Gly	Pro	Val	Ser	Pro 345	Thr	Trp	Gly	Val	Phe 350	His	Gly
Gly	Ala	Pro 355	Gly	Ala	Asp	Ser	Leu 360	Leu	Leu	Ser	Tyr	Leu 365	Phe	Glu	Arg

<210> 295

<211> 94

<212> PRT

<213> homo sapiens

<400> 295

Ala	Leu	Arg	Ser	Pro	Pro	Arg	Met	Arg	Ile	Val	Leu	Ser	Asn	Arg	Leu	
1				5					10					15		
Thr	Ser	Thr	Ser	Phe	Ser	Lys	Cys	Asn	Phe	Phe	Asp	Thr	His	Phe	Leu	
			20					25					30			
Ala	Ser	Ser	Asn	Ser	Phe	Leu	Arg	Pro	Lys	Ile	His	Met	Val	Ser	Ser	
		35					40					45				
Ala	Ser	Ile	Ser	Val	Arg	Pro	Arg	Pro	Asn	His	Ser	Leu	Lys	Asp	Leu	
	50					55					60					
Asp	Thr	Gly	Phe	Ser	Ser	Ser	Trp	Pro	His	Ala	Asn	Leu	Arg	Tyr	Pro	
65					70					75					80	
Phe	His	Ala	Cys	Arg	Lys	Thr	Ser	Ile	Thr	Pro	Phe	Trp	Arg			
				85					90							

<210> 296

<211> 94

<212> PRT

<213> homo sapiens

<400> 296

Leu	Leu	Arg	His	Pro	Leu	Pro	Gly	Phe	Leu	Lys	Phe	Phe	Pro	Gln	Thr	
1				5					10					15		
Gln	Asp	Pro	His	Gly	Val	Gln	Arg	Val	Asp	Gln	Cys	Glu	Thr	Glu	Ala	
			20					25					30			
Lys	Pro	Leu	Thr	Glu	Gly	Pro	Gly	His	Arg	Leu	Gln	Leu	Val	Met	Ala	
		35					40					45				
Pro	Cys	Lys	Leu	Ala	Val	Ser	Phe	Pro	Cys	Met	Gln	Glu	Asp	Val	Asn	
	50					55					60					
His	Ala	Leu	Leu	Ala	Ile	Val	Gln	Met	His	Trp	Cys	Ala	Leu	Cys	Pro	
65					70					75					80	
Gly	Arg	Trp	Gln	Gly	Arg	Leu	Gly	Gly	His	Phe	Cys	Ser	Ser			
				85					90							

<210> 297

<211> 146

<212> PRT

<213> homo sapiens

<400> 297

Ser	Gly	Pro	Leu	Leu	Ala	Gly	Pro	Ala	Thr	Leu	Thr	Gly	Arg	Met	Ser	
1				5					10					15		
Glu	Val	Arg	Leu	Pro	Pro	Leu	Arg	Ala	Leu	Asp	Asp	Phe	Val	Leu	Gly	
			20					25					30			
Ser	Ala	Arg	Leu	Ala	Ala	Pro	Asp	Pro	Cys	Asp	Pro	Gln	Arg	Trp	Cys	
		35					40					45				

His	Arg	Val	Ile	Asn	Asn	Leu	Leu	Tyr	Tyr	Gln	Thr	Asn	Tyr	Leu	Leu
	50					55					60				
Cys	Phe	Gly	Ile	Gly	Leu	Ala	Leu	Ala	Gly	Tyr	Val	Arg	Pro	Leu	His
65					70					75					80
Thr	Leu	Leu	Ser	Ala	Leu	Val	Val	Ala	Val	Ala	Leu	Gly	Val	Leu	Val
				85					90					95	
Trp	Ala	Ala	Glu	Thr	Arg	Ala	Leu	Cys	Ala	Ala	Ala	Ala	Ala	Ala	Thr
			100					105					110		
Leu	Gln	Pro	Ala	Trp	Pro	Gln	Cys	Leu	Pro	Ser	Ala	Ser	Trp	Cys	Ser
		115					120					125			
Gly	Ser	Arg	Ala	Ala	Leu	Ala	Pro	Ser	Cys	Ser	Ala	Ser	Pro	Gly	Arg
	130					135					140				
Cys	Phe														
145															

<210> 298

<211> 152

<212> PRT

<213> homo sapiens

<400> 298

Thr	Gln	Arg	His	Ser	His	Pro	Pro	Phe	Ser	Met	Leu	Ile	Pro	Lys	Leu
1				5					10					15	
Gly	Pro	Gly	Ala	Arg	His	Ser	Gln	Ile	Leu	Asn	Pro	Gly	Pro	Lys	Leu
			20					25					30		
Phe	Gln	Thr	Pro	Pro	Tyr	Leu	Pro	Thr	Gln	Val	Lys	Thr	Leu	Pro	Asn
		35					40					45			
Leu	Glu	Leu	Arg	Thr	Gln	Val	Phe	His	Ala	Pro	Val	Trp	Met	Glu	Ser
	50					55					60				
Gly	Ile	Leu	Thr	Val	Gly	Pro	Leu	Val	Gln	Val	Ile	Pro	Thr	Leu	Thr
65					70					75					80
Ser	Pro	Ile	Cys	Leu	Pro	Pro	Ala	Leu	Leu	Arg	His	Phe	Ala	Pro	His
				85					90					95	
Pro	Asn	Val	Pro	His	His	Arg	Gln	Pro	Arg	Gly	Glu	Val	Gly	Thr	Gly
			100					105					110		
Leu	Ser	Arg	Glu	Trp	Gly	Val	Tyr	Val	Ser	Val	Ala	Ala	Thr	Ile	Lys
		115					120					125			
Pro	Val	Ala	Ser	Leu	Met	Pro	Lys	Lys	Lys	Lys	Lys	Ser	Thr	Gly	Arg
	130					135					140				
Lys	Tyr	Ser	Ser	Ser	Ser	Arg	Pro								
145					150										

<210> 299

<211> 172

<212> PRT

<213> homo sapiens

<400> 299

Arg 1	Thr	Thr	Thr	Thr 5	Thr	Ile	Phe	Ala	Ala 10	Gly	Arg	Leu	Phe	Phe 15	Phe
Phe	Trp	His	Glu 20	Arg	Cys	Asn	Arg	Leu 25	Tyr	Cys	Cys	Ser	Asn 30	Thr	Asn
Ile	Tyr	Ala 35	Pro	Phe	Pro	Ala	Glu 40	Ala	Cys	Pro	His	Leu 45	Thr	Pro	Trp
Leu	Ser 50	Met	Val	Trp	Asn	Ile 55	Gly	Val	Arg	Gly	Lys 60	Met	Pro	Lys	Gln
Ser 65	Trp	Arg	Glu	Ala	Asn 70	Gly	Thr	Gly	Glu	Gly 75	Arg	Asp	His	Leu	Asp 80
Gln	Gly	Ser	Asn	Ser 85	Gln	Asp	Thr	Arg	Leu 90	His	Pro	His	Arg	Gly 95	Met
Glu	His	Leu	Gly 100	Ser	Glu	Phe	Lys	Ile 105	Trp	Gln	Cys	Leu	Asp 110	Leu	Gly
Trp	Lys	Val 115	Gly	Trp	Gly	Leu	Glu 120	Lys	Leu	Trp	Ser	Arg 125	Val	Gln	Asp
Leu	Arg 130	Val	Pro	Cys	Ser	Arg 135	Pro	Gln	Phe	Gly	Asp 140	Glu	His	Gly	Glu
Gly 145	Trp	Met	Gly	Val	Ser 150	Leu	Gly	Ser	Gln	Phe 155	Glu	Ile	Gly	His	Gly 160
Cys	Ser	Gly	Leu	Lys 165	Pro	Gln	Phe	Trp	Gly 170	Trp	Met				

<210> 300

<211> 178

<212> PRT

<213> homo sapiens

<400> 300

Trp 1	Phe	Trp	Arg	Glu 5	Ser	Tyr	Trp	Gln	Thr 10	Ile	Lys	Val	Asp	Leu 15	Gln
Val	Glu	His	Pro 20	Tyr	Gln	Phe	Leu	Leu 25	Lys	Tyr	Ala	Lys	Gln 30	Leu	Lys
Gly	Asp	Lys 35	Asn	Lys	Ile	Gln	Lys 40	Leu	Val	Gln	Met	Ala 45	Trp	Thr	Phe
Val	Asn 50	Asp	Ser	Leu	Cys	Thr 55	Thr	Leu	Ser	Leu	Gln 60	Trp	Glu	Pro	Glu
Ile 65	Ile	Ala	Val	Ala	Val 70	Met	Tyr	Leu	Ala	Gly 75	Arg	Leu	Cys	Lys	Phe 80
Glu	Ile	Gln	Glu	Trp 85	Thr	Ser	Lys	Pro	Met 90	Tyr	Arg	Arg	Trp	Trp 95	Glu
Gln	Phe	Val	Gln 100	Asp	Val	Pro	Val	Asp 105	Val	Leu	Glu	Asp	Ile 110	Cys	His



Gln	Ile	Leu	Asp	Leu	Tyr	Ser	Gln	Gly	Lys	Gln	Gln	Met	Pro	His	His
		115					120					125			
Thr	Pro	His	Gln	Leu	Gln	Gln	Pro	Pro	Ser	Pro	Glu	Pro	Pro	Thr	Pro
	130					135					140				
Leu	Pro	Gly	Pro	Cys	Gly	Cys	Trp	Ala	Ser	His	Leu	Lys	Glu	Gly	Lys
145					150					155					160
Val	Val	Gln	Pro	Glu	Pro	Val	Glu	Gln	Cys	Pro	Val	Trp	Pro	Pro	Lys
				165					170					175	
Pro	Lys														

<210> 301  
 <211> 113  
 <212> PRT  
 <213> homo sapiens  
 <400> 301

Cys	Ile	Ser	Gln	Asp	Val	Cys	Ala	Asn	Leu	Lys	Tyr	Lys	Asn	Gly	Pro
1				5					10					15	
Pro	Asn	Pro	Cys	Ile	Gly	Asp	Gly	Gly	Ser	Ser	Leu	Phe	Lys	Met	Ser
			20					25					30		
Arg	Ser	Thr	Phe	Trp	Lys	Thr	Ser	Ala	Thr	Lys	Ser	Trp	Ile	Phe	Thr
		35					40					45			
His	Lys	Glu	Asn	Asn	Arg	Cys	Leu	Ile	Thr	Pro	Pro	Ile	Ser	Cys	Asn
	50					55					60				
Ser	Pro	His	Leu	Leu	Ser	Leu	Pro	Pro	Arg	Cys	Leu	Gly	Pro	Val	Val
65					70					75					80
Ala	Gly	Pro	Pro	Thr	Ser	Arg	Arg	Gly	Arg	Leu	Tyr	Ser	Pro	Asn	Pro
				85					90					95	
Trp	Ser	Asn	Ala	Leu	Ser	Gly	Leu	Gln	Asn	Gln	Asn	Lys	Thr	Gly	Ser
			100					105					110		
Leu															

<210> 302  
 <211> 90  
 <212> PRT  
 <213> homo sapiens

<400> 302

Gly	Gly	Arg	Pro	Ser	Asn	His	Arg	Ala	Gln	Ala	Ala	Gly	Trp	Glu	Ala
1				5					10					15	
Gln	Glu	Met	Gly	Ala	Val	Ala	Ala	Asp	Gly	Gly	Cys	Asp	Glu	Ala	Ser
			20					25					30		
Val	Val	Phe	Leu	Val	Ser	Lys	Asp	Pro	Gly	Phe	Gly	Gly	Arg	Cys	Leu
		35					40					45			
Pro	Lys	Arg	Arg	Pro	Gly	His	Leu	Glu	Gln	Thr	Ala	Pro	Thr	Ile	Ser
	50					55					60				

Tyr 65	Thr	Trp	Val	Trp	Arg 70	Ser	Ile	Leu	Val	Phe 75	Gln	Ile	Cys	Thr	Asn 80
Val	Leu	Arg	Asp	Thr 85	Ser	Leu	Leu	Leu	Leu 90						

<210> 303  
 <211> 158  
 <212> PRT  
 <213> homo sapiens

<400> 303

Thr 1	Gln	Val	Met	Val 5	Gln	Ser	Met	Phe	Ala 10	Pro	Thr	Asp	Thr	Ser 15	Asp
Met	Glu	Ala	Val 20	Trp	Lys	Glu	Ala	Lys 25	Pro	Glu	Asp	Leu	Met 30	Asp	Ser
Lys	Leu	Arg 35	Cys	Val	Phe	Glu	Leu 40	Pro	Ala	Glu	Asn	Asp 45	Lys	Pro	His
Asp	Val 50	Glu	Ile	Asn	Lys	Ile 55	Ile	Ser	Thr	Thr	Ala 60	Ser	Lys	Thr	Glu
Thr 65	Pro	Ile	Val	Ser	Lys 70	Ser	Leu	Ser	Ser	Ser 75	Leu	Asp	Asp	Thr	Glu 80
Val	Lys	Lys	Val	Met 85	Glu	Glu	Cys	Lys	Arg 90	Leu	Gln	Gly	Glu	Val 95	Gln
Arg	Leu	Arg	Glu 100	Glu	Asn	Lys	Gln	Phe 105	Lys	Glu	Glu	Asp	Gly 110	Leu	Arg
Met	Arg	Lys 115	Thr	Val	Gln	Ser	Asn 120	Ser	Pro	Ile	Ser	Ala 125	Leu	Ala	Pro
Thr	Gly 130	Lys	Glu	Glu	Gly	Leu 135	Ser	Thr	Arg	Leu	Leu 140	Ala	Leu	Val	Val
Leu 145	Phe	Phe	Ile	Val	Gly 150	Val	Ile	Ile	Gly	Lys 155	Ile	Ala	Leu		

<210> 304  
 <211> 112  
 <212> PRT  
 <213> homo sapiens

<400> 304

Val 1	Asn	Lys	Ala	Leu 5	Pro	Phe	Ile	Ser	Lys 10	Ala	Leu	Gly	Gln	Ser 15	Val
Asn	Thr	Arg	Leu 20	Ser	Leu	Met	Thr	Ser 25	Thr	Ser	Asp	Ala	Ala 30	Thr	Val
Gln	Phe	Leu 35	Trp	Ala	Ser	Asp	Ser 40	Val	His	Gln	Ser	Gln 45	Gly	Ala	Asp
Gly	Leu 50	Asp	Arg	Thr	Glu	Asp 55	Thr	Glu	Ser	Ser	Leu 60	Gly	Arg	Glu	Trp

Ala 65	Thr	Trp	Gly	Leu	Leu 70	Cys	Gly	Ala	Asp	Arg 75	Thr	Pro	Gln	His	Ala 80
Gly	Leu	Gln	Leu	Pro 85	Lys	Gly	Gln	His	Gln 90	Gln	Ala	Arg	Lys	Gly 95	Val
Ile	Leu	Arg	Glu 100	Val	Ile	Gln	His	His 105	Val	Pro	Arg	Pro	Thr 110	Asn	Val

<210> 305

<211> 105

<212> PRT

<213> homo sapiens

<400> 305

Phe 1	Lys	Gly	Lys	Thr 5	Cys	Glu	Met	Ser	Ser 10	Tyr	Ile	Asn	Phe	Phe 15	Leu
His	Met	Val	Met 20	Ile	Asn	Leu	Asn	Pro 25	Met	Ile	Trp	Trp	Ile 30	His	Gln
Ser	Asn	Leu 35	Pro	Ser	Cys	Ala	Cys 40	Tyr	Leu	Tyr	Lys	Ala 45	Ile	Phe	Pro
Ile	Ile 50	Thr	Pro	Thr	Ile	Lys 55	Asn	Lys	Thr	Thr	Arg 60	Ala	Lys	Ser	Arg
Val 65	Leu	Arg	Pro	Ser	Ser 70	Phe	Pro	Val	Gly	Ala 75	Asn	Ala	Glu	Met	Gly 80
Leu	Leu	Leu	Cys	Thr 85	Val	Phe	Leu	Ile	Arg 90	Ser	Pro	Ser	Ser	Ser 95	Leu
Asn	Cys	Leu	Phe 100	Ser	Ser	Arg	Ser	Leu 105							

<210> 306

<211> 126

<212> PRT

<213> homo sapiens

<400> 306

Arg 1	Pro	Pro	Gln	Arg 5	Thr	Leu	Arg	His	Ser 10	Ala	Gln	Leu	Gly	Ala 15	Ala
Pro	Ala	Ala	Leu 20	Pro	Gln	Pro	Leu	Trp 25	Glu	Leu	Pro	Arg	Ala 30	His	Gly
Ser	Gln	Arg 35	Gln	Pro	Gly	Pro	Gly 40	Glu	Ala	Ala	Asp	His 45	Ala	Glu	Gln
Glu	Arg 50	Glu	Glu	Ala	Ala	Glu 55	Arg	Pro	Gly	Ser	Ser 60	Pro	Glu	Glu	Gly
Gln 65	Glu	Gly	Ser	Gly	Ala 70	Phe	Gly	Gly	His	Thr 75	Gly	His	Arg	Ala	Cys 80
Ala	Arg	Cys	Leu	Gly 85	Arg	Gly	Ala	Leu	Gly 90	Gly	Arg	Ile	Pro	Cys 95	Gly
Leu	Leu	Cys	Gln	Leu	Phe	Arg	Arg	Asp	Gly	Cys	Pro	Ala	Asp	Ser	Glu

	100							105				110				
	Val	Gln	His	His	Ile	His	Gln	His	Trp	Gln	Gln	Leu	Leu	Pro		
			115					120					125			
<210>	307															
<211>	240															
<212>	PRT															
<213>	homo sapiens															
<400>	307															
	Asn	Val	Gly	Arg	Cys	Cys	Glu	Ala	Gln	Ala	Arg	Ala	Gly	Ala	Ala	Ser
	1				5					10					15	
	Leu	Asn	Ala	Ser	Leu	Asp	Gly	Leu	His	Asn	Ala	Leu	Phe	Ala	Thr	Gln
				20					25					30		
	Arg	Ser	Leu	Glu	Gln	His	Gln	Arg	Leu	Phe	His	Ser	Leu	Phe	Gly	Asn
			35					40					45			
	Phe	Gln	Gly	Leu	Met	Glu	Ala	Asn	Val	Ser	Leu	Asp	Leu	Gly	Lys	Leu
		50					55					60				
	Gln	Thr	Met	Leu	Ser	Arg	Lys	Gly	Lys	Lys	Gln	Gln	Lys	Asp	Leu	Glu
	65					70					75					80
	Ala	Pro	Arg	Lys	Arg	Asp	Lys	Lys	Glu	Ala	Glu	Pro	Leu	Val	Asp	Ile
					85					90					95	
	Arg	Val	Thr	Gly	Pro	Val	Pro	Gly	Ala	Leu	Gly	Ala	Ala	Leu	Trp	Glu
				100					105					110		
	Ala	Gly	Ser	Pro	Val	Ala	Phe	Tyr	Ala	Ser	Phe	Ser	Glu	Gly	Thr	Ala
			115					120					125			
	Ala	Leu	Gln	Thr	Val	Lys	Phe	Asn	Thr	Thr	Tyr	Ile	Asn	Ile	Gly	Ser
		130					135					140				
	Ser	Tyr	Phe	Pro	Glu	His	Gly	Tyr	Phe	Arg	Ala	Pro	Glu	Arg	Gly	Val
	145					150					155					160
	Tyr	Leu	Phe	Ala	Val	Ser	Val	Glu	Phe	Gly	Pro	Gly	Pro	Gly	Thr	Gly
					165					170					175	
	Gln	Leu	Val	Phe	Gly	Gly	His	His	Arg	Thr	Pro	Val	Cys	Thr	Thr	Gly
				180					185					190		
	Gln	Gly	Ser	Gly	Ser	Thr	Ala	Thr	Val	Phe	Ala	Met	Ala	Glu	Leu	Gln
			195					200					205			
	Lys	Gly	Glu	Arg	Val	Trp	Phe	Glu	Leu	Thr	Gln	Gly	Ser	Ile	Thr	Lys
		210					215					220				
	Arg	Ser	Leu	Ser	Gly	Thr	Ala	Phe	Gly	Gly	Phe	Leu	Met	Phe	Lys	Thr
	225					230					235					240

<210> 308  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 308

Lys 1	Ala	Gly	Ile	Glu 5	Gly	His	Arg	Gly	Ser 10	Cys	Leu	Pro	Glu	Arg 15	Arg
Ala	Gln	Gly	Thr 20	Trp	His	Arg	Pro	Cys 25	Asp	Pro	Tyr	Val	His 30	Gln	Arg
Leu	Arg	Phe 35	Leu	Leu	Val	Pro	Leu 40	Pro	Gly	Ser	Phe	Gln 45	Val	Phe	Leu
Leu	Leu 50	Leu	Pro	Phe	Pro	Ala 55	Gln	His	Gly	Leu	Gln 60	Leu	Pro	Gln	Val
Gln 65	Ala	Asp	Val	Gly	Phe 70	His	Glu	Pro	Leu	Glu 75	Val	Pro	Lys	Glu	Ala 80
Val	Glu	Glu	Pro	Leu 85	Val	Leu	Leu	Gln	Ala 90	Ala	Leu	Ser	Gly	Glu 95	Glu
Cys	Val	Val	Glu 100	Ala	Val	Lys	Gly	Gly 105	Val	Glu	Gly	Gly	Gly 110	Pro	Gly
Pro	Gly	Leu 115	Gly	Leu	Ala	Ala	Pro 120	Pro	Asp	Ile					

<210> 309  
 <211> 84  
 <212> PRT  
 <213> homo sapiens

<400> 309

Pro 1	Thr	Thr	Thr	Leu 5	Val	Ile	Pro	Leu	Phe 10	Phe	Leu	Ser	Ser	Arg 15	Lys
Arg	Lys	Gln	Lys 20	Asp	Ser	Phe	Gln	Thr 25	Ala	Leu	Cys	Ser	Leu 30	His	Cys
Ser	Phe	Pro 35	Lys	Gln	Ala	Ala	Ser 40	Thr	Gly	Lys	Ala	His 45	Val	Val	Thr
Pro	Tyr 50	Phe	Ser	Glu	Val	Leu 55	Leu	Phe	His	Gly	Val 60	Thr	Leu	Leu	Ser
Glu 65	Ser	Lys	Phe	Arg	Lys 70	Gln	Val	Leu	Pro	Leu 75	Ala	Asp	Lys	Asn	His 80
Thr	Ser	Phe	Leu												

<210> 310  
 <211> 128  
 <212> PRT  
 <213> homo sapiens

<400> 310

Cys 1	Asp	Arg	Val	Pro 5	Leu	Phe	Leu	Ser	Tyr 10	Trp	Cys	Ala	Val	Ala 15	Asp
Ser	Trp	Leu	Thr 20	Ala	Ser	Ser	Val	Ser 25	His	Val	Lys	Gly	Ile 30	Leu	Ser
Pro	Gln	Pro	Thr	Glu	Cys	Ala	Pro	Pro	Gly	Pro	Ala	Asn	Cys	Phe	Phe

			35				40					45				
Asn	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Val	Glu	Thr	Gly	Ser	Pro	Ser	
	50					55					60					
Val	Ala	Gln	Asp	Gly	Leu	Glu	Leu	Leu	Gly	Ser	Ser	Asn	Pro	Pro	Thr	
65					70					75					80	
Leu	Ala	Ser	Gln	Ser	Ala	Glu	Ile	Thr	Gly	Met	Ser	His	Tyr	Ala	Gln	
				85					90					95		
Pro	Glu	Gln	Asp	Asp	Leu	Asn	Leu	Ile	Asn	Ser	Thr	Pro	Lys	Gln	Gln	
			100					105					110			
Leu	Ser	Leu	Ser	Gln	Gly	Cys	Gln	Gly	Gly	Leu	Cys	Glu	Gly	Lys	Asp	
		115					120					125				

<210> 311

<211> 96

<212> PRT

<213> homo sapiens

<400> 311

Trp	Val	Ala	Gly	Arg	Arg	His	Leu	Leu	Ser	Val	Gln	Thr	Lys	Ser	Leu
1				5					10					15	
Gln	Val	Leu	Gly	Leu	Asp	Leu	Cys	Val	Thr	Pro	Glu	Ser	Gln	Cys	Ile
			20					25					30		
Arg	Tyr	Leu	Tyr	Lys	Lys	Leu	Val	Trp	Phe	Leu	Ser	Ala	Lys	Gly	Lys
		35					40					45			
Thr	Cys	Phe	Leu	Asn	Leu	Leu	Ser	Asp	Asn	Lys	Val	Thr	Pro	Trp	Lys
	50					55					60				
Arg	Arg	Thr	Ser	Glu	Lys	Tyr	Gly	Val	Thr	Thr	Trp	Ala	Phe	Pro	Val
65					70					75					80
Leu	Ala	Ala	Cys	Phe	Gly	Lys	Leu	Gln	Cys	Arg	Leu	Gln	Arg	Ala	Val
				85					90					95	

<210> 312

<211> 57

<212> PRT

<213> homo sapiens

<400> 312

Ile	Ser	Thr	Ser	Ile	Ala	Ala	Leu	Trp	Leu	Pro	Gly	Gly	Gln	Asp	Ala
1				5					10					15	
Gly	Gly	Gly	Ala	Leu	Trp	Pro	Leu	Cys	Gly	Ser	Arg	Gly	Leu	Cys	Val
			20					25					30		
Ser	Asp	Arg	Phe	Pro	Gly	Asn	Phe	Arg	Ala	Arg	Leu	Thr	Ser	Trp	Lys
		35					40					45			
Phe	Lys	Tyr	Ser	Ile	Ala	Leu	Glu	Phe							
	50					55									

<210> 313

<211> 52

<212> PRT  
<213> homo sapiens

<400> 313

Ser	Ala	His	Gln	Leu	Gln	His	Cys	Gly	Tyr	Gln	Gly	Val	Arg	Met	Arg	
1				5					10					15		
Ala	Val	Glu	Pro	Ser	Gly	Leu	Cys	Val	Val	Ala	Glu	Asp	Ser	Val	Ser	
			20					25					30			
Ala	Thr	Val	Phe	Arg	Glu	Thr	Ser	Gly	Arg	Asp	Ser	His	Leu	Gly	Asn	
		35					40					45				
Ser	Asn	Thr	Gln													
	50															

<210> 314  
<211> 43  
<212> PRT  
<213> homo sapiens

<400> 314

Asn	Ser	Arg	Ala	Ile	Glu	Tyr	Leu	Asn	Phe	Gln	Asp	Val	Ser	Leu	Ala	
1				5					10					15		
Arg	Lys	Phe	Pro	Gly	Lys	Arg	Ser	Leu	Thr	Gln	Ser	Pro	Arg	Leu	Pro	
			20					25					30			
His	Lys	Gly	Gln	Arg	Ala	Pro	Pro	Pro	Ala	Ser						
		35					40									

<210> 315  
<211> 247  
<212> PRT  
<213> homo sapiens

<400> 315

Gly	Ser	Ser	Gly	Ser	Arg	Phe	Glu	Val	Val	Val	Val	Leu	Glu	Glu	Arg	
1				5					10					15		
Arg	Gly	Gly	Arg	Gly	Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser	
			20					25					30			
Arg	Gly	Lys	Arg	Glu	Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Gly	
		35					40					45				
Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	Gly	
	50					55					60					
Thr	Val	Lys	Asp	Glu	Leu	Thr	Glu	Ser	Pro	Lys	Tyr	Ile	Gln	Lys	Gln	
					70					75					80	
Ile	Ser	Tyr	Asn	Tyr	Ser	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	Glu	Glu	
				85					90					95		
Thr	Pro	Glu	Gly	Glu	Glu	His	His	Pro	Val	Ala	Asp	Thr	Glu	Asn	Lys	
			100					105					110			
Glu	Asn	Glu	Val	Glu	Glu	Val	Lys	Glu	Glu	Gly	Pro	Lys	Glu	Met	Thr	
		115					120					125				

Leu	Asp	Glu	Trp	Lys	Ala	Ile	Gln	Asn	Lys	Asp	Arg	Ala	Lys	Val	Glu
	130					135					140				
Phe	Asn	Ile	Arg	Lys	Pro	Asn	Glu	Gly	Ala	Asp	Gly	Gln	Trp	Lys	Lys
145					150					155					160
Gly	Phe	Val	Leu	His	Lys	Ser	Lys	Ser	Glu	Glu	Ala	His	Ala	Glu	Asp
				165					170					175	
Ser	Val	Met	Asp	His	His	Phe	Arg	Lys	Pro	Ala	Asn	Asp	Ile	Thr	Ser
			180					185					190		
Gln	Leu	Glu	Ile	Asn	Phe	Gly	Asp	Leu	Gly	Arg	Pro	Gly	Arg	Gly	Gly
		195					200					205			
Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Pro	Asn	Arg	Gly
	210					215					220				
Ser	Arg	Thr	Asp	Lys	Ser	Ser	Ala	Ser	Ala	Pro	Asp	Val	Asp	Asp	Pro
225					230					235					240
Glu	Ala	Phe	Pro	Ala	Leu	Ala									
				245											

<210> 316

<211> 75

<212> PRT

<213> homo sapiens

<400> 316

Phe	Met	Lys	Asn	Lys	Ser	Leu	Leu	Pro	Leu	Pro	Ile	Ser	Thr	Phe	Ile
1				5					10					15	
Trp	Phe	Ser	Asp	Ile	Lys	Phe	Tyr	Phe	Cys	Pro	Val	Leu	Ile	Leu	Asn
			20					25					30		
Ser	Leu	Pro	Leu	Ile	Gln	Ser	His	Leu	Phe	Trp	Thr	Leu	Leu	Phe	Tyr
		35					40					45			
Leu	Phe	Asn	Phe	Ile	Leu	Leu	Ile	Phe	Ser	Val	Cys	His	Trp	Met	Met
	50					55					60				
Phe	Phe	Thr	Phe	Arg	Cys	Phe	Leu	Ser	His	Ile					
65					70					75					

<210> 317

<211> 78

<212> PRT

<213> homo sapiens

<400> 317

Ser	Phe	Gly	Ile	Leu	Lys	His	Ala	Lys	Ala	Leu	Asn	Arg	Arg	Val	His
1				5					10					15	
Lys	Gly	Thr	Arg	Val	Val	Leu	Trp	His	Pro	Val	Lys	Pro	Glu	Leu	Gly
			20					25					30		
Met	Pro	Leu	Gly	His	Pro	His	Gln	Glu	Gln	Lys	His	Leu	Thr	Cys	Arg
		35					40					45			



Ser	Cys	Cys	His	Gly	Leu	Gly	Ala	His	His	Ala	His	Val	His	Leu	Val
	50					55					60				
Leu	Pro	Cys	Arg	His	Val	Leu	Gly	Gly	Gln	Gly	Leu	Gln	Asn		
65					70					75					

<210> 318  
 <211> 235  
 <212> PRT  
 <213> homo sapiens

<400> 318

Leu	His	Leu	Gly	Ala	Gln	Arg	Ala	Leu	Ala	Pro	Gly	Leu	Phe	Arg	Leu
1				5					10					15	
Gln	Gly	Met	Leu	Arg	Ala	Leu	Leu	Gly	Arg	Gln	Leu	Phe	Arg	Ala	Arg
			20					25					30		
Gly	Pro	Pro	Val	Val	Arg	Glu	Pro	Leu	Pro	Arg	Thr	Thr	Arg	Leu	Ala
		35					40					45			
Val	Arg	His	Val	Trp	Pro	Pro	Cys	Asp	Arg	Pro	Leu	Arg	Val	Gly	Pro
	50					55					60				
Gly	Ser	Pro	Leu	Pro	Pro	Gly	Pro	Leu	His	Met	His	Leu	Leu	Pro	Ala
65					70					75					80
Pro	Ala	His	Gln	Gly	Val	Leu	Pro	Gly	Ala	Arg	Arg	Gln	Ala	Leu	Leu
				85					90					95	
Pro	Ala	Leu	Leu	Pro	Glu	Ala	Leu	Arg	Leu	Thr	Ala	Arg	Ser	Ala	Arg
			100					105					110		
Pro	Leu	Pro	Arg	Arg	Pro	Arg	Pro	Pro	Gly	Lys	Ala	Gly	Ser	Ser	Arg
		115					120					125			
Pro	Arg	Gly	Leu	Ala	Leu	Arg	Ala	Gly	Gly	Pro	Thr	His	Trp	Arg	Ala
	130					135					140				
Pro	Pro	Leu	Arg	Tyr	Tyr	Glu	Ser	Ser	Gly	Val	Lys	Phe	Arg	Asn	Gly
145					150					155					160
Pro	Ala	Arg	Pro	Lys	Pro	Thr	Arg	Pro	Gln	Ser	Gly	Leu	His	Thr	Asp
				165					170					175	
Lys	Asn	Ser	Arg	Ala	Gly	Leu	His	Ser	Ile	Pro	Thr	Leu	Glu	Gly	Ala
			180					185					190		
Pro	Leu	Leu	Gly	Glu	Gly	Pro	Cys	Asn	Ser	Ser	Glu	Ser	Glu	Ala	Arg
		195					200					205			
Pro	Gly	Arg	Pro	Cys	Ser	Leu	His	Pro	His	Cys	Ser	Val	His	Phe	Phe
	210					215					220				
Tyr	Leu	His	Lys	His	Thr	His	Ser	Thr	Ser	Lys					
225					230					235					

<210> 319  
 <211> 478  
 <212> PRT  
 <213> homo sapiens

<400> 319

Gly 1	Ser	Arg	Pro	Pro 5	Pro	Cys	Ser	Pro	Arg 10	Ala	Thr	Gly	Pro	Arg 15	Pro
Ala	Met	Glu	Asp 20	Leu	Asp	Ala	Leu	Leu 25	Ser	Asp	Leu	Glu	Thr 30	Thr	Thr
Ser	His	Met 35	Pro	Arg	Ser	Gly	Ala 40	Pro	Lys	Glu	Arg	Pro 45	Ala	Glu	Pro
Leu	Thr 50	Pro	Pro	Pro	Ser	Tyr 55	Gly	His	Gln	Pro	Gln 60	Thr	Gly	Ser	Gly
Glu 65	Ser	Ser	Gly	Ala	Ser 70	Gly	Asp	Lys	Asp	His 75	Leu	Tyr	Ser	Thr	Val 80
Cys	Lys	Pro	Arg	Ser 85	Pro	Lys	Pro	Ala	Ala 90	Pro	Ala	Ala	Pro	Pro 95	Phe
Ser	Ser	Ser	Ser 100	Gly	Val	Leu	Gly	Thr 105	Gly	Leu	Cys	Glu	Leu 110	Asp	Arg
Leu	Leu	Gln 115	Glu	Leu	Asn	Ala	Thr 120	Gln	Phe	Asn	Ile	Thr 125	Asp	Glu	Ile
Met	Ser 130	Gln	Phe	Pro	Ser	Ser 135	Lys	Val	Ala	Ser	Gly 140	Glu	Gln	Lys	Glu
Asp 145	Gln	Ser	Glu	Asp	Lys 150	Lys	Arg	Pro	Ser	Leu 155	Pro	Ser	Ser	Pro	Ser 160
Pro	Gly	Leu	Pro	Lys 165	Ala	Ser	Ala	Thr	Ser 170	Ala	Thr	Leu	Glu	Leu 175	Asp
Arg	Leu	Met	Ala 180	Ser	Leu	Ser	Asp	Phe 185	Arg	Val	Gln	Asn	His 190	Leu	Pro
Ala	Ser	Gly 195	Pro	Thr	Gln	Pro	Pro 200	Val	Val	Ser	Ser	Thr 205	Asn	Glu	Gly
Ser	Pro 210	Ser	Pro	Pro	Glu	Pro 215	Thr	Gly	Lys	Gly	Ser 220	Leu	Asp	Thr	Met
Leu 225	Gly	Leu	Leu	Gln	Ser 230	Asp	Leu	Ser	Arg	Arg 235	Gly	Val	Pro	Thr	Gln 240
Ala	Lys	Gly	Leu	Cys 245	Gly	Ser	Cys	Asn	Lys 250	Pro	Ile	Ala	Gly	Gln 255	Val
Val	Thr	Ala	Leu 260	Gly	Arg	Ala	Trp	His 265	Pro	Glu	His	Phe	Val 270	Cys	Gly
Gly	Cys	Ser 275	Thr	Ala	Leu	Gly	Gly 280	Ser	Ser	Phe	Phe	Glu 285	Lys	Asp	Gly
Ala	Pro 290	Phe	Cys	Pro	Glu	Cys 295	Tyr	Phe	Glu	Arg	Phe 300	Ser	Pro	Arg	Cys
Gly 305	Phe	Cys	Asn	Gln	Pro 310	Ile	Arg	His	Lys	Met 315	Val	Thr	Ala	Leu	Gly 320
Thr	His	Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro

325								330				335			
Phe	Gly	Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg
			340					345					350		
Arg	Asp	Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly
		355					360					365			
Pro	Ile	Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Ala	Leu	Trp	His	Pro
	370					375					380				
Asp	Cys	Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser
385					390					395					400
Phe	Phe	Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala
				405					410					415	
Arg	Arg	Gly	Ser	Leu	Cys	Ala	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg
			420					425					430		
Cys	Val	Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Thr	Cys
		435					440					445			
Thr	Phe	Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala
	450					455					460				
Gly	Lys	Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly		
465					470					475					

<210> 320

<211> 285

<212> PRT

<213> homo sapiens

<400> 320

Glu	Gln	Gly	Leu	Gly	Val	Trp	Arg	Thr	Arg	Leu	Phe	Arg	Glu	Gly	Ala
1				5					10					15	
Ala	Ser	Gly	Gly	Glu	Gly	Glu	Pro	Ser	Gly	Leu	Ser	Ala	Glu	Glu	Leu
			20					25					30		
Gln	Glu	Ala	Gly	Leu	Ala	Val	Gly	Leu	Ala	Gly	Ala	Leu	Leu	Glu	Gly
		35					40					45			
Pro	Leu	Gly	Glu	Arg	Ala	Gln	Ala	Glu	Gly	Ala	Cys	Glu	Val	Val	Arg
	50					55					60				
Val	Glu	Ala	Ala	Thr	Gln	Gly	Arg	His	Ala	Ala	Ala	Gly	His	Arg	Glu
65					70					75					80
Ala	Thr	Arg	Gly	Ala	Gln	Arg	Ala	Ala	Ser	Cys	Val	Glu	Val	Val	Leu
				85					90					95	
Ala	Gln	Arg	Ala	Ala	Leu	Val	Leu	Glu	Lys	Ala	Ala	Ser	Arg	Glu	Gly
			100					105					110		
Arg	Glu	Ala	Phe	Pro	Ala	Asp	Glu	Thr	Val	Arg	Val	Pro	Glu	Arg	Ala
		115					120					125			
Glu	Arg	Arg	Asp	Val	Val	Ile	Gln	Asp	Gly	Ala	Leu	Ala	Ala	Leu	Ala
	130					135					140				

Ala 145	Arg	Gly	Glu	Gln	Leu 150	Gln	Glu	Val	Pro	Ala 155	Ala	Val	Gly	Ala	Ala 160
Leu	Ala	Leu	Val	Glu 165	Thr	Leu	Ile	Ser	Glu 170	Gly	Leu	Pro	Ala	Thr 175	Asp
Ala	Ala	Glu	Met 180	Leu	Trp	Val	Pro	Val 185	Ser	Ala	Gln	Gly	Gly 190	His	His
Leu	Val	Ser 195	Asp	Gly	Leu	Val	Ala 200	Glu	Ala	Thr	Ser	Trp 205	Arg	Glu	Ala
Leu	Lys 210	Val	Ala	Leu	Gly	Ala 215	Glu	Gly	Gly	Ser	Ile 220	Leu	Leu	Glu	Glu
Ala 225	Ala	Ala	Ser	Gln	Gly 230	Gly	Gly	Thr	Ala	Ser 235	Ala	Asn	Glu	Val	Leu 240
Gly	Val	Pro	Gly	Ala 245	Ala	Gln	Ser	Arg	His 250	His	Leu	Pro	Ser	Asn 255	Arg
Phe	Ile	Ala	Gly 260	Ala	Thr	Glu	Ala	Phe 265	Gly	Leu	Gly	Gly	Asn 270	Thr	Pro
Ala	Ala	Glu 275	Val	Gly	Leu	Gln	Gln 280	Pro	Gln	His	Gly	Val 285			

<210> 321  
 <211> 99  
 <212> PRT  
 <213> homo sapiens

<400> 321

Gly 1	Leu	His	Leu	Gln 5	Pro	Leu	Leu	Trp	Arg 10	Gln	Ser	Thr	Glu	Glu 15	Glu
Val	Arg	Glu	Glu 20	Gly	Gln	Ala	Leu	Thr 25	Glu	Pro	Lys	Ser	Cys 30	Gly	Ala
Gln	Gly	Gly 35	Ala	Gln	His	Arg	Gly 40	Leu	Thr	Pro	Cys	Pro 45	Thr	Gly	Asn
Gly 50	Leu	Gly	Leu	Ala	Gln	Pro 55	Lys	Ile	Pro	Ala	Leu 60	Ser	Asn	Ser	Trp
Arg 65	Val	Asp	Ser	Val	Leu 70	Ala	Cys	Leu	Val	Ser 75	Ser	Asp	Ile	Phe	His 80
Thr	Val	Glu	Gln	Asn 85	His	Gln	Pro	Cys	Thr 90	Asp	Val	Thr	Leu	Cys 95	Arg

Lys Arg Pro

<210> 322  
 <211> 99  
 <212> PRT  
 <213> homo sapiens

<400> 322

Glu 1	Thr	Gln	Ser	Ser 5	Gln	Arg	Leu	Thr	Cys 10	Pro	Arg	Ser	Leu	Gly 15	Leu
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Asp	Leu	Ser	Leu	Arg	Leu	Arg	Leu	Gln	Asn	Pro	His	Ser	Ile	Cys	Tyr
			20					25					30		
Ile	Ser	Gln	Gly	Trp	Gly	Gln	Gly	Ser	Cys	Glu	Gln	Lys	Glu	Lys	Tyr
		35					40					45			
Gln	Leu	Leu	Lys	Gly	Leu	Gly	Phe	Val	Gly	Arg	Ala	Arg	Gln	Gly	Gln
	50					55					60				
Arg	Gly	Ile	Gln	Asn	Lys	Gly	Ala	Ser	Thr	Ser	Ala	Trp	Asp	Gly	Pro
65					70					75					80
Ile	His	Ser	Gly	Arg	Gly	Cys	Gly	Val	Ser	Pro	Val	Leu	Arg	Asn	His
				85					90					95	
Leu	Ala	Ser													

<210> 323  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 323

Ser	Asn	Pro	Lys	Ala	Pro	Val	Ser	Met	Trp	Val	Lys	Gly	Pro	Thr	Met
1				5					10					15	
Gly	Thr	Tyr	Thr	Gln	Glu	Asp	Glu	Ser	Ser	Leu	Ala	Ser	Glu	Ser	Asp
			20					25					30		
Cys	Leu	Pro	Gln	Thr	Pro	Pro	Gln	Asn	Arg	Leu	Leu	Ser	His	Leu	Pro
		35					40					45			
Leu	His	Ser	Asp	Lys	Thr	Gln	Ala	His	Ile	Pro	Gly	Pro	Gly	Val	Phe
	50					55					60				
Ala	Cys	Ile	Cys	Ile	Asp	Gly	Asn	Ala	Gly	Pro	Ala	Lys	Ala	Phe	Phe
65					70					75					80

Tyr Ile Lys

<210> 324  
 <211> 111  
 <212> PRT  
 <213> homo sapiens

<400> 324

Val	Phe	Pro	Thr	Val	Leu	Arg	Gly	Val	Leu	Val	Pro	Ser	Ser	Val	Thr
1				5					10					15	
Ser	Lys	Pro	Gly	Leu	Ile	Val	Pro	Ile	Gly	Asp	Glu	Gly	Gly	Met	Arg
			20					25					30		
Arg	Ser	His	Leu	Gln	Leu	Leu	Ser	Val	Glu	Arg	Thr	Ser	Gly	Thr	Glu
		35					40					45			
Lys	Asn	Arg	Gly	Pro	His	Gly	Ser	Leu	Glu	Gly	Arg	Gly	Thr	Arg	Val
	50					55					60				
Gly	Glu	Leu	Ile	Ala	Glu	Arg	Arg	Asp	Val	Gln	Arg	Pro	Ser	Ala	Pro
65					70					75					80



260

265

270

&lt;210&gt; 326

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 326

Thr 1	Leu	Val	Phe	Gly 5	Arg	Leu	Arg	Thr	Lys 10	Pro	Phe	Arg	Ile	Pro 15	Gly
Phe	Leu	Gln	Arg 20	Lys	Arg	Arg	Trp	Gln 25	Ile	Gln	Glu	Ile	Lys 30	Pro	Met
Gly	Ala	Glu 35	His	Leu	Trp	Ile	Pro 40	Ala	Ala	Leu	Arg	Asn 45	Lys	Val	Glu
Ala	Pro 50	Glu	Arg	Trp	Ser	Pro 55	Pro	Trp	Cys	Pro	Trp 60	Ala	Trp	Cys	Trp
Gln 65	Trp	Glu	Pro	Trp	Leu 70	Trp	Gly	Trp	Pro	Glu 75	Pro	Gly	Thr	Gly	Arg 80
Thr	Ser	Thr	Glu	Phe 85	Gln	Ser	Glu	Ala	Thr 90	Gly	Gln	Thr	Leu	Ala 95	Cys
Gln	Thr	Ser	Arg 100	Thr	Pro	Gly	Asn	Leu 105	Glu	Pro	Met	Thr	Thr 110	Trp	Glu
Pro	Leu	Arg 115	Ser	Leu	Arg	Arg	His 120	Pro	Ser	Glu	Glu	Lys 125	Lys	Ser	Leu
Leu	Pro 130	Pro	Leu	Arg	Ala	Pro 135	Gln	Arg	Pro	Lys	Asn 140	Pro	Arg	Arg	Gln
Lys 145	Gly	His	Pro	Arg	Arg 150	Lys	Pro	Arg	Trp	Pro 155	Thr	Lys	Thr	Ser	Cys 160
Ser	Ser	Pro	Ala	Pro 165	Trp	Pro	Pro	Arg	Pro 170	Arg	Thr	Ala	Pro	Arg 175	Lys
Pro	Arg	Arg	Cys 180	Arg	Arg	Leu	Leu	Pro 185	Ala	Pro	Met	Thr	Ile 190	Thr	Phe
Arg	Ile	Met 195	Ser	Ile	Leu	Gly	Pro 200	Ser	Ala	Pro	Gly	Asp 205	Pro	Thr	Pro
Cys	Ser 210	Asn	Thr	Cys	Leu	Gly 215	Phe	Ser	Tyr	Cys	Pro 220	Gln	Arg	Arg	Ala
Gly 225	Pro	Leu	Leu	Ser	Asp 230	Ile	Lys	Ala	Trp	Pro 235	Asn	Cys	Ser	Tyr	Trp 240

Gly

&lt;210&gt; 327

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 327

Ala 1	Val	Val	Arg	Val 5	Thr	Trp	Tyr	Lys	Gly 10	Glu	Gly	Ile	Thr	Leu 15	Pro
Pro	Val	Leu	Thr 20	Pro	Ala	Leu	Val	Arg 25	Gly	Glu	Ser	Ile	Pro 30	Ile	Arg
Leu	Phe	Leu 35	Ala	Gly	Tyr	Glu	Leu 40	Thr	Pro	Thr	Met	Arg 45	Asp	Ile	Asn
Lys	Lys 50	Phe	Ser	Val	Arg	Tyr 55	Tyr	Leu	Asn	Leu	Val 60	Leu	Ile	Asp	Glu
Glu 65	Glu	Arg	Arg	Tyr	Phe 70	Lys	Gln	Gln	Glu	Val 75	Val	Leu	Trp	Arg	Lys 80
Gly	Asp	Ile	Val	Arg 85	Lys	Ser	Met	Ser	His 90	Gln	Ala	Ala	Ile	Ala 95	Ser
Gln	Arg	Phe	Glu 100	Gly	Thr	Thr	Ser	Leu 105	Gly	Glu	Val	Arg	Thr 110	Pro	Ser
Gln	Leu	Ser 115	Asp	Asn	Asn	Cys	Arg 120	Gln							

<210> 328

<211> 140

<212> PRT

<213> homo sapiens

<400> 328

Gly 1	Glu	Thr	Arg	Val 5	His	Ser	Gln	Gln	Gly 10	Gly	Gly	Ile	Lys	Ala 15	Pro
Ser	Trp	Asp	Trp 20	Phe	Phe	Arg	Glu	Pro 25	Gly	Pro	Leu	Val	Lys 30	Gly	Leu
Leu	Gly	His 35	Val	Lys	Gln	Tyr	Leu 40	Glu	Gln	Pro	Arg	Pro 45	Trp	Gly	Tyr
Gln	Val 50	Glu	Arg	Arg	Glu	Gly 55	Arg	Arg	Leu	Pro	Cys 60	Thr	His	Leu	Pro
Trp 65	Trp	Ala	Gly	Phe	Ser 70	Leu	Leu	Gly	Ser	Thr 75	Leu	Pro	Pro	Ser	Val 80
His	Asp	Thr	Asp	Pro 85	Arg	Ala	Ser	Pro	Cys 90	Pro	Arg	Pro	Ser	Tyr 95	Arg
Leu	Leu	Phe	Gln 100	Asp	Ile	Thr	Asp	Asn 105	Pro	Glu	Arg	Met	Glu 110	Lys	Gly
Gly	Ala	Trp 115	Val	Pro	Ala	Val	Ser 120	Gly	Gln	Lys	Glu	Val 125	Ala	Cys	Gly
Asn	Leu 130	Arg	Ser	Pro	His	Pro 135	Arg	Phe	Pro	Lys	Arg 140				

<210> 329

<211> 127

<212> PRT

<213> homo sapiens



<400> 329

Val 1	Phe	Pro	Cys	His 5	Leu	Val	Gly	Ala	Gly 10	Pro	Thr	Pro	Ala	Thr 15	Thr
Ser	Gly	Thr	Ala 20	Lys	Gly	Ser	Thr	Arg 25	Cys	Asp	Tyr	Pro	Gly 30	Pro	Cys
Trp	Gln	Leu 35	Arg	Ile	Pro	Gly	Thr 40	Cys	Ser	Asp	Pro	Val 45	Ser	Gly	Ser
Ser	Glu 50	Ser	Gln	Glu	Pro	Arg 55	Met	Arg	Ala	Leu	Cys 60	Ser	Pro	Ser	Ser
Lys 65	Thr	Gln	Gly	Ser	Pro 70	Pro	Arg	Lys	Gly	Ala 75	His	Val	Pro	Gln	Arg 80
Gly	Trp	Leu	Pro	Gly 85	Cys	Tyr	Leu	Phe	Tyr 90	Pro	Thr	Ser	Ala	Ala 95	Glu
Ser	Gln	Gly	Glu 100	Thr	Ala	Ser	His	Pro 105	Lys	Pro	Leu	Gly	Phe 110	Ser	Arg
Glu	Lys	Asn 115	Leu	Ser	Gln	Lys	His 120	Asp	Leu	Phe	Ser	Gly 125	Cys	Lys	

<210> 330

<211> 418

<212> PRT

<213> homo sapiens

<400> 330

Gly 1	Ser	Thr	Ser	Thr 5	Lys	Asn	Thr	Lys	Ile 10	Ser	Gln	Ala	Cys	Gly 15	Val
Ile	Val	Glu	Leu 20	Ile	Lys	Ser	Lys	Lys 25	Met	Ala	Gly	Gly	Ala 30	Val	Leu
Leu	Ala	Gly 35	Pro	Pro	Gly	Thr	Gly 40	Lys	Thr	Ala	Leu	Ala 45	Leu	Ala	Ile
Ala	Gln 50	Glu	Leu	Gly	Ser	Lys 55	Val	Pro	Phe	Cys	Pro 60	Met	Val	Gly	Ser
Glu 65	Val	Tyr	Ser	Thr	Glu 70	Ile	Lys	Lys	Thr	Glu 75	Val	Leu	Met	Glu	Asn 80
Phe	Arg	Arg	Ala	Ile 85	Gly	Leu	Arg	Ile	Lys 90	Glu	Thr	Lys	Glu	Val 95	Tyr
Glu	Gly	Glu	Val 100	Thr	Glu	Leu	Thr	Pro 105	Cys	Glu	Thr	Glu	Asn 110	Pro	Met
Gly	Gly	Tyr 115	Gly	Lys	Thr	Ile	Ser 120	His	Val	Ile	Ile	Gly 125	Leu	Lys	Thr
Ala	Lys 130	Gly	Thr	Lys	Gln	Leu 135	Lys	Leu	Asp	Pro	Ser 140	Ile	Phe	Glu	Ser
Leu 145	Gln	Lys	Glu	Arg	Val 150	Glu	Ala	Gly	Asp	Val 155	Ile	Tyr	Ile	Glu	Ala 160

Asn	Ser	Gly	Ala	Val 165	Lys	Arg	Gln	Gly	Arg 170	Cys	Asp	Thr	Tyr	Ala 175	Thr
Glu	Phe	Asp	Leu 180	Glu	Ala	Glu	Glu	Tyr 185	Val	Pro	Leu	Pro	Lys 190	Gly	Asp
Val	His	Lys 195	Lys	Lys	Glu	Ile	Ile 200	Gln	Asp	Val	Thr	Leu 205	His	Asp	Leu
Asp	Val 210	Ala	Asn	Ala	Arg	Pro 215	Gln	Gly	Gly	Gln	Asp 220	Ile	Leu	Ser	Met
Met 225	Gly	Gln	Leu	Met	Lys 230	Pro	Lys	Lys	Thr	Glu 235	Ile	Thr	Asp	Lys	Leu 240
Arg	Gly	Glu	Ile	Asn 245	Lys	Val	Val	Asn	Lys 250	Tyr	Ile	Asp	Gln	Gly 255	Ile
Ala	Glu	Leu	Val 260	Pro	Gly	Val	Leu	Phe 265	Val	Asp	Glu	Val	His 270	Met	Leu
Asp	Ile	Glu 275	Cys	Phe	Thr	Tyr	Leu 280	His	Arg	Ala	Leu	Glu 285	Ser	Ser	Ile
Ala	Pro 290	Ile	Val	Ile	Phe	Ala 295	Ser	Asn	Arg	Gly	Asn 300	Cys	Val	Ile	Arg
Gly 305	Thr	Glu	Asp	Ile	Thr 310	Ser	Pro	His	Gly	Ile 315	Pro	Leu	Asp	Leu	Leu 320
Asp	Arg	Val	Met	Ile 325	Ile	Arg	Thr	Met	Leu 330	Tyr	Thr	Pro	Gln	Glu 335	Met
Lys	Gln	Ile	Ile 340	Lys	Ile	Arg	Ala	Gln 345	Thr	Glu	Gly	Ile	Asn 350	Ile	Ser
Glu	Glu	Ala 355	Leu	Asn	His	Leu	Gly 360	Glu	Ile	Gly	Thr	Lys 365	Thr	Thr	Leu
Arg	Tyr 370	Ser	Val	Gln	Leu	Leu 375	Thr	Pro	Ala	Asn	Leu 380	Leu	Ala	Lys	Ile
Asn 385	Gly	Lys	Asp	Ser	Ile 390	Glu	Lys	Glu	His	Val 395	Glu	Glu	Ile	Ser	Glu 400
Leu	Phe	Tyr	Asp	Ala 405	Lys	Ser	Ser	Ala	Lys 410	Ile	Leu	Gly	Leu	Thr 415	Arg

Gln Gly

<210> 331

<211> 142

<212> PRT

<213> homo sapiens

<400> 331

Val 1	Pro	Gln	Cys	Gly 5	Leu	Gly	Ala	Asn	Leu 10	Pro	Gln	Val	Val	Gln 15	Cys
Leu	Leu	Thr	Asp 20	Val	Asp	Ser	Phe	Arg 25	Leu	Gly	Thr	Asp	Phe 30	Asn	Asp

Leu	Phe	His	Phe	Leu	Trp	Ser	Ile	Gln	His	Gly	Pro	Asp	Tyr	His	His
		35					40					45			
Ser	Val	Gln	Lys	Val	Lys	Arg	Asp	Ala	Val	Arg	Gly	Cys	Asp	Val	Leu
	50					55					60				
Ser	Ala	Ser	Asp	Asp	Thr	Val	Ala	Ser	Val	Gly	Cys	Lys	Asp	Asp	Asp
65					70					75					80
Gly	Ser	Asp	Arg	Arg	Leu	Gln	Gly	Ala	Val	Gln	Val	Gly	Glu	Ala	Leu
				85					90					95	
Asn	Val	Gln	His	Val	Asp	Leu	Ile	Asn	Lys	Gln	His	Thr	Arg	Asp	Gln
			100					105					110		
Leu	Ser	Asn	Ala	Leu	Val	Asp	Val	Leu	Val	His	His	Leu	Ile	Asn	Leu
		115					120					125			
Pro	Ser	Lys	Phe	Val	Cys	Asp	Phe	Cys	Leu	Leu	Trp	Leu	His		
	130					135					140				

<210> 332  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 332

Leu	Ala	His	His	Gly	Gln	Asp	Ile	Leu	Ser	Pro	Leu	Gly	Pro	Arg	Ile
1				5					10					15	
Ser	His	Ile	Gln	Val	Met	Gln	Gly	His	Ile	Leu	Asp	Asp	Phe	Phe	Leu
			20					25					30		
Phe	Val	His	Ile	Pro	Phe	Trp	Gln	Gly	Asp	Ile	Leu	Phe	Ser	Phe	Lys
		35					40					45			
Val	Glu	Phe	Cys	Gly	Ile	Gly	Ile	Thr	Pro	Ala	Leu	Pro	Leu	His	Gly
	50					55					60				
Pro	Thr	Val	Gly	Phe	Asn	Val	Asn	His	Ile	Ser	Ser	Phe	Tyr	Ser	Leu
65					70					75					80
Phe	Leu	Gln	Thr	Phe	Lys	Asn	Ala	Gly	Val	Gln	Phe	Gln	Leu	Phe	Gly
				85					90					95	
Ser	Phe	Gly	Cys	Phe	Glu	Ser	Tyr	Asp	His	Met	Ala	Asn	Gly	Phe	Ala
			100					105					110		
Ile	Ser	Ser	His	Gly	Ile	Leu	Cys	Leu	Thr	Arg	Ser				
		115					120								

<210> 333  
 <211> 176  
 <212> PRT  
 <213> homo sapiens

<400> 333

Gln	Ala	Met	Gly	Lys	Lys	Gln	Lys	Asn	Lys	Ser	Glu	Asp	Ser	Thr	Lys
1				5					10					15	
Asp	Asp	Ile	Asp	Leu	Asp	Ala	Leu	Ala	Ala	Glu	Ile	Glu	Gly	Ala	Gly

20							25					30				
Ala	Ala	Lys 35	Glu	Gln	Glu	Pro	Gln 40	Lys	Ser	Lys	Gly	Lys 45	Lys	Lys	Lys	
Glu	Lys 50	Lys	Lys	Gln	Asp	Phe 55	Asp	Glu	Asp	Asp	Ile 60	Leu	Lys	Glu	Leu	
Glu 65	Glu	Leu	Ser	Leu	Glu 70	Ala	Gln	Gly	Ile	Lys 75	Ala	Asp	Arg	Glu	Thr 80	
Val	Ala	Val	Lys	Pro 85	Thr	Glu	Asn	Asn	Glu 90	Glu	Glu	Phe	Thr	Ser 95	Lys	
Asp	Lys	Lys	Lys 100	Lys	Gly	Gln	Lys	Gly 105	Lys	Lys	Gln	Ser	Phe 110	Asp	Asp	
Asn	Asp	Ser 115	Glu	Glu	Leu	Glu	Asp 120	Lys	Asp	Ser	Lys	Ser 125	Lys	Lys	Thr	
Ala	Lys 130	Pro	Lys	Val	Glu	Met 135	Tyr	Ser	Gly	Ser	Leu 140	Thr	Asn	Phe	Leu	
Lys 145	Lys	Leu	Lys	Gly	Lys 150	Leu	Lys	Asn	Gln	Ile 155	Arg	Ser	Gly	Met	Gly 160	
Gln	Arg	Arg	Met	Arg 165	Ile	Thr	Val	Lys	Lys 170	Leu	Lys	Ser	Val	Gln 175	Glu	

<210> 334

<211> 193

<212> PRT

<213> homo sapiens

<400> 334

Arg 1	Phe	Lys	Ile	Lys 5	Lys	Asp	Cys	Lys	Thr 10	Glu	Ser	Gly	Asn	Val 15	Leu	
Trp	Glu	Phe	Asn 20	Lys	Leu	Pro	Lys	Lys 25	Ala	Lys	Gly	Lys	Ala 30	Gln	Lys	
Ser	Asn	Lys 35	Lys	Trp	Asp	Gly	Ser 40	Glu	Glu	Asp	Glu	Asp 45	Asn	Ser	Lys	
Lys	Ile 50	Lys	Glu	Arg	Ser	Arg 55	Ile	Asn	Ser	Ser	Gly 60	Glu	Ser	Gly	Asp	
Glu 65	Ser	Asp	Glu	Phe	Leu 70	Gln	Ser	Arg	Lys	Gly 75	Gln	Lys	Lys	Asn	Gln 80	
Lys	Asn	Lys	Pro	Gly 85	Pro	Asn	Ile	Glu	Ser 90	Gly	Asn	Glu	Asp	Asp 95	Asp	
Ala	Ser	Phe	Lys 100	Ile	Lys	Thr	Val	Ala 105	Gln	Lys	Lys	Ala	Glu 110	Lys	Lys	
Glu	Arg	Glu 115	Arg	Lys	Lys	Arg	Asp 120	Glu	Glu	Lys	Ala	Lys 125	Leu	Arg	Lys	
Leu	Lys 130	Glu	Lys	Glu	Glu	Leu 135	Glu	Thr	Gly	Lys	Lys 140	Asp	Gln	Ser	Lys	

Gln 145	Lys	Glu	Ser	Gln	Arg 150	Lys	Phe	Glu	Glu	Glu 155	Thr	Val	Lys	Ser	Lys 160
Val	Thr	Val	Asp	Thr 165	Gly	Val	Ile	Pro	Ala 170	Ser	Glu	Glu	Lys	Ala 175	Glu
Thr	Pro	Thr	Ala 180	Ala	Glu	Asp	Asp	Asn 185	Glu	Gly	Asp	Lys	Lys 190	Asn	Glu

Arg

<210> 335  
 <211> 118  
 <212> PRT  
 <213> homo sapiens

<400> 335

Glu 1	Thr	Val	Ala	Phe 5	Ala	Arg	Pro	Phe	Phe 10	Pro	Ser	Leu	Phe	Ser 15	Phe
Pro	Pro	Leu	Ser 20	Ser	Phe	Leu	Phe	Leu 25	Leu	Ile	Phe	Arg	Ser 30	Phe	Cys
Leu	Leu	His 35	Cys	His	Leu	Leu	Gln 40	Leu	Trp	Glu	Ser	Leu 45	Leu	Ser	Leu
Gln	Arg 50	Gln	Glu	Leu	Leu	Gln 55	Tyr	Gln	Gln	Ser	Leu 60	Trp	Ile	Leu	Gln
Phe 65	Leu	Leu	Gln	Ile	Ser 70	Phe	Glu	Ile	Pro	Phe 75	Val	Tyr	Ser	Asp	Pro 80
Phe	Tyr	Leu	Phe	Leu 85	Thr	Leu	Leu	Phe 90	Leu	Ser	Ala	Ser	Ala	Val 95	Ser
Leu	Phe	Leu	His 100	Leu	Ala	Phe	Phe	Ser 105	Arg	Ala	Pro	Ser	Phe 110	Leu	Pro
Ser	Phe	Gly 115	Pro	Leu	Ser										

<210> 336  
 <211> 230  
 <212> PRT  
 <213> homo sapiens

<400> 336

Leu 1	Gln	Arg	Leu	Leu 5	Pro	Pro	Gly	Ala	Glu 10	Arg	Pro	Ala	His	Leu 15	Cys
Thr	Gly	Pro	Gly 20	Gly	Glu	Asp	Gly	Ala 25	Gly	Gly	Arg	Val	Pro 30	Gly	Thr
Arg	Pro	Gln 35	Arg	Pro	Pro	Ala	Leu 40	Gln	Arg	Ala	Glu	Asp 45	Gly	Arg	Gln
Gly	Gly 50	Leu	Arg	Val	Ala	Gly 55	Thr	Ala	Gly	Pro	Pro 60	Pro	Gly	Val	Pro
Leu 65	Arg	Pro	Gly	Gln	Gly 70	Gly	Ser	Gly	His	Gln 75	Glu	Gln	Gly	Ala	Ser 80

His	Pro	Gly	Ser	Leu 85	Asp	Gln	Gly	Leu	Thr 90	Gly	Ala	Lys	Arg	Pro 95	Gln
Gly	Cys	Pro	Ala 100	Cys	Gly	Arg	Arg	Pro 105	Pro	Cys	Val	Gly	Gly 110	Val	Pro
Gly	Ser	Ala 115	His	Arg	Pro	Gln	Pro 120	Glu	Gly	Ala	Ala	Leu 125	Arg	Arg	Gly
Arg	Ser 130	Arg	Leu	Gln	Gln	Ala 135	Gly	Pro	Cys	Cys	Cys 140	Arg	Val	Leu	Trp
Leu 145	Arg	Arg	Cys	His	Pro 150	Ala	Gly	Leu	Pro	Arg 155	Arg	Pro	Pro	Ala	Ala 160
Asp	Pro	Gly	Ala	Arg 165	Ala	Ala	Ala	Gly	Gly 170	Arg	His	Val	Leu	Cys 175	Arg
Ser	Pro	Leu	His 180	Pro	Gly	Leu	Arg	Pro 185	Pro	Leu	Pro	Gln	Trp 190	Gly	Leu
Leu	Arg	Pro 195	Glu	Gly	Gly	Cys	Leu 200	Cys	Val	Pro	Val	Ser 205	Arg	Gly	Ile
Leu	Arg 210	Thr	Ala	Leu	Arg	Glu 215	Gly	Ala	Gly	Gly	Glu 220	Val	Ser	Gly	Gly
Arg 225	Gly	Tyr	Leu	Gly	Leu 230										

<210> 337

<211> 416

<212> PRT

<213> homo sapiens

<400> 337

Gln 1	Asp	Gly	Ser	Gly 5	Pro	Phe	Leu	Ala	Asp 10	Phe	Asn	Gly	Phe	Ser 15	His
Leu	Glu	Leu	Arg 20	Gly	Leu	His	Thr	Phe 25	Ala	Arg	Asp	Leu	Gly 30	Glu	Lys
Met	Ala	Leu 35	Glu	Val	Val	Phe	Leu 40	Ala	Arg	Gly	Pro	Ser 45	Gly	Leu	Leu
Leu	Tyr 50	Asn	Gly	Gln	Lys	Thr 55	Asp	Gly	Lys	Gly	Asp 60	Phe	Val	Ser	Leu
Ala 65	Leu	Arg	Asp	Arg	Arg 70	Leu	Glu	Phe	Arg	Tyr 75	Asp	Leu	Gly	Lys	Gly 80
Ala	Ala	Val	Ile	Arg 85	Ser	Arg	Glu	Pro	Val 90	Thr	Leu	Gly	Ala	Trp 95	Thr
Arg	Val	Ser	Leu 100	Glu	Arg	Asn	Gly	Arg 105	Lys	Gly	Ala	Leu	Arg 110	Val	Gly
Asp	Gly	Pro 115	Arg	Val	Leu	Gly	Glu 120	Ser	Pro	Val	Pro	His 125	Thr	Val	Leu
Asn	Leu	Lys	Glu	Pro	Leu	Tyr	Val	Gly	Gly	Ala	Pro	Asp	Phe	Ser	Lys

	130					135					140					
Leu 145	Ala	Arg	Ala	Ala	Ala 150	Val	Ser	Ser	Gly	Phe 155	Asp	Gly	Ala	Ile	Gln 160	
Leu	Val	Ser	Leu	Gly 165	Gly	Arg	Gln	Leu	Leu 170	Thr	Pro	Glu	His	Val 175	Leu	
Arg	Gln	Val	Asp 180	Val	Thr	Ser	Phe	Ala 185	Gly	His	Pro	Cys	Thr 190	Arg	Ala	
Ser	Gly	His 195	Pro	Cys	Leu	Asn	Gly 200	Ala	Ser	Cys	Val	Pro 205	Arg	Glu	Ala	
Ala	Tyr 210	Val	Cys	Leu	Cys	Pro 215	Gly	Gly	Phe	Ser	Gly 220	Pro	His	Cys	Glu	
Lys 225	Gly	Leu	Val	Glu	Lys 230	Ser	Ala	Gly	Asp	Val 235	Asp	Thr	Leu	Ala	Phe 240	
Asp	Gly	Arg	Thr	Phe 245	Val	Glu	Tyr	Leu	Asn 250	Ala	Val	Thr	Glu	Ser 255	Glu	
Lys	Ala	Leu	Gln 260	Ser	Asn	His	Phe	Glu 265	Leu	Ser	Leu	Arg	Thr 270	Glu	Ala	
Thr	Gln	Gly 275	Leu	Val	Leu	Trp	Ser 280	Gly	Lys	Ala	Thr	Glu 285	Arg	Ala	Asp	
Tyr	Val 290	Ala	Leu	Ala	Ile	Val 295	Asp	Gly	His	Leu	Gln 300	Leu	Ser	Tyr	Asn	
Leu 305	Gly	Ser	Gln	Pro	Val 310	Val	Leu	Arg	Ser	Thr 315	Val	Pro	Val	Asn	Thr 320	
Asn	Arg	Trp	Leu	Arg 325	Val	Val	Ala	His	Arg 330	Glu	Gln	Arg	Glu	Gly 335	Ser	
Leu	Gln	Val	Gly 340	Asn	Glu	Ala	Pro	Val 345	Thr	Gly	Ser	Ser	Pro 350	Leu	Gly	
Ala	Thr	Gln 355	Leu	Asp	Thr	Asp	Gly 360	Ala	Leu	Trp	Leu	Gly 365	Gly	Leu	Pro	
Glu	Leu 370	Pro	Val	Gly	Pro	Ala 375	Leu	Pro	Lys	Ala	Tyr 380	Gly	Thr	Gly	Phe	
Val 385	Gly	Cys	Leu	Arg	Asp 390	Val	Val	Val	Gly	Arg 395	His	Pro	Leu	His	Leu 400	
Leu	Glu	Asp	Ala	Val 405	Thr	Lys	Pro	Glu	Leu 410	Arg	Pro	Cys	Pro	Thr 415	Pro	

<210> 338

<211> 241

<212> PRT

<213> homo sapiens

<400> 338

Asn 1	Gln	His	Met	Lys 5	Asn	Thr	Ala	Met	Ala 10	Arg	Pro	Arg	Tyr	Pro 15	Gly
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Arg	Arg	Gln	Arg	Ser	Thr	Pro	Ser	His	Ser	Glu	Leu	Leu	Ser	Ile	Ala
			20					25					30		
Pro	Arg	Arg	Ala	Trp	Gly	Val	Ala	Glu	Gly	Tyr	Gly	His	Val	Gln	Gly
		35					40					45			
Gly	Trp	Ala	Gly	Pro	Ala	Glu	Gly	Gln	Asp	Thr	Gln	Ile	Gly	Pro	Gly
	50					55					60				
Leu	Ala	Ser	Ala	Pro	Gln	Gln	Pro	Gly	Leu	Ala	Gln	Ala	Ala	Arg	Glu
65					70					75					80
Gln	Arg	Arg	Ala	Val	Pro	Ser	Ser	Asn	Ile	Val	Trp	Lys	Ser	Gln	Tyr
				85					90					95	
Trp	Arg	Arg	Arg	Pro	Arg	Gln	Gly	Pro	Glu	His	Thr	Gln	Glu	Gly	Ala
			100					105					110		
Ala	Gln	Ile	Gly	Ala	Trp	Lys	Gly	Pro	Val	Gly	Ser	Pro	Gly	Gly	Arg
		115					120					125			
Ala	Pro	Ser	Asp	Leu	Ser	Ser	Pro	Phe	Leu	Ser	Gly	Thr	Arg	Val	Pro
	130					135					140				
Pro	Asp	Gly	Ala	Arg	Val	Ile	Gln	Glu	Pro	Gly	Leu	Leu	Pro	Gly	Gly
145					150					155					160
Asp	Thr	Val	Gly	Gln	Ala	Gln	Cys	Lys	Ala	Gly	Ala	Gln	His	Leu	Glu
				165					170					175	
Ala	Gly	Val	Cys	Val	Leu	Arg	Leu	Pro	Ser	Thr	Pro	Ser	Pro	Pro	Arg
			180					185					190		
Cys	His	Leu	Ala	Cys	Pro	Ser	Leu	Ser	Thr	Arg	Ser	Val	Cys	Ser	Thr
		195					200					205			
Ala	Ala	Trp	Thr	Glu	Gly	Arg	Pro	Gly	Gln	Gln	Ser	Leu	Arg	Pro	Thr
	210					215					220				
Leu	Arg	Gln	Glu	Asn	His	Ile	Lys	Lys	Arg	Gln	Val	Tyr	Lys	Asn	Arg
225					230					235					240
Lys															

<210> 339

<211> 79

<212> PRT

<213> homo sapiens

<400> 339

Leu	Leu	Gln	Pro	Gln	Gly	Glu	Met	Pro	Pro	Gly	Asn	Pro	Pro	Met	Ser
1				5					10					15	
Thr	Arg	Gly	Gln	Glu	Ala	Thr	Val	Leu	Arg	Thr	Pro	Glu	Asn	Leu	Ala
			20					25					30		
Gly	Glu	Leu	Phe	Leu	Val	His	Pro	Ser	Leu	Gln	Leu	Tyr	Leu	Cys	Pro
		35					40					45			
Ala	Asp	Asn	Val	Lys	Asp	Trp	Ser	Lys	Val	Val	Leu	Ala	Tyr	Glu	Pro
	50					55					60				



Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Pro	Gln	Gln	Gly
65					70					75				

<210> 340

<211> 62

<212> PRT

<213> homo sapiens

<400> 340

Phe	Pro	Val	Gly	Val	Leu	Gln	Ser	Cys	Gln	Tyr	Gln	Trp	Pro	Thr	Gln
1				5					10					15	
Ala	His	Arg	Pro	Gly	Arg	Pro	Cys	Ser	Ser	Pro	Ser	Arg	Tyr	Leu	Gln
			20					25					30		
Gly	Arg	Asp	Thr	Ala	Gly	Gly	Lys	Gly	Glu	Gln	Glu	Arg	Ala	Leu	Gln
		35					40					45			
Pro	Gly	Ser	Pro	Glu	Tyr	Glu	Glu	Arg	Trp	Pro	Pro	Ala	Pro		
	50					55					60				

<210> 341

<211> 80

<212> PRT

<213> homo sapiens

<400> 341

Ser	Leu	Leu	Gly	Cys	Cys	Ser	Leu	Ala	Ser	Thr	Asn	Gly	Pro	His	Arg
1				5					10					15	
Leu	Ile	Gly	Gln	Asp	Asp	Leu	Ala	Pro	Val	Leu	His	Val	Ile	Cys	Arg
			20					25					30		
Ala	Glu	Ile	Gln	Leu	Glu	Gly	Arg	Val	Asn	Lys	Lys	Glu	Leu	Ser	Ser
		35					40					45			
Gln	Val	Leu	Arg	Ser	Thr	Lys	Asn	Gly	Gly	Leu	Leu	Pro	Pro	Ser	Gly
	50					55					60				
His	Trp	Gly	Ile	Ser	Arg	Trp	His	Leu	Pro	Leu	Gly	Leu	Glu	Lys	Ser
65					70					75					80

<210> 342

<400> 342

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<210> 343

<400> 343

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<210> 344

<400> 344

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<210> 345

<211> 257

<212> PRT

<213> homo sapiens

<400> 345

Lys 1	Asn	Leu	Ser	Gln 5	Leu	Glu	Pro	Arg	Glu 10	Asn	Ala	Lys	Glu	Glu 15	Val
Arg	Lys	Glu	Arg 20	Gly	Met	Gly	Trp	Val 25	Ala	Ala	Gly	Ala	Ala 30	Gln	Leu
Leu	Ser	Leu 35	Leu	Ser	Thr	Ser	Thr 40	Ala	Ser	Asp	Ser	Ser 45	Val	Ile	Ser
Ser	Ser 50	Ala	Cys	Thr	Ser	Gly 55	Leu	Leu	Pro	Arg	Arg 60	Arg	Ser	Pro	Ala
Ser 65	Pro	Arg	Ser	Ala	His 70	Leu	His	His	Leu	Gly 75	Gly	Leu	Glu	His	Phe 80
His	Leu	Ala	Leu	Ala 85	Asp	Leu	Leu	Asp	Val 90	Glu	Gly	Glu	Gly	Trp 95	His
Leu	Val	Asp	Arg 100	Gly	Leu	Gly	Ala	Arg 105	Val	His	His	Val	Val 110	Gly	Arg
Glu	Gly	Phe 115	Ala	Gln	Leu	Val	Pro 120	Arg	Arg	Leu	Gln	Phe 125	Leu	Ala	Pro
Leu	Gly 130	Gly	His	Gln	Ala	Arg 135	Ala	Gln	Leu	Val	His 140	Ala	Leu	Leu	Gln
Gly 145	Val	Pro	Arg	Leu	Leu 150	Gln	Val	Phe	Leu	Gly 155	Leu	Glu	Ala	Arg	Leu 160
Leu	Gln	Val	Leu	Ala 165	Gly	Thr	His	Leu	Gly 170	Leu	Leu	His	Leu	Leu 175	Leu
Gly	Glu	Gly	Leu 180	Leu	Glu	Val	Val	His 185	Ala	Pro	Gln	Ala	Leu 190	Arg	Leu
Ile	Arg	Ser 195	Ala	Arg	Asp	Ser	Ser 200	Ile	Thr	Ser	Ser	Thr 205	Ser	Thr	Ala
Ser	Ser 210	Asp	Glu	Ser	Ser	Ser 215	Ala	Ala	Ala	Ser	Ser 220	Ser	Gly	Arg	Ser
Pro 225	Ser	Pro	Ser	Ser	Ser 230	Pro	Ser	Phe	Ser	Gly 235	Ser	Ala	Ser	Asp	Ser 240
Phe	Ser	Asp	Leu	Leu 245	Met	Leu	Ser	Leu	Ala 250	Gly	Ser	Phe	Thr	Ser 255	Ser

Trp

<210> 346

<211> 237

<212> PRT

<213> homo sapiens

<400> 346

Lys 1	Ser	Arg	Arg	Arg 5	Cys	Gln	Arg	Arg	Arg 10	Ala	Arg	Ser	Trp	Ala 15	Arg
Ala	Ser	Gly	Pro 20	Arg	Arg	Thr	Gln	Arg 25	Arg	Trp	Ser	Phe	Arg 30	Arg	Thr

Arg	Arg	Trp 35	Arg	Leu	Arg	Arg	Leu 40	Leu	Arg	Ser	Pro	Ala 45	Gln	Ser	Val
Ser	Ser 50	Ala	Gly	Pro	Ala	Ala 55	Arg	Gly	Arg	Leu	Gln 60	Glu	Gly	Leu	Leu
Gln 65	Gly	Glu	Asp	Gly	Glu 70	Asp	Gln	Gly	Ala	Tyr 75	Pro	Arg	Glu	Pro	Gly 80
Glu	Asp	Ala	Pro	Gln 85	Asp	Gln	Gly	Lys	Pro 90	Gly	Glu	Asp	Ala	Ala 95	His
Pro	Gly	Glu	Ala 100	His	Glu	Gln	Ala	Gly 105	His	Ala	Pro	Gly	Ala 110	Arg	Arg
Ala	Ala	Arg 115	Glu	Thr	Glu	Asp	Val 120	Ala	Gly	Gln	Val	Ala 125	Gln	Ile	Leu
His	Ala 130	Arg	Pro	Arg	Gly	Val 135	Arg	Ala	Leu	Gln	Asp 140	Arg	Gly	Leu	Gln
Gly 145	Ala	Thr	Leu	His	Leu 150	Pro	Arg	Gln	Glu	Asp 155	Pro	Arg	Gly	Pro	Gly 160
Gly	Ser	Ala	Gln	Gly 165	His	Arg	Asp	Gly	Gly 170	Gly	Gly	Arg	Ser	Gly 175	Gly
Arg	Pro	Ala	Thr 180	Cys	Gly	Ala	Gly	Ala 185	Ala	Pro	Thr	Cys	Thr 190	Arg	Cys
Trp	Arg	Ser 195	Pro	Arg	Ser	Arg	Thr 200	Pro	Cys	Trp	Trp	Thr 205	Arg	Ala	Thr
Ala	Thr 210	Glu	Arg	Pro	Pro	Leu 215	Pro	Pro	Thr	Pro	Phe 220	Leu	Ala	Pro	Ser
Glu 225	Leu	Pro	Leu	Ser	His 230	Ser	Leu	Ser	Ala	Arg 235	Ala	Gly			

<210> 347

<211> 263

<212> PRT

<213> homo sapiens

<400> 347

Gly 1	Arg	Leu	Pro	Gly 5	Tyr	Pro	Asp	Arg	Arg 10	Gly	Pro	Gly	Ala	Ser 15	Ser
Ala	Gly	Ala	Gln 20	Ala	Ala	Glu	Glu	Pro 25	Ser	Gly	Ala	Gly	Ser 30	Glu	Glu
Leu	Ile	Lys 35	Ser	Asp	Gln	Val	Asn 40	Gly	Val	Leu	Val	Leu 45	Ser	Leu	Leu
Asp	Lys 50	Ile	Ile	Gly	Ala	Val 55	Asp	Gln	Ile	Gln	Leu 60	Thr	Gln	Ala	Gln
Leu 65	Glu	Glu	Arg	Gln	Ala 70	Glu	Met	Glu	Gly	Ala 75	Val	Gln	Ser	Ile	Gln 80
Gly	Glu	Leu	Ser	Lys 85	Leu	Gly	Lys	Ala	His 90	Ala	Thr	Thr	Ser	Asn 95	Thr

Val	Ser	Lys	Leu 100	Leu	Glu	Lys	Val	Arg 105	Lys	Val	Ser	Val	Asn 110	Val	Lys
Thr	Val	Arg 115	Gly	Ser	Leu	Glu	Arg 120	Gln	Ala	Gly	Gln	Ile 125	Lys	Lys	Leu
Glu	Val 130	Asn	Glu	Ala	Glu	Leu 135	Leu	Arg	Arg	Arg	Asn 140	Phe	Lys	Val	Met
Ile 145	Tyr	Gln	Asp	Glu	Val 150	Lys	Leu	Pro	Ala	Lys 155	Leu	Ser	Ile	Ser	Lys 160
Ser	Leu	Lys	Glu	Ser 165	Glu	Ala	Leu	Pro	Glu 170	Lys	Glu	Gly	Glu	Glu	Leu
Gly	Glu	Gly	Glu 180	Arg	Pro	Glu	Glu	Asp 185	Ala	Ala	Ala	Leu	Glu 190	Leu	Ser
Ser	Asp	Glu 195	Ala	Val	Glu	Val	Glu 200	Glu	Val	Ile	Glu	Glu 205	Ser	Arg	Ala
Glu	Arg 210	Ile	Lys	Arg	Arg	Ala 215	Cys	Gly	Ala	Trp	Thr 220	Thr	Ser	Arg	Arg
Pro 225	Ser	Pro	Arg	Arg	Arg 230	Trp	Arg	Arg	Pro	Arg 235	Cys	Val	Pro	Ala	Arg 240
Thr	Trp	Arg	Arg	Arg 245	Ala	Ser	Arg	Pro	Arg 250	Lys	Thr	Trp	Arg	Arg 255	Arg
Gly	Thr	Pro	Trp 260	Arg	Ser	Ala									

<210> 348

<211> 106

<212> PRT

<213> homo sapiens

<400> 348

Ser 1	Ser	Gly	Ser	Ser 5	Arg	Phe	Gly	Ser	Ser 10	Gly	Ser	Arg	Arg	Arg 15	Tyr
Ala	Ser	Leu	Tyr 20	Phe	Cys	Cys	Ala	Ile 25	Glu	Asp	Gln	Asp	Asn 30	Glu	Leu
Ile	Thr	Leu 35	Glu	Ile	Ile	His	Arg 40	Tyr	Val	Glu	Leu	Leu 45	Asp	Lys	Tyr
Phe 50	Gly	Ser	Val	Cys	Glu	Leu 55	Asp	Ile	Ile	Phe	Asn 60	Phe	Glu	Lys	Ala
Tyr 65	Phe	Ile	Leu	Asp	Glu 70	Phe	Leu	Leu	Gly	Gly 75	Glu	Val	Gln	Glu	Thr 80
Ser	Lys	Lys	Asn	Val 85	Leu	Lys	Ala	Ile	Glu 90	Gln	Ala	Asp	Leu	Leu 95	Gln
Glu	Glu	Ala	Glu 100	Thr	Pro	Arg	Ser	Gly 105	Ser						

<210> 349

<211> 78  
 <212> PRT  
 <213> homo sapiens

<400> 349

Leu 1	Phe	Leu	Met	Pro 5	Gln	Asn	Lys	Val	Arg 10	Met	Val	Ile	Cys	Gln 15	Glu
Phe	Phe	Ile	Thr 20	Val	Ser	Tyr	Lys	Lys 25	Arg	Val	Ala	Leu	Phe 30	Thr	Val
Leu	Cys	Val 35	Lys	Ser	Leu	Phe	Lys 40	Ala	Arg	Met	Phe	Pro 45	Leu	Gly	Tyr
Leu 50	Leu	Lys	Leu	Asn	Leu	Phe 55	Cys	Phe	Pro	Pro	Leu 60	Arg	Ser	Ala	Ala
His 65	Phe	Thr	Ala	Ala	Ser 70	Phe	Leu	Ser	Met	Ala 75	Leu	Pro	Ser		

<210> 350  
 <211> 65  
 <212> PRT  
 <213> homo sapiens

<400> 350

Thr 1	Cys	Leu	His	Gly 5	Leu	Tyr	Phe	His	Leu 10	Tyr	Met	Leu	Gly	Trp 15	Ile
Lys	Leu	Cys	Cys 20	Asp	Cys	Asp	Gln	His 25	Ser	Gly	His	Val	Ser 30	Thr	Val
Leu	Ser	His 35	Arg	Gln	Leu	Val	Val 40	Ile	Asn	Val	Gln	Arg 45	Thr	Lys	Lys
Lys 50	Lys	Gly	Ala	Ala	Ser	Leu 55	Gly	Gly	Ile	Thr	Gly 60	Ser	Gly	Val	Lys
Arg 65															

<210> 351  
 <211> 196  
 <212> PRT  
 <213> homo sapiens

<400> 351

Leu 1	Pro	Gly	Leu	Pro 5	Leu	Arg	Gln	Leu	Gly 10	Gly	Val	Cys	His	Gly 15	His
Arg	Pro	Gly	Leu 20	Leu	Leu	His	Gln	Gln 25	His	Gly	Gly	Gly	Ala 30	Gly	Ala
Val	Gln	Gln 35	Pro	Gln	Arg	Glu	Glu 40	Glu	Ala	Leu	His	Asp 45	Pro	Gly	Gln
Gly	Ser 50	Ala	Pro	Ala	Glu	Leu 55	Cys	Gln	Phe	Gln	Gln 60	His	Val	Pro	Arg
Phe	Pro	Leu	Gln	Gln	Pro	Gln	Ala	Val	Gln	Glu	Gly	Gly	Gly	Ala	Gly

65						70						75						80
Ala	Gly	Gln	Gly	Leu	Val	Leu	Trp	Gln	Pro	Gly	Ala	Gly	Leu	Gln	Gly			
				85					90					95				
Val	Gln	Pro	Gly	Asp	Asp	Gly	Ala	Pro	Asp	Leu	Gln	His	Gly	Asp	Ala			
			100					105					110					
Ala	Gly	Asp	Ser	His	His	Asp	Asp	Pro	Ala	Gln	Glu	Leu	Pro	Ala	Ala			
		115					120					125						
Glu	His	Arg	Ala	Gln	Gly	Pro	Gly	Gly	Pro	Arg	Pro	Ala	Leu	Arg	Gly			
	130					135					140							
Gly	Ala	Arg	Ser	Asn	Cys	Arg	Val	Cys	Leu	Val	Gln	Met	Cys	Pro	Glu			
145					150					155					160			
Ala	Pro	Glu	Gly	Ser	His	Gln	Leu	Met	Pro	Ala	Ser	Asp	Pro	Gln	Gln			
				165					170					175				
Gly	Trp	Phe	Ala	Ala	Ala	Ala	Gln	Gly	Glu	Pro	Val	Ser	Asp	Pro	Gly			
			180					185					190					
His	His	His	His															
			195															

<210> 352  
 <211> 361  
 <212> PRT  
 <213> homo sapiens

<400> 352

Ser	Leu	Ala	Ser	Leu	Ser	Asp	Ser	Leu	Gly	Val	Ser	Val	Met	Ala	Thr
1				5					10				15		
Asp	Gln	Asp	Ser	Tyr	Ser	Thr	Ser	Ser	Thr	Glu	Glu	Glu	Leu	Glu	Gln
			20					25					30		
Phe	Ser	Ser	Pro	Ser	Val	Lys	Lys	Lys	Pro	Ser	Met	Ile	Leu	Gly	Lys
		35					40					45			
Ala	Arg	His	Arg	Leu	Ser	Phe	Ala	Ser	Phe	Ser	Ser	Met	Phe	His	Ala
	50					55					60				
Phe	Leu	Ser	Asn	Asn	Arg	Lys	Leu	Tyr	Lys	Lys	Val	Val	Glu	Leu	Ala
65					70				75						80
Gln	Asp	Lys	Gly	Ser	Tyr	Phe	Gly	Ser	Leu	Val	Gln	Asp	Tyr	Lys	Val
				85					90					95	
Tyr	Ser	Leu	Glu	Met	Met	Ala	Arg	Gln	Thr	Ser	Ser	Thr	Glu	Met	Leu
			100					105					110		
Gln	Glu	Ile	Arg	Thr	Met	Met	Thr	Gln	Leu	Lys	Ser	Tyr	Leu	Leu	Gln
		115					120					125			
Ser	Thr	Glu	Leu	Lys	Ala	Leu	Val	Asp	Pro	Ala	Leu	His	Ser	Glu	Glu
	130					135					140				
Glu	Leu	Glu	Ala	Ile	Val	Glu	Ser	Ala	Leu	Tyr	Lys	Cys	Val	Leu	Lys
145					150					155					160

Pro	Leu	Lys	Glu	Ala 165	Ile	Asn	Ser	Cys	Leu 170	His	Gln	Ile	His	Ser 175	Lys
Asp	Gly	Ser	Leu 180	Gln	Gln	Leu	Lys	Glu 185	Asn	Gln	Leu	Val	Ile 190	Leu	Ala
Thr	Thr	Thr 195	Thr	Asp	Leu	Gly	Val 200	Thr	Thr	Ser	Val	Pro 205	Glu	Val	Pro
Met	Met 210	Glu	Lys	Ile	Leu	Gln 215	Lys	Phe	Thr	Ser	Met 220	His	Lys	Ala	Tyr
Ser 225	Pro	Glu	Lys	Lys	Ile 230	Ser	Ile	Leu	Leu	Lys 235	Thr	Cys	Lys	Leu	Ile 240
Tyr	Asp	Ser	Met	Ala 245	Leu	Gly	Asn	Pro	Gly 250	Lys	Pro	Tyr	Gly	Ala 255	Asp
Asp	Phe	Leu	Pro 260	Val	Leu	Met	Tyr	Val 265	Leu	Ala	Arg	Ser	Asn 270	Leu	Thr
Glu	Met	Leu 275	Leu	Asn	Val	Glu	Tyr 280	Met	Met	Glu	Leu	Met 285	Asp	Pro	Ala
Leu	Gln 290	Leu	Gly	Glu	Gly	Ser 295	Tyr	Tyr	Leu	Thr	Thr 300	Thr	Tyr	Gly	Ala
Leu 305	Glu	His	Ile	Lys	Ser 310	Tyr	Asp	Lys	Ile	Thr 315	Val	Thr	Arg	Gln	Leu 320
Ser	Val	Glu	Val	Gln 325	Asp	Ser	Ile	His	Arg 330	Trp	Glu	Arg	Arg	Arg 335	Thr
Leu	Asn	Lys	Ala 340	Arg	Ala	Ser	Arg	Ser 345	Ser	Val	Gln	Pro	Leu 350	His	Leu
Arg	Val	Val 355	Pro	Gly	Ala	Arg	Ala 360	Ala							

<210> 353

<211> 161

<212> PRT

<213> homo sapiens

<400> 353

Val 1	Asp	Gly	Phe	Leu 5	Gln	Gly	Leu	Gln	Asp 10	Thr	Phe	Val	Gln	Gly 15	Arg
Leu	Tyr	Asn	Cys 20	Phe	Glu	Leu	Leu	Leu 25	Gly	Val	Gln	Gly	Gly 30	Val	His
Gln	Gly	Leu 35	Glu	Leu	Gly	Ala	Leu 40	Gln	Gln	Val	Ala	Leu 45	Glu	Leu	Gly
His	His 50	Gly	Ala	Asn	Leu	Leu 55	Gln	His	Leu	Arg	Ala 60	Gly	Gly	Leu	Ala
Arg 65	His	His	Leu	Gln	Ala 70	Val	His	Leu	Val	Val 75	Leu	His	Gln	Ala	Ala 80
Lys	Val	Arg	Ala	Leu 85	Val	Leu	Arg	Gln	Leu 90	His	His	Leu	Leu	Val 95	Gln





<210> 355  
 <211> 253  
 <212> PRT  
 <213> homo sapiens

<400> 355

Ala 1	Gly	Glu	Gly	Val 5	Asp	Gly	Leu	Thr	Gln 10	Glu	Thr	Pro	Leu	Lys 15	Pro
Val	Ser	Gln	Leu 20	Pro	Gly	Pro	Ala	Gly 25	Ala	Pro	Thr	Gly	Arg 30	Arg	Gly
Gln	Ala	Glu 35	Asp	Pro	Gly	Ser	Val 40	Met	Ala	Ser	Ala	Leu 45	Arg	Pro	Pro
Arg	Val 50	Pro	Lys	Pro	Lys	Gly 55	Val	Leu	Pro	Ser	His 60	Tyr	Tyr	Glu	Ser
Phe 65	Leu	Glu	Lys	Lys	Gly 70	Pro	Cys	Asp	Arg	Asp 75	Tyr	Lys	Lys	Phe	Trp 80
Ala	Gly	Leu	Gln	Gly 85	Leu	Thr	Ile	Tyr	Phe 90	Tyr	Asn	Ser	Asn	Arg 95	Asp
Phe	Gln	His	Val 100	Glu	Lys	Leu	Asn	Leu 105	Gly	Ala	Phe	Glu	Lys 110	Leu	Thr
Asp	Glu	Ile 115	Pro	Trp	Gly	Ser	Ser 120	Arg	Asp	Pro	Gly	Thr 125	His	Phe	Ser
Leu	Ile 130	Leu	Arg	Asn	Gln	Glu 135	Ile	Lys	Phe	Lys	Val 140	Glu	Thr	Leu	Glu
Cys 145	Arg	Glu	Met	Trp	Lys 150	Gly	Phe	Ile	Leu	Thr 155	Val	Val	Glu	Leu	Arg 160
Val	Pro	Thr	Asp	Leu 165	Thr	Leu	Leu	Pro	Gly 170	His	Leu	Tyr	Met	Met 175	Ser
Glu	Val	Leu	Ala 180	Lys	Glu	Glu	Ala	Arg 185	Arg	Ala	Leu	Glu	Thr 190	Pro	Ser
Cys	Phe	Leu 195	Lys	Val	Ser	Arg	Leu 200	Glu	Ala	Gln	Leu	Leu 205	Leu	Glu	Arg
Tyr	Pro 210	Glu	Cys	Gly	Asn	Leu 215	Leu	Leu	Arg	Pro	Ser 220	Gly	Asp	Gly	Ala
Asp 225	Gly	Val	Gly	His	His 230	Ala	Ala	Asp	Ala	Gln 235	Arg	Asp	Ala	Arg	Gly 240
Pro	Ala	Leu	Gln	Gly 245	Glu	Ala	Gly	Gly	Ala 250	Pro	Ser	Thr			

<210> 356  
 <211> 118  
 <212> PRT  
 <213> homo sapiens

<400> 356

Leu 1	Thr	Thr	Ala	Ser 5	Arg	Glu	Val	Gln	Glu 10	Asn	Gly	Cys	Ser	Thr 15	Ser
Ile	Thr	Tyr	Leu 20	Gly	Pro	Leu	Pro	Leu 25	His	Leu	Val	Met	Pro 30	Asp	His
Val	Arg	Pro 35	Val	Val	His	Leu	Pro 40	Arg	Gly	Asp	Arg	His 45	Arg	Arg	Arg
Arg	Pro 50	Arg	Trp	Ala	Ala	Ala 55	Ala	Gly	Ser	Arg	Thr 60	Arg	Gly	Ser	Ala
Pro 65	Gly	Ala	Val	Val	Pro 70	Pro	Ala	Gly	Ser	Pro 75	Ser	Gly	Ser	Thr	Arg 80
Val	Ser	Pro	Val	His 85	Gly	Ala	Pro	Pro	Leu 90	Trp	Pro	Arg	Leu	Gln 95	Thr
Ser	Cys	Ile	Gly 100	Ala	Gln	Glu	Ala	Gly 105	Ser	Ser	Arg	Ser	Gly 110	His	Gly
Ala	Pro	Pro 115	Pro	Leu	Arg										

<210> 357

<211> 223

<212> PRT

<213> homo sapiens

<400> 357

Asp 1	His	Thr	Cys	Gly 5	Cys	Ala	Gly	Asn	Leu 10	Gln	Glu	Ala	Ile	Met 15	Leu
Arg	Ser	Gly	Val 20	Thr	Ser	Gln	Gly	Ile 25	His	Pro	Gly	Ser	Pro 30	Trp	Cys
Cys	Thr	Pro 35	Thr	Gln	Ala	Glu	Leu 40	Ile	Val	Gly	Asp	Gln 45	Ser	Gly	Ala
Ile 50	His	Ile	Trp	Asp	Leu	Lys 55	Thr	Asp	His	Asn	Glu 60	Gln	Leu	Ile	Pro
Glu 65	Pro	Glu	Val	Ser	Ile 70	Thr	Ser	Ala	His	Ile 75	Asp	Pro	Asp	Ala	Ser 80
Tyr	Met	Ala	Ala	Val 85	Asn	Ser	Thr	Gly	Asn 90	Cys	Tyr	Val	Trp	Asn 95	Leu
Thr	Gly	Gly	Ile 100	Gly	Asp	Glu	Val	Thr 105	Gln	Leu	Ile	Pro	Lys 110	Thr	Lys
Ile	Pro	Ala 115	His	Thr	Arg	Tyr	Ala 120	Leu	Gln	Cys	Arg	Phe 125	Ser	Pro	Asp
Ser	Thr 130	Leu	Leu	Ala	Thr	Cys 135	Ser	Ala	Asp	Gln	Thr 140	Cys	Lys	Ile	Trp
Arg 145	Thr	Ser	Asn	Phe	Ser 150	Leu	Met	Thr	Glu	Leu 155	Ser	Ile	Lys	Ser	Gly 160
Asn	Pro	Gly	Glu	Ser 165	Ser	Arg	Gly	Trp	Met 170	Trp	Gly	Cys	Ala	Phe 175	Ser

Gly	Asp	Ser	Gln	Tyr	Ile	Val	Thr	Ala	Ser	Ser	Asp	Asn	Leu	Ala	Arg
			180					185					190		
Leu	Trp	Cys	Val	Glu	Thr	Gly	Glu	Ile	Lys	Arg	Glu	Tyr	Gly	Gly	His
		195					200					205			
Gln	Lys	Ala	Val	Val	Cys	Leu	Ala	Phe	Asn	Asp	Ser	Val	Leu	Gly	
	210					215					220				

<210> 358  
 <211> 193  
 <212> PRT  
 <213> homo sapiens

<400> 358

Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Pro	Glu	Gln	His	Leu	Arg	Val
1				5					10					15	
Gly	Leu	Leu	Leu	Leu	Pro	Pro	Arg	Leu	Ser	Pro	Arg	Pro	Gly	Pro	Ala
			20					25					30		
Trp	Pro	Val	Pro	Asn	Pro	Val	Gly	Trp	Pro	Gly	His	Leu	His	Gln	Gly
		35					40					45			
Gly	Gln	Leu	Leu	Ala	Gly	Thr	Asn	Lys	Pro	Phe	His	Leu	Ala	Met	Val
	50					55					60				
Val	Val	Phe	Ser	Met	Asp	Arg	Gly	Pro	Glu	Thr	Arg	Ala	Gly	Arg	Gly
	65				70					75					80
Arg	Glu	His	Thr	Ser	Leu	Gly	Val	Gly	Thr	Ser	Leu	Arg	Pro	Leu	Ser
				85					90					95	
Ser	Phe	Gly	Pro	Ser	Ala	Asp	Phe	Pro	Arg	Gln	Cys	Arg	Leu	Ala	Gln
			100					105					110		
Ser	Arg	Ser	Val	Gln	Pro	Gly	Leu	Gly	Arg	Ala	Leu	Ser	His	Leu	Asp
		115					120					125			
Lys	Gln	Leu	Gly	Ala	Glu	Ser	Pro	Arg	Ala	Ala	Trp	Pro	Ser	Arg	Ser
	130					135					140				
Arg	Arg	His	Arg	Gly	Pro	Ser	Gly	Pro	Val	Ala	Gln	Ala	Gly	Arg	Gly
	145				150					155					160
Gly	Ser	Ala	Leu	Thr	Trp	Val	Leu	His	Gly	Ser	Leu	Gln	Leu	Pro	Pro
				165					170					175	
Pro	Ala	Pro	Gly	Ser	Pro	Glu	Gly	Ser	Gln	Ala	Ser	Pro	Ala	His	Cys
			180					185					190		

His

<210> 359  
 <211> 251  
 <212> PRT  
 <213> homo sapiens

<400> 359

Pro	Gly	Cys	Cys	Met	Gly	Pro	Ser	Ser	Cys	His	His	Leu	His	Gln	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1			5			10			15						
Val	Pro	Arg	Gly 20	His	Arg	Leu	Ala	Gln 25	His	Thr	Val	Ile	Glu 30	Gly	Gln
Ala	Asp	Asn 35	Ser	Leu	Leu	Val	Ala 40	Ala	Ile	Leu	Ser	Leu 45	Asp	Leu	Ser
Ser	Leu 50	His	Thr	Pro	Glu	Pro 55	Gly	Gln	Val	Val	Arg 60	Gly	Ser	Ser	Asp
Asp 65	Val	Leu	Gly	Val	Pro 70	Arg	Glu	Gly	Ala	Ala 75	Pro	His	Pro	Ala	Ala 80
Gly	Gly	Leu	Pro	Gly 85	Val	Ala	Ala	Leu	Asp 90	Ala	Gln	Leu	Arg	His 95	Gln
Gly	Glu	Val	Gly 100	Arg	Pro	Pro	Asp	Leu 105	Ala	Arg	Leu	Ile	Ser 110	Arg	Ala
Gly	Gly	Glu 115	Glu	Arg	Gly	Val	Gly 120	Ala	Glu	Ala	Thr	Leu 125	Gln	Gly	Val
Ala	Arg 130	Val	Gly	Arg	Asp	Leu 135	Ser	Leu	Gly	Asp	Glu 140	Leu	Gly	His	Leu
Val 145	Thr	Asn	Ala	Pro	Arg 150	Gln	Ile	Pro	Asp	Ile 155	Ala	Val	Ser	Gly	Ala 160
Ile	Asp	Ser	Cys	His 165	Val	Ala	Gly	Val	Gly 170	Ile	Asp	Val	Gly	Gly 175	Arg
Asp	Gly	Asp	Leu 180	Gly	Leu	Arg	Asp	Gln 185	Leu	Leu	Val	Val	Val 190	Cys	Phe
Gln	Val	Pro 195	Asp	Val	Asp	Ser	Pro 200	Ala	Leu	Val	Thr	His 205	Asp	Glu	Leu
Cys	Leu 210	Gly	Trp	Gly	Ala	Ala 215	Pro	Gly	Thr	Pro	Arg 220	Val	Asn	Ala	Leu
Gly 225	Gly	His	Thr	Gly	Pro 230	Gln	His	Asp	Cys	Phe 235	Leu	Gln	Val	Thr	Ser 240
Thr	Ser	Ala	Cys	Met 245	Ile	Leu	Thr	Ser	Ser 250	Cys					

<210> 360

<211> 50

<212> PRT

<213> homo sapiens

<400> 360

Gly 1	Asn	Ile	Pro	His 5	Ser	Asn	Leu	Thr	Asp 10	Ala	Ser	Ser	Pro	Lys 15	Arg
Ile	Lys	Ile	Val 20	Ala	Cys	Thr	Asp	Gln 25	Glu	Asn	Ile	Leu	Gly 30	Arg	Met
Lys	Tyr	Val 35	Cys	Leu	Phe	Phe	Phe 40	Lys	Asn	Lys	Gly	Phe 45	Trp	Asn	Ser

Gly Glu  
50

<210> 361  
<211> 59  
<212> PRT  
<213> homo sapiens

<400> 361

Lys	Gly	Asn	Gln	Leu	Tyr	Gln	Gly	Glu	Thr	Arg	Ala	Leu	Gly	Thr	Met
1				5					10					15	
Thr	Thr	Arg	Thr	Ala	Phe	Ile	Leu	His	His	Ser	Asp	Cys	Phe	Gln	Ser
			20					25					30		
Ser	Asn	Asp	Cys	Gln	Ala	Thr	Ser	Gln	Met	Thr	Asp	Asn	Phe	Cys	Cys
		35					40					45			
Ser	Phe	Leu	Tyr	Lys	Met	Leu	Arg	Gln	Gln	Ala					
	50					55									

<210> 362  
<211> 67  
<212> PRT  
<213> homo sapiens

<400> 362

Asp	Lys	Ile	Leu	Leu	Ser	Pro	Arg	Met	Glu	Cys	Ser	Gly	Met	Ile	Met
1				5					10					15	
Ala	His	Cys	Ser	Leu	Asp	Leu	Pro	Gly	Ser	His	Leu	Ser	Leu	Pro	Ser
			20					25					30		
Ser	Trp	Asp	His	Arg	His	Val	Pro	Pro	Cys	Pro	Ala	Asn	Phe	Tyr	Phe
		35					40					45			
Gly	Arg	Asp	Lys	Val	Ser	Pro	Cys	Cys	Leu	Gly	Arg	Phe	Gln	Thr	Pro
	50					55					60				
Gly	Leu	Lys													
65															

<210> 363  
<211> 84  
<212> PRT  
<213> homo sapiens

<400> 363

Met	Arg	Arg	Cys	Ile	His	Pro	Ser	His	Ser	Leu	Ser	Gly	Ser	Arg	Gln
1				5					10					15	
Thr	Gln	Ser	Pro	Leu	Ser	His	Ser	Ala	Ser	Asn	Gly	Ser	Thr	Thr	Lys
			20					25					30		
Val	Ala	Gln	Gln	Met	Arg	Arg	Ala	Ala	Ala	Val	Val	Gly	Glu	Ser	Thr
		35					40					45			
Glu	Glu	Thr	Arg	Leu	Gly	Arg	Ala	Leu	Gly	Ala	Ala	Gly	Phe	Thr	Asn
	50					55					60				

Lys	Gln	Leu	Ser	Glu	Asn	Thr	Ala	Gln	Gly	Glu	Glu	Lys	Arg	Val	Met
65					70					75					80

Cys	Leu	Gln	Asn
-----	-----	-----	-----

<210> 364

<211> 127

<212> PRT

<213> homo sapiens

<400> 364

Cys	Ala	Tyr	Arg	Thr	Glu	Lys	Trp	Lys	Ser	His	Thr	Val	Pro	Cys	Ser
1				5					10					15	
Pro	Glu	Val	Lys	Leu	Val	Leu	Thr	Leu	Ala	Leu	Arg	Ala	Phe	Ser	Ser
			20					25					30		
Met	Glu	Pro	Leu	Gly	Leu	Gly	Arg	Lys	Ala	Arg	Val	Ser	Ala	His	Arg
		35					40					45			
His	Thr	Ser	Tyr	Leu	Gln	Asp	Ile	Asp	Cys	Leu	Cys	Arg	Gly	Ser	Thr
	50					55					60				
Gly	Gln	Pro	Thr	Ala	Asn	Thr	Ala	Ala	Ser	Leu	Val	Ser	Ala	Ser	Leu
65					70					75					80
Leu	Pro	Val	His	Pro	Gly	Asp	Tyr	Ser	Trp	Ile	Asn	Leu	Pro	Lys	Asn
				85					90					95	
Ser	Ala	Phe	Ile	Met	Ser	Leu	Phe	Cys	Ser	Lys	Thr	Gln	Asn	Gly	Ser
			100					105					110		
Leu	Pro	Pro	Arg	Gly	Arg	Pro	Ser	His	His	Cys	Ile	Pro	Asn	Arg	
		115					120					125			

<210> 365

<211> 114

<212> PRT

<213> homo sapiens

<400> 365

Pro	Tyr	Val	His	Ser	Pro	Ala	Trp	Ser	Pro	Trp	Gly	Leu	Val	Gly	Arg
1				5					10					15	
Leu	Val	Ser	Val	His	Thr	Asp	Ile	Pro	Ala	Thr	Phe	Arg	Thr	Leu	Ile
			20					25					30		
Val	Ser	Ala	Glu	Val	Ala	Leu	Gly	Ser	Gln	Leu	Gln	Thr	Gln	Gln	Pro
		35					40					45			
Pro	Trp	Phe	Gln	Leu	Leu	Ser	Phe	Gln	Tyr	Ile	Leu	Glu	Thr	Thr	Pro
	50					55					60				
Gly	Leu	Ile	Phe	Leu	Arg	Thr	Gln	His	Ser	Leu	Cys	His	Phe	Ser	Val
65					70					75					80
Arg	Lys	Pro	Lys	Met	Ala	Pro	Cys	His	Leu	Glu	Ala	Asp	Gln	Val	Ile
				85					90					95	
Thr	Val	Ser	Pro	Thr	Ala	Ser	Thr	Val	Cys	Ile	Trp	Tyr	Ile	Val	Gln
			100					105					110		

Ala Pro

<210> 366

<211> 30

<212> PRT

<213> homo sapiens

<400> 366

Asn	Leu	His	Ser	Asn	Ile	Lys	Val	Phe	Phe	Tyr	Asn	Val	Pro	Lys	Ile
1				5					10					15	

Ser	Gly	Pro	Gln	Gln	Ala	Val	Phe	Val	Pro	Val	Phe	Phe	Asn		
			20					25					30		

<210> 367

<211> 44

<212> PRT

<213> homo sapiens

<400> 367

Lys	Glu	Cys	Met	Ser	Glu	Ala	Gln	Phe	Leu	Ala	Thr	Thr	Leu	Thr	Lys
1				5					10					15	

Gly	Asn	Asn	Cys	Arg	Gly	Ile	Leu	Gln	Leu	Ile	His	Thr	Gln	His	Leu
			20					25					30		

Leu	His	Thr	Val	Phe	Thr	Asp	Ser	Asn	Leu	Val	Gly				
		35					40								

<210> 368

<211> 34

<212> PRT

<213> homo sapiens

<400> 368

Asn	Val	Asp	Phe	Arg	Cys	Lys	Asn	Met	Leu	Glu	Ile	Arg	Phe	Ser	Ala
1				5					10					15	

Ile	Lys	Pro	Asn	Thr	Lys	Lys	Ile	Lys	Lys	Asn	Val	Cys	Gln	Lys	Pro
			20					25					30		

Asn Ser

<210> 369

<211> 147

<212> PRT

<213> homo sapiens

<400> 369

Gln	Pro	Ser	Ser	Leu	Leu	His	His	Cys	Pro	Tyr	Pro	Tyr	Pro	Pro	Arg
1				5					10					15	

His	Leu	Leu	Ala	Thr	Pro	Leu	Leu	Lys	Pro	Gln	Leu	Leu	Ala	Gly	Ser
			20					25					30		

Pro	Ala	His	Ala	Ser	Leu	Ile	Ser	Phe	Leu	Ala	Ser	Pro	Gln	Arg	Ala
		35					40					45			

Ser	Arg	Gln	His	Gly	Gly	Pro	Ser	Gln	Arg	Ala	Gly	Thr	Leu	Ser	Cys	
	50					55					60					
Pro	Leu	Val	Glu	Leu	Gly	Gly	Ser	Ser	Gly	Gly	Arg	Gly	Leu	Cys	His	
65					70					75					80	
Gly	Ser	Ala	Asp	Pro	Thr	Asn	Arg	Ala	Ala	Glu	Pro	Gln	Glu	Arg	Gly	
				85					90					95		
Glu	Pro	Ala	Ala	Gly	Asp	Arg	Arg	Pro	Leu	Pro	Glu	Trp	Gly	Arg	Val	
			100					105					110			
Ser	Leu	Ala	Glu	Ser	Pro	Gly	Ala	Glu	Phe	Arg	Cys	Pro	Gly	Ser	Leu	
		115					120					125				
Gly	Glu	Trp	Gly	Glu	Ile	Pro	Glu	Lys	Glu	Ser	Ser	Ala	His	Pro	Lys	
	130					135					140					
Thr	Glu	Glu														
145																

<210> 370

<211> 244

<212> PRT

<213> homo sapiens

<400> 370

Asn	His	Ser	Cys	Trp	Gln	Gly	Pro	Gln	Leu	Met	Pro	Ala	Ser	Ser	Pro	
1				5					10					15		
Phe	Leu	Leu	Ala	Pro	Lys	Gly	Pro	Pro	Gly	Asn	Met	Gly	Gly	Pro	Val	
			20					25					30			
Arg	Glu	Pro	Ala	Leu	Ser	Val	Ala	Leu	Trp	Leu	Ser	Trp	Gly	Ala	Ala	
		35					40					45				
Leu	Gly	Ala	Val	Ala	Cys	Ala	Met	Ala	Leu	Leu	Thr	Gln	Gln	Thr	Glu	
	50					55					60					
Leu	Gln	Ser	Leu	Arg	Arg	Glu	Val	Ser	Arg	Leu	Gln	Gly	Thr	Gly	Gly	
65					70					75					80	
Pro	Ser	Gln	Asn	Gly	Glu	Gly	Tyr	Pro	Trp	Gln	Ser	Leu	Pro	Glu	Gln	
				85					90					95		
Ser	Ser	Asp	Ala	Leu	Glu	Ala	Trp	Glu	Ser	Gly	Glu	Arg	Ser	Arg	Lys	
			100					105					110			
Arg	Arg	Ala	Val	Leu	Thr	Gln	Lys	Gln	Lys	Asn	Asp	Ser	Asp	Val	Thr	
		115					120					125				
Glu	Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala	
	130					135					140					
Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu	Tyr	
145					150					155					160	
Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln	Val	Val	
				165					170					175		
Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg	Cys	Ile	Arg	
			180					185					190			



Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser	Cys	Tyr	Ser	Ala
		195					200					205			
Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu	Ser	Val	Ile	Ile	Pro
	210					215					220				
Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro	His	Gly	Thr	Phe	Leu	Gly
225					230					235					240
Phe	Val	Lys	Leu												

<210> 371  
 <211> 185  
 <212> PRT  
 <213> homo sapiens

<400> 371

Thr	Pro	Ala	Ser	Trp	Ile	Arg	Thr	Pro	Tyr	Pro	Trp	Ala	Cys	Arg	Pro
1				5					10					15	
Leu	Pro	Arg	Leu	Arg	Ala	Gly	Cys	His	Ile	Thr	Ser	Val	Thr	Ser	Glu
			20					25					30		
Ser	Phe	Phe	Cys	Phe	Trp	Val	Ser	Thr	Ala	Leu	Leu	Phe	Arg	Asp	Leu
		35					40					45			
Ser	Pro	Leu	Ser	Gln	Ala	Ser	Arg	Ala	Ser	Glu	Leu	Cys	Ser	Gly	Arg
	50					55					60				
Leu	Cys	Gln	Gly	Tyr	Pro	Ser	Pro	Phe	Trp	Glu	Gly	Pro	Pro	Val	Pro
65					70					75					80
Cys	Ser	Arg	Leu	Thr	Ser	Leu	Leu	Arg	Leu	Cys	Ser	Ser	Val	Cys	Trp
				85					90					95	
Val	Ser	Arg	Ala	Met	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Ala	Pro	Gln
			100					105					110		
Leu	Asn	Gln	Arg	Ala	Thr	Glu	Ser	Ala	Gly	Ser	Leu	Thr	Gly	Pro	Pro
		115					120					125			
Met	Leu	Pro	Gly	Gly	Pro	Leu	Gly	Ala	Ser	Lys	Lys	Gly	Asp	Glu	Ala
	130					135					140				
Gly	Met	Ser	Trp	Gly	Pro	Cys	Gln	Gln	Leu	Trp	Phe	Gln	Glu	Trp	Gly
145					150					155					160
Ser	Lys	Glu	Val	Ala	Gly	Arg	Val	Arg	Val	Arg	Ala	Val	Val	Gln	Lys
				165					170					175	
Gly	Arg	Arg	Leu	Leu	Arg	Lys	Glu	Lys							
			180					185							

<210> 372  
 <211> 148  
 <212> PRT  
 <213> homo sapiens

<400> 372

Val	Leu	Tyr	His	Cys	Ala	Ser	Arg	Tyr	Arg	Arg	Arg	Ala	Arg	Gln	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



<210> 374  
 <211> 152  
 <212> PRT  
 <213> homo sapiens

<400> 374

Ile 1	Pro	Cys	Leu	Leu 5	Cys	Val	Ser	Arg	Gly 10	Lys	Gly	Gln	Arg	Gln 15	Lys
Thr	Asp	Ser	Leu 20	Val	Val	Leu	Ser	Asn 25	Asn	Ala	Val	Gly	Leu 30	Pro	Phe
Gly	Val	Cys 35	His	Asp	Asn	Asp	Thr 40	Pro	Gly	Gly	Asn	Ala 45	Glu	Ala	Asp
Asp	His 50	Leu	Arg	Asn	Gly	Pro 55	Trp	Thr	Arg	Gly	Val 60	Ser	His	Leu	His
Gly 65	Leu	Pro	Cys	His	Pro 70	Val	His	Val	Pro	Ala 75	Arg	Pro	His	Gln	Pro 80
Gln	Pro	Arg	Lys	His 85	Ala	Thr	Ala	Pro	Ala 90	Gly	Leu	Gln	Gln	Ala 95	Val
Phe	Cys	Trp	Gly 100	Gly	Arg	Arg	Ser	Gly 105	Cys	Ser	Trp	Gly	Arg 110	Arg	Phe
Gly	Gly	Arg 115	Gly	Gly	Gly	Thr	Gly 120	Arg	Arg	Ser	Asp	Ile 125	Gly	Leu	Lys
Arg	Leu 130	Gly	Gln	Pro	Arg	Pro 135	His	Ala	Leu	Glu	Leu 140	Gly	Leu	Asn	Leu
Gly 145	Arg	Leu	Trp	Phe	Lys 150	Leu	Ala								

<210> 375  
 <211> 107  
 <212> PRT  
 <213> homo sapiens

<400> 375

Gly 1	Ala	Glu	Leu	Gln 5	Leu	Arg	Ser	Cys	Ala 10	Met	Ala	Val	Ser	Gln 15	Glu
Gly	Leu	Asp	Gly 20	Glu	Val	Lys	Ala	Pro 25	Asp	Ala	Arg	Ile	Phe 30	Ile	Pro
Cys	Ala	Asn 35	Thr	Ala	Phe	Thr	Pro 40	Asp	Leu	Gln	Val	Leu 45	Gln	Gln	Val
Leu	Ser 50	Ser	Phe	Thr	Val	Ser 55	Ser	Pro	Leu	Phe	His 60	Ser	Gly	Phe	Ile
Cys 65	Tyr	Thr	Pro	Asn	Leu 70	Phe	Ser	Gln	Ser	Thr 75	Pro	Gln	Ser	Leu	Pro 80
Cys	Trp	Gly	Gln	His 85	Arg	Lys	Arg	Gln	Asn 90	Leu	Arg	Lys	Glu	Lys 95	Gly
Asn	Leu	Gln	Pro	Ala	Met	Asp	Leu	Met	Ile	Pro					

100

105

<210> 376  
 <211> 113  
 <212> PRT  
 <213> homo sapiens

<400> 376

Ile 1	Pro	Lys	Asn	Phe 5	Tyr	His	Asn	Ile	His 10	Arg	Ser	Leu	Tyr	Gln 15	Leu
Tyr	Leu	Glu	Val 20	Lys	Gln	Ala	Trp	Glu 25	Ser	Ile	Asp	Cys	Ser 30	Ala	Cys
Pro	Arg	Val 35	Glu	Ala	Leu	Asn	Lys 40	Ala	Thr	Lys	Thr	Pro 45	Glu	Ile	Thr
Asp	Leu 50	Thr	Phe	Gln	Trp	Pro 55	Thr	Gly	Pro	Gly	Ser 60	Gly	Gln	Val	Gly
His 65	Gln	Ala	Asn	His	Leu 70	Phe	Pro	Cys	Ala	Ser 75	Leu	Cys	Lys	Ser	Trp 80
Ser	Val	Pro	Leu	Ala 85	Arg	Pro	Ser	Leu	Val 90	Gln	Asp	Leu	Gly	Pro 95	Gln
Thr	Lys	Glu	Ser 100	Arg	Gly	Leu	Gly	Phe 105	Pro	Asp	Pro	Arg	Met 110	Val	Ser
Leu															

<210> 377  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 377

Phe 1	Gly	Gly	Pro	Gln 5	Ala	Gln	Pro	His	Ser 10	Ala	Val	Gly	Ser	Ser 15	Leu
Ser	Ser	Gln	Ile 20	Gln	Val	Asn	Leu	Ser 25	Phe	Lys	Asn	Lys	Gly 30	Glu	Pro
Gln	Thr	Cys 35	Ser	Thr	Thr	Arg	Asp 40	Asn	Asn	Thr	Pro	Trp 45	Gln	Glu	Asp
His 50	Val	Leu	Asp	Cys	Leu	Arg 55	Thr	Ala	Thr	Val	Arg 60	Gln	Glu	Ala	Cys
Cys 65	Asp	Pro	Leu	Cys	Ser 70	Met	Pro	Ile	Ala	Gln 75	Ala	Ser	Ser	Ile	Pro 80
Tyr	His	Leu	Pro	Pro 85	Met	Leu	Phe	Phe	Gly 90	Thr	Thr	Thr	Leu	Ala 95	Lys
Arg	Glu	Tyr	Gly 100	Lys	Gln	Arg	Pro	Arg 105	Ala	Leu	Leu	Gln	Tyr 110	Arg	His
Phe	Glu	Val 115	Gly	Arg	Gln	His	Met 120	Leu	His	Ser	Lys				

<210> 378  
 <211> 66  
 <212> PRT  
 <213> homo sapiens

<400> 378

His 1	Lys	Ile	Ile	Leu 5	Ile	Ser	Arg	Tyr	Arg 10	Arg	Asn	Ser	Val	Val 15	Thr
Cys	Gln	Ala	Ile 20	Leu	Tyr	Thr	Pro	Met 25	Ile	Leu	Gln	Arg	Lys 30	His	Pro
Ser	Leu	Leu 35	Leu	Pro	Leu	Leu	Trp 40	Gln	Leu	Lys	Cys	Ile 45	Cys	Ser	Ser
Thr	Leu 50	Lys	Arg	Arg	Lys	Arg 55	Asn	Asn	Leu	Ser	Leu 60	Ile	Pro	Lys	Leu
Pro 65	His														

<210> 379  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 379

Pro 1	Glu	Lys	Ser	Pro 5	Gly	Ala	Gly	Pro	Leu 10	Leu	Gly	Gly	Ser	Pro 15	Phe
Phe	Phe	Phe	Phe 20	Tyr	Val	Ser	Lys	Ser 25	Thr	Glu	Phe	Ile	Leu 30	Lys	His
Ser	Ile	Lys 35	Phe	Glu	Ser	His	Glu 40	Thr	Lys	Ala	Ser	Leu 45	His	Tyr	Met
Leu	Ile 50	Leu	Ala	Lys	Ser	Lys 55	Asp	Gln	His	Thr	Ile 60	Asp	Ile	His	Asp
Asn 65	Val	Val													

<210> 380  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 380

Phe 1	Cys	Ile	His	Phe 5	Glu	Cys	Leu	His	Val 10	Lys	Thr	Gln	Leu	Ile 15	Tyr
Tyr	Phe	Asn	Ile 20	Lys	Pro	Ile	Ser	Phe 25	Glu	Ala	Lys	Leu	Ile 30	Leu	Leu
Phe	Tyr	Lys 35	Ser	Asn	Gly	Asp	Ser 40	Phe	Phe	Arg	Met	Leu 45	Lys	Ala	Gln
Cys	Leu 50	Arg	Phe	Met	Leu	Ala 55	Ala	Leu	Leu	Ala	Leu 60	Leu	Leu	Pro	Glu

Met Lys Thr Lys Gln Asn Arg  
65 70

<210> 381  
<211> 107  
<212> PRT  
<213> homo sapiens

<400> 381

Met	Asp	Gly	Ala	Gln	Gly	Arg	Leu	Leu	Pro	Val	Ser	Ser	Arg	His	Ser
1				5					10					15	
Asn	Leu	Ala	Leu	Leu	Lys	Pro	Thr	Ser	Arg	Asp	Leu	Thr	Ala	Pro	Pro
			20					25					30		
Glu	Gly	Ala	Ser	Leu	Met	Thr	Val	Gly	Gly	Ile	Thr	Ala	Pro	Arg	Asp
		35					40					45			
Val	Gln	Val	Trp	Asn	Pro	Arg	Thr	Trp	Glu	Ser	Val	Thr	Leu	Arg	Gly
	50					55					60				
Lys	Arg	Asp	Pro	Ala	Pro	Val	Leu	Gln	Phe	Arg	Ile	Ser	Trp	Trp	Gly
65					70					75					80
Asp	Asp	Arg	Gly	Trp	Leu	Arg	Trp	Ala	Leu	Ser	Asn	His	Gly	Gly	Pro
				85					90					95	
Tyr	Lys	Gly	Arg	Gly	Val	Thr	Arg	Val	Cys	Ala					
			100					105							

<210> 382  
<211> 143  
<212> PRT  
<213> homo sapiens

<400> 382

Glu	Val	Glu	Asn	His	Thr	Asn	Leu	Leu	Ser	Tyr	Ser	Ser	Arg	Gly	Gln
1				5					10					15	
Glu	Ser	Lys	Met	Val	Phe	Thr	Arg	Leu	Lys	Ser	Cys	Gln	Cys	Gly	Phe
			20					25					30		
Val	Ser	Pro	Arg	Arg	Leu	Trp	Gly	Arg	Ile	Gln	Cys	Leu	Phe	Gln	Leu
		35					40					45			
Leu	Gln	Gly	Pro	Pro	His	Arg	Leu	Ala	Pro	Gly	Leu	Leu	Ala	Ile	Phe
	50					55					60				
Thr	Ala	Arg	Ser	Phe	Leu	Ala	Ser	Cys	Ala	Asp	Pro	Arg	Asp	Ser	Pro
65					70					75					80
Ser	Leu	Ile	Arg	Ala	Pro	Met	Ile	Thr	Gln	Gly	Pro	Pro	Gln	Pro	Ser
				85					90					95	
Thr	Val	Ile	Ser	Pro	Pro	Arg	Asn	Pro	Glu	Leu	Lys	His	Arg	Arg	Arg
			100					105					110		
Val	Pro	Phe	Ala	Thr	Gln	Gly	Asn	Thr	Phe	Pro	Arg	Pro	Gly	Val	Pro
		115					120					125			
Asn	Leu	Asp	Ile	Ser	Gly	Gly	Cys	Tyr	Ser	Thr	His	Arg	His	Gln	

130 135 140

<210> 383  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 383

Ser	His	Thr	His	Ala	Gln	Leu	Ser	Asn	His	Gly	Gly	Val	Gln	Glu	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Gly	Val	Pro	Lys	Pro	Trp	Gly	Ser	Asp	Ser	Gly	Ala
			20					25					30		
Leu	Ser	Arg	Pro	Gly	Cys	Lys	Leu	Lys	Thr	Pro	Gly	Gly	Phe	Gln	Asn
		35					40					45			
Ala	Gln	Cys	Leu	Gly	His	Asn	Leu	Asp	Gln	Leu	Asn	Leu	Asn	Leu	Gln
	50					55					60				
Arg	Asp	Ile	Thr	Ala	Pro	Gln	Glu	Thr	Pro	Arg	Gly	Ser	Gln	Ser	Ala
65					70					75					80
Lys	Pro	Glu	Glu	Thr	Ile										
				85											

<210> 384  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 384

Leu	Glu	Pro	Ile	Arg	Phe	Gln	Gln	Lys	Val	Met	Glu	Lys	Glu	Thr	Glu
1				5					10					15	
Lys	Arg	Ile	Ser	Glu	Ile	Glu	Asp	Ala	Ala	Phe	Leu	Ala	Arg	Glu	Lys
			20					25					30		
Ala	Lys	Gln	Asp	Ala	Glu	Tyr	Tyr	Ala	Ala	His	Lys	Tyr	Ala	Thr	Ser
		35					40					45			
Asn	Lys	His	Lys	Leu	Thr	Pro	Glu	Tyr	Leu	Glu	Leu	Lys	Lys	Tyr	Gln
	50					55					60				
Ala	Ile	Ala	Ser	Asn	Ser	Lys	Ile	Tyr	Phe	Gly	Ser	Asn	Ile	Pro	Asn
65					70					75					80
Met	Phe	Val	Asp	Ser	Ser	Cys	Ala	Leu	Lys	Tyr	Ser	Asp	Ile	Arg	Thr
				85					90					95	
Gly	Arg	Glu	Ser	Ser	Leu	Pro	Ser	Lys	Glu	Ala	Leu	Glu	Pro	Ser	Gly
			100					105					110		
Glu	Asn	Val	Ile	Gln	Asn	Lys	Glu	Ser	Thr	Gly					
		115					120								

<210> 385  
 <211> 83  
 <212> PRT  
 <213> homo sapiens

<400> 385

Asp 1	Asn	Ser	Cys	Val 5	Arg	Tyr	Val	Glu	Ala 10	Gln	Gln	Lys	Ser	His 15	Gly
Thr	Thr	Ser	Arg 20	Asn	Leu	Ser	Ala	Val 25	Arg	Pro	Val	Ser	Leu 30	Met	Thr
Val	Cys	Trp 35	Leu	Cys	Gln	Thr	Leu 40	Tyr	Leu	Gly	Lys	Glu 45	Ser	Pro	Asp
Leu	Asn 50	Gly	Ser	Phe	Pro	Trp 55	Ala	Leu	Ser	Tyr	Arg 60	Gly	Ile	Cys	Asn
Met 65	Glu	Lys	Ile	Ile	Phe 70	His	Phe	Cys	Ser	Phe 75	Asn	Ser	Ile	Asn	Ser 80
Leu	Tyr	Lys													

<210> 386

<211> 88

<212> PRT

<213> homo sapiens

<400> 386

Cys 1	Leu	Thr	Phe	Gln 5	Cys	Arg	Gln	Tyr	Leu 10	Ser	Ile	Arg	Leu	Ser 15	Ser
Phe	Met	Ser	Ser 20	Ser	Leu	Glu	Arg	Asn 25	Thr	Tyr	Arg	Ile	Leu 30	Asp	Lys
Thr	Val	Ala 35	Glu	Lys	Thr	Ile	Cys 40	Val	Ser	Asp	Ser	Trp 45	Leu	Tyr	Pro
Pro	Ile 50	Ser	Gly	Ala	Pro	Arg 55	Thr	Ile	Ala	Gly	Glu 60	Val	Glu	Gln	Met
Lys 65	Cys	Lys	Phe	Ser	Val 70	Asn	Leu	Lys	Ser	Pro 75	Tyr	Asn	Asp	Cys	Ser 80
His	Leu	Thr	Pro	Trp 85	Ala	Thr	Ser								

<210> 387

<211> 105

<212> PRT

<213> homo sapiens

<400> 387

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys 35	Val	Lys	Ile	Asn	Gln 40	Gly	Gly	Met	Lys	His 45	Ile	Phe	Leu
Ala	Thr 50	Lys	Leu	Glu	Phe	Leu 55	Arg	Glu	Gln	Met	Gln 60	Arg	Asp	Leu	Leu



Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 388

<211> 173

<212> PRT

<213> homo sapiens

<400> 388

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys
Pro	Pro	Ser 35	Ser	Leu	Phe	Leu	Pro 40	Gly	Ala	Tyr	Lys	Ala 45	Gln	Met	Tyr
Ser	Asp 50	Val	Trp	Thr	Asn	Thr 55	Lys	Lys	Lys	Lys	Lys 60	Lys	Lys	Lys	Lys
Lys 65	Ala	Phe	Leu	Ser	His 70	Arg	His	Lys	Thr	Gln 75	Ile	Ile	Tyr	Cys	Tyr 80
Glu	Ala	Leu	Phe	Thr 85	Asn	Gly	Gln	Phe	Leu 90	His	Phe	Ile	Ala	Ala 95	Cys
Glu	Arg	Leu	Pro 100	Asp	Gly	Arg	Pro	Ile 105	Ser	Leu	Val	Leu	Gln 110	Thr	Ser
Ser	Gln	Ala 115	Ala	Phe	Tyr	Gln	Lys 120	Gly	Glu	Asn	Ser	Cys 125	Leu	Ser	Phe
Leu	Lys 130	Asn	Ala	Phe	Leu	Tyr 135	Leu	Ser	Ile	Arg	His 140	Tyr	Thr	Ser	Glu
Leu 145	Tyr	Lys	Arg	Pro	Gly 150	Gly	Thr	Met	Ser	Leu 155	Val	Asp	Thr	Phe	His 160
Cys	Ser	Val	Ala	Pro 165	Phe	Leu	Ala	Trp	Glu 170	Ala	Ser	Ala			

<210> 389

<211> 105

<212> PRT

<213> homo sapiens

<400> 389

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys	Val	Lys	Ile	Asn	Gln	Gly	Gly	Met	Lys	His	Ile	Phe	Leu

		35					40					45				
Ala	Thr	Lys	Leu	Glu	Phe	Leu	Arg	Glu	Gln	Met	Gln	Arg	Asp	Leu	Leu	
	50					55					60					
Leu	Leu	Ala	Arg	Leu	Gln	Gly	Pro	Leu	Trp	Ser	His	Thr	Glu	Ala	Val	
65					70					75					80	
Thr	Gly	His	Lys	Pro	Arg	Arg	Ala	Arg	Gly	Ser	Cys	Ala	Glu	Ala	Pro	
				85					90					95		
Gly	Pro	Leu	Ser	Gly	Ser	Phe	Pro	Ser								
			100					105								

<210> 390

<211> 262

<212> PRT

<213> homo sapiens

<400> 390

Arg	Cys	Pro	Arg	Arg	Gly	Arg	Glu	Met	Asp	Ser	Gly	Cys	Trp	Leu	Phe	
1				5					10					15		
Gly	Gly	Glu	Phe	Glu	Asp	Ser	Val	Phe	Glu	Glu	Arg	Pro	Glu	Arg	Arg	
			20					25					30			
Ser	Gly	Pro	Pro	Ala	Ser	Tyr	Cys	Ala	Lys	Leu	Cys	Glu	Pro	Gln	Trp	
		35					40					45				
Phe	Tyr	Glu	Glu	Thr	Glu	Ser	Ser	Asp	Asp	Val	Glu	Val	Leu	Thr	Leu	
	50					55					60					
Lys	Lys	Phe	Lys	Gly	Asp	Leu	Ala	Tyr	Arg	Arg	Gln	Glu	Tyr	Gln	Lys	
65					70					75					80	
Ala	Leu	Gln	Glu	Tyr	Ser	Ser	Ile	Ser	Glu	Lys	Leu	Ser	Ser	Thr	Asn	
				85					90					95		
Phe	Ala	Met	Lys	Arg	Asp	Val	Gln	Glu	Gly	Gln	Ala	Arg	Cys	Leu	Ala	
			100					105					110			
His	Leu	Gly	Arg	His	Met	Glu	Ala	Leu	Glu	Ile	Ala	Ala	Asn	Leu	Glu	
		115					120					125				
Asn	Lys	Ala	Thr	Asn	Thr	Asp	His	Leu	Thr	Thr	Val	Leu	Tyr	Leu	Gln	
	130					135					140					
Leu	Ala	Ile	Cys	Ser	Ser	Leu	Gln	Asn	Leu	Glu	Lys	Thr	Ile	Phe	Cys	
145					150					155					160	
Leu	Gln	Lys	Leu	Ile	Ser	Leu	His	Pro	Phe	Asn	Pro	Trp	Asn	Trp	Gly	
				165					170					175		
Lys	Leu	Ala	Glu	Ala	Tyr	Leu	Asn	Leu	Gly	Pro	Ala	Leu	Ser	Ala	Ala	
			180					185					190			
Leu	Ala	Ser	Ser	Gln	Lys	Gln	His	Ser	Phe	Thr	Ser	Ser	Asp	Lys	Thr	
		195					200					205				
Ile	Lys	Ser	Phe	Phe	Pro	His	Ser	Gly	Lys	Asp	Cys	Leu	Leu	Cys	Phe	
	210					215					220					

Pro	Glu	Thr	Leu	Pro	Glu	Ser	Ser	Leu	Ile	Phe	Cys	Gly	Arg	Asp	Thr
225					230					235					240
Arg	Asn	Gly	Arg	Lys	Ile	Gly	Lys	Phe	Cys	Lys	Cys	Ala	Asn	Leu	Val
				245					250					255	
Gly	Glu	Arg	Gly	Thr	Gly										
			260												

<210> 391  
 <211> 66  
 <212> PRT  
 <213> homo sapiens

<400> 391

Lys	Pro	Val	Pro	Leu	Ser	Pro	Thr	Arg	Leu	Ala	His	Leu	Gln	Asn	Phe
1				5					10					15	
Pro	Ile	Phe	Leu	Pro	Phe	Leu	Val	Ser	Leu	Pro	Gln	Lys	Ile	Lys	Glu
			20					25					30		
Leu	Ser	Gly	Lys	Val	Ser	Gly	Lys	His	Lys	Arg	Gln	Ser	Phe	Pro	Glu
		35					40					45			
Cys	Gly	Lys	Lys	Asp	Leu	Ile	Val	Leu	Ser	Leu	Glu	Val	Lys	Leu	Cys
	50					55					60				
Cys	Phe														
65															

<210> 392  
 <211> 78  
 <212> PRT  
 <213> homo sapiens

<400> 392

Gln	Ala	Gly	Gly	Arg	Val	Pro	Trp	Leu	Asn	Gly	Leu	Cys	Trp	Leu	Leu
1				5					10					15	
Tyr	Phe	Pro	Ser	Leu	Gln	Gln	Ser	Pro	Ala	Pro	Pro	Tyr	Ala	Tyr	Pro
			20					25					30		
Gly	Glu	Pro	Asp	Thr	Glu	Pro	Asp	Leu	Pro	Gly	His	Pro	Phe	Ser	Trp
		35					40					45			
Gln	Asn	Trp	Leu	Met	Thr	Ile	Phe	Gln	Arg	Tyr	Trp	Asn	Thr	Pro	Ala
	50					55					60				
Val	Leu	Ser	Asp	Thr	Leu	Val	Val	Cys	Arg	Pro	Gly	Leu	Leu		
65					70					75					

<210> 393  
 <211> 79  
 <212> PRT  
 <213> homo sapiens

<400> 393

Thr	Ser	Leu	Glu	Gly	Ile	Asp	Leu	Gln	Pro	Ser	His	Leu	Thr	Ile	Tyr
1				5					10					15	

Thr	Ala	Ala	Leu	Lys	Glu	Lys	Thr	Pro	Asp	Phe	Arg	Arg	Leu	Ser	Pro
			20					25					30		
Arg	Val	Ser	Glu	Thr	Ala	Asp	Ser	Arg	Lys	Val	Ala	Arg	Gly	Pro	Arg
		35					40					45			
Phe	Val	Met	Arg	Asp	Asn	Pro	Gly	Arg	Gly	Gly	Asp	His	Arg	Gly	Leu
	50					55					60				
Gln	Ala	Pro	Gly	Trp	Met	Lys	Glu	Gly	Arg	Gly	Trp	Gly	Val	Leu	
65					70					75					

<210> 394  
 <211> 72  
 <212> PRT  
 <213> homo sapiens

<400> 394

Val	Thr	Pro	Pro	Pro	Pro	Ser	Gln	Ile	Ser	Ser	Phe	Leu	Pro	Pro	Ser
1				5					10					15	
Thr	Ala	Pro	Phe	Thr	Lys	Pro	Pro	Ile	Pro	Asp	Pro	Pro	Ser	Ser	Thr
			20					25					30		
Pro	Ala	Pro	Gly	Asp	Pro	Tyr	Asp	His	Pro	Arg	Ala	Arg	Gly	Cys	Pro
		35					40					45			
Ala	Leu	Gln	Ile	Gly	Ala	His	Gly	Arg	Pro	Tyr	Gly	Ser	Pro	Arg	Ser
	50					55					60				
Pro	Arg	Arg	Glu	Glu	Arg	Asp	Val								
65					70										

<210> 395  
 <211> 98  
 <212> PRT  
 <213> homo sapiens

<400> 395

Pro	Pro	Pro	Pro	Pro	Pro	Lys	Phe	His	Pro	Ser	Phe	Arg	Leu	Leu	Gln
1				5					10					15	
Pro	Pro	Leu	Gln	Asn	Pro	Pro	Ser	Pro	Thr	Leu	Leu	His	Pro	Pro	Arg
			20					25					30		
Arg	Leu	Glu	Thr	Pro	Met	Ile	Thr	Pro	Ala	Pro	Gly	Val	Val	Pro	His
		35					40					45			
Tyr	Lys	Ser	Gly	Pro	Thr	Gly	Asp	Leu	Thr	Gly	Val	Arg	Gly	Leu	Arg
	50					55					60				
Asp	Ala	Arg	Arg	Glu	Thr	Ser	Glu	Val	Trp	Arg	Leu	Phe	Leu	Gln	Gly
65					70					75					80
Cys	Cys	Val	Asp	Cys	Glu	Val	Gly	Gly	Leu	Lys	Ile	Asn	Ser	Leu	Glu
				85					90					95	
Gly	Gly														

<210> 396  
 <211> 80

<212> PRT  
<213> homo sapiens

<400> 396

Asn 1	Trp	Arg	Gln	Thr 5	Val	Trp	Gln	Arg	Val 10	Arg	Glu	Gly	Ala	Cys 15	Ala	
Gln	Glu	Ser	Ser 20	Arg	Pro	Ala	Ser	Gly 25	Cys	Arg	Phe	Leu	Arg 30	Cys	Ala	
Ile	Gly	Ala 35	Ser	Ala	Phe	Ser	Gly 40	Asp	Arg	Gly	Ser	Ala 45	Val	Ala	Thr	
Asn	Thr 50	Gln	Pro	His	Thr	His 55	Asn	His	Thr	His	Lys 60	Trp	Gly	Gln	Pro	
His 65	Pro	Val	Gln	Ala	Phe 70	Thr	Asn	Val	Ile	Ser 75	Val	Leu	Phe	Tyr	Phe 80	

<210> 397  
<211> 309  
<212> PRT  
<213> homo sapiens

<400> 397

Tyr 1	Asp	Asn	Ser	Ser 5	Thr	Cys	Lys	Lys	Gly 10	Lys	Val	Phe	Pro	Gly 15	Lys	
Ile	Ser	Val	Thr 20	Val	Ser	Glu	Thr	Phe 25	Asp	Pro	Glu	Glu	Lys 30	His	Ser	
Met	Ala	Tyr 35	Gln	Asp	Leu	His	Ser 40	Glu	Ile	Thr	Ser	Leu 45	Phe	Lys	Asp	
Val	Phe 50	Gly	Thr	Ser	Val	Tyr 55	Gly	Gln	Thr	Val	Ile 60	Leu	Thr	Val	Ser	
Thr 65	Ser	Leu	Ser	Pro	Arg 70	Ser	Glu	Met	Arg	Ala 75	Asp	Asp	Lys	Phe	Val 80	
Asn	Val	Thr	Ile	Val 85	Thr	Ile	Leu	Ala	Glu 90	Thr	Thr	Ser	Asp	Asn 95	Glu	
Lys	Thr	Val	Thr 100	Glu	Lys	Ile	Asn	Lys 105	Ala	Ile	Arg	Ser	Ser 110	Ser	Ser	
Asn	Phe	Leu 115	Asn	Tyr	Asp	Leu	Thr 120	Leu	Arg	Cys	Asp	Tyr 125	Tyr	Gly	Cys	
Asn	Gln 130	Thr	Ala	Asp	Asp	Cys 135	Leu	Asn	Gly	Leu	Ala 140	Cys	Asp	Cys	Lys	
Ser 145	Asp	Leu	Gln	Arg	Pro 150	Asn	Pro	Gln	Ser	Pro 155	Phe	Cys	Val	Ala	Ser 160	
Ser	Leu	Lys	Cys	Pro 165	Asp	Ala	Cys	Asn	Ala 170	Gln	His	Lys	Gln	Cys 175	Leu	
Ile	Lys	Lys	Ser 180	Gly	Gly	Ala	Pro	Glu 185	Cys	Ala	Cys	Val	Pro 190	Gly	Tyr	

Gln	Glu	Asp	Ala	Asn	Gly	Asn	Cys	Gln	Lys	Cys	Ala	Phe	Gly	Tyr	Ser	
		195					200					205				
Gly	Leu	Asp	Cys	Lys	Asp	Lys	Phe	Gln	Leu	Ile	Leu	Thr	Ile	Val	Gly	
	210					215					220					
Thr	Ile	Ala	Gly	Ile	Val	Ile	Leu	Ser	Met	Ile	Ile	Ala	Leu	Ile	Val	
225					230					235					240	
Thr	Ala	Arg	Ser	Asn	Asn	Lys	Thr	Lys	His	Ile	Glu	Glu	Glu	Asn	Leu	
				245					250					255		
Ile	Asp	Glu	Asp	Phe	Gln	Asn	Leu	Lys	Leu	Arg	Ser	Thr	Gly	Phe	Thr	
			260					265					270			
Asn	Leu	Gly	Ala	Glu	Gly	Ser	Val	Phe	Pro	Lys	Val	Arg	Ile	Thr	Ala	
		275					280					285				
Ser	Arg	Asp	Ser	Gln	Met	Gln	Asn	Pro	Tyr	Ser	Arg	His	Ser	Ser	Met	
	290					295					300					
Pro	Arg	Pro	Asp	Tyr												
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<210> 398  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 398

Gln	Ala	Leu	Ile	Ala	Ser	Thr	Thr	Phe	Asn	Val	Ile	Asp	Ser	Tyr	Leu	
1				5					10					15		
Ala	Ser	Glu	Leu	Asp	Ser	Leu	Gln	Thr	Phe	Thr	Thr	Ser	Ile	Gln	Arg	
			20					25					30			
Gly	Trp	Gln	Met	Ser	Asp	Gly	Arg	Lys	Thr	Pro	Glu	Ala	Arg	Ser	Leu	
		35					40					45				
Leu	Val	Leu	Thr	Ser	Pro	Ser	Val	Phe	Leu	Asn	Thr	Leu	Asn	Asn	Ser	
	50					55					60					
Leu	Tyr	Ile	Gly	Trp	Gly	Pro	Trp	Arg	Val	Pro	His	Ser	Tyr	Asp	Ser	
	65				70					75					80	
Asn	Ser	Gln	Gly	Gly	Ala	Cys	Cys	Cys	Val	Leu	Asn	Arg	Asp	Phe	Ala	
				85					90					95		
Ser	Gly	Cys	Leu	Trp	Arg	Pro	Leu	Ser								
			100					105								

<210> 399  
 <211> 75  
 <212> PRT  
 <213> homo sapiens

<400> 399

Cys	Phe	Ser	Cys	Phe	Val	Ile	Cys	Ser	Val	Ser	Leu	Cys	Thr	Leu	Asn	
1				5					10					15		
Ile	Tyr	Pro	Leu	Cys	Asp	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Ser	Arg	

			20					25					30			
Thr	Ser	Thr	Phe	Asp	Phe	Ser	Gln	Pro	Gln	Pro	Arg	Lys	Asn	Gly	Ser	
		35					40					45				
Trp	Asp	Lys	Gln	Leu	Val	Phe	Val	Ser	Lys	Thr	Gln	Ile	Gly	His	Ile	
	50					55					60					
Asn	Ala	Thr	Ala	Phe	Arg	Ser	Phe	Asp	Phe	Asp						
65					70					75						

<210> 400  
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 <213> homo sapiens

<400> 400																
Arg	Lys	Lys	Ala	Val	Cys	Phe	Met	Asn	Asp	Leu	Ile	Cys	Phe	Leu	Asp	
1				5					10					15		
Asn	Thr	Phe	Lys	Asn	Asn	Val	Leu	Ser	Gln	Ala	Trp	Trp	Cys	Val	His	
			20					25					30			
Leu	Val	Pro	Thr	Ile	Trp	Glu	Ala	Glu	Ala	Gly	Gly	Ser	Leu	Glu	Pro	
		35					40					45				
Arg	Ser	Leu	Lys	Leu	Gln	Cys	Pro	Val	Val	Ala	Pro	Val	Asn	Asn	Cys	
	50					55					60					
Thr	Pro	Ala	Trp	Ala	Thr											
65					70											

<210> 401  
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Leu	Val	Pro	Gln	Gly	Ser	Leu	Leu	Gln	Thr	His	Pro	Phe	Val	Phe	Phe	
1				5					10					15		
Ser	Phe	Leu	Glu	Met	Arg	Ser	Arg	Tyr	Val	Ala	Gln	Ala	Gly	Val	Gln	
			20					25					30			
Leu	Phe	Thr	Gly	Ala	Thr	Thr	Gly	His	Cys	Ser	Phe	Lys	Leu	Leu	Gly	
		35					40					45				
Ser	Ser	Asp	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ile	Val	Gly	Thr	Arg	Cys	
	50					55					60					
Thr	His	His	His	Ala												
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<210> 402  
 <211> 80  
 <212> PRT  
 <213> homo sapiens

<400> 402																
Pro	Pro	Leu	Trp	Val	Ala	Thr	Val	Arg	Asn	Gly	Cys	Cys	His	Val	Phe	

1				5					10					15		
Trp	Thr	Leu	Pro 20	Ala	Asn	Arg	Ser	Leu 25	Pro	Gly	Phe	Gly	Asn 30	Thr	Ser	
Ile	Thr	Ser 35	Leu	Leu	Leu	Phe	Cys 40	Arg	Asp	Lys	Thr	Phe 45	Glu	Val	Ala	
Arg	Pro 50	Arg	Thr	Ser	Lys	Asp 55	Ser	Cys	Tyr	Ser	Ala 60	Thr	Val	Tyr	Thr	
Ala 65	His	Leu	Ser	Tyr	Ser 70	His	Val	Leu	Ser	Ser 75	Leu	Val	Arg	Leu	Phe 80	

<210> 403  
 <211> 81  
 <212> PRT  
 <213> homo sapiens

<400> 403

Leu 1	Thr	Asn	Met	Ser 5	Asp	His	Leu	Phe	Gly 10	Trp	Leu	Leu	Leu	Glu 15	Met	
Ala	Val	Val	Met 20	Phe	Ser	Gly	Leu	Cys 25	Gln	Pro	Thr	Asp	Pro 30	Cys	Gln	
Val	Leu	Glu 35	Ile	Leu	Leu	Leu	Pro 40	Arg	Cys	Tyr	Phe	Ser 45	Ala	Gly	Ile	
Lys	Leu 50	Leu	Arg	Trp	Pro	Asp 55	Pro	Glu	His	Pro	Arg 60	Ile	Pro	Val	Thr	
Val 65	Leu	Gln	Tyr	Thr	Leu 70	Leu	Ile	Tyr	Pro	Ile 75	Leu	Met	Cys	Phe	Leu 80	

Leu

<210> 404  
 <211> 75  
 <212> PRT  
 <213> homo sapiens

<400> 404

Val 1	Ser	His	Tyr	Pro 5	His	Ser	Val	Ser	Lys 10	Pro	Pro	Lys	His	Gln 15	Thr	
Lys	Gln	Met	Val 20	Val	Ala	Leu	Thr	His 25	Ser	Arg	Leu	Thr	Ser 30	Glu	Phe	
Lys	Trp	Glu 35	Asn	Thr	Pro	Tyr	Thr 40	Thr	Val	Ile	Ile	Pro 45	Leu	Trp	Thr	
Leu	Asn 50	Ile	Thr	Tyr	Phe	Leu 55	Lys	Ile	Ile	Leu	Leu 60	Lys	Lys	Lys	Ala	
His 65	Glu	Asn	Arg	Ile	Asn 70	Glu	Gln	Cys	Ile	Leu 75						

<210> 405  
 <211> 328  
 <212> PRT



<213> homo sapiens

<400> 405

Arg 1	Tyr	Leu	Asn	Met 5	Gly	Asn	Leu	Leu	Lys 10	Val	Leu	Thr	Cys	Thr 15	Asp
Leu	Glu	Gln	Gly 20	Pro	Asn	Phe	Phe	Leu 25	Asp	Phe	Glu	Asn	Ala 30	Gln	Pro
Thr	Glu	Ser 35	Glu	Lys	Glu	Ile	Tyr 40	Asn	Gln	Val	Asn	Val 45	Val	Leu	Lys
Asp	Ala 50	Glu	Gly	Ile	Leu	Glu 55	Asp	Leu	Gln	Ser	Tyr 60	Arg	Gly	Ala	Gly
His 65	Glu	Ile	Arg	Glu	Ala 70	Ile	Gln	His	Pro	Ala 75	Asp	Glu	Lys	Leu	Gln 80
Glu	Lys	Ala	Trp	Gly 85	Ala	Val	Val	Pro	Leu 90	Val	Gly	Lys	Leu	Lys 95	Lys
Phe	Tyr	Glu	Phe 100	Ser	Gln	Arg	Leu	Glu 105	Ala	Ala	Leu	Arg	Gly 110	Leu	Leu
Gly	Ala	Leu 115	Thr	Ser	Thr	Pro	Tyr 120	Ser	Pro	Thr	Gln	His 125	Leu	Glu	Arg
Glu	Gln 130	Ala	Leu	Ala	Lys	Gln 135	Phe	Ala	Glu	Ile	Leu 140	His	Phe	Thr	Leu
Arg 145	Phe	Asp	Glu	Leu	Lys 150	Met	Thr	Asn	Pro	Ala 155	Ile	Gln	Asn	Asp	Phe 160
Ser	Tyr	Tyr	Arg	Arg 165	Thr	Leu	Ser	Arg	Met 170	Arg	Ile	Asn	Asn	Val 175	Pro
Ala	Glu	Gly	Glu 180	Asn	Glu	Val	Asn	Asn 185	Glu	Leu	Ala	Asn	Arg 190	Met	Ser
Leu	Phe	Tyr 195	Ala	Glu	Ala	Thr	Pro 200	Met	Leu	Lys	Thr	Leu 205	Ser	Asp	Ala
Thr	Thr 210	Lys	Phe	Val	Ser	Glu 215	Asn	Lys	Asn	Leu	Pro 220	Ile	Glu	Asn	Thr
Thr 225	Asp	Cys	Leu	Ser	Thr 230	Met	Ala	Ser	Val	Cys 235	Arg	Val	Met	Leu	Glu 240
Thr	Pro	Glu	Tyr	Arg 245	Ser	Arg	Phe	Thr	Asn 250	Glu	Glu	Thr	Val	Ser 255	Phe
Cys	Leu	Arg	Val 260	Met	Val	Gly	Val	Ile 265	Ile	Leu	Tyr	Asp	His 270	Val	His
Pro	Val	Gly 275	Ala	Phe	Ala	Lys	Thr 280	Ser	Lys	Ile	Asp	Met 285	Lys	Gly	Cys
Ile	Lys 290	Val	Leu	Lys	Asp	Gln 295	Pro	Pro	Asn	Ser	Val 300	Glu	Gly	Leu	Leu
Asn 305	Ala	Leu	Arg	Tyr	Thr 310	Thr	Lys	His	Leu	Asn 315	Asp	Glu	Thr	Thr	Ser 320

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<400> 406

<400> 407

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all, until, until, all, from, from  
to, except, until, to, to, to, to  
with, through, through, with, through, through

[illegible][illegible]

130

<210> 410  
 <211> 142  
 <212> PRT  
 <213> homo sapiens

<400> 410

Trp 1	Lys	Gln	Arg	Arg 5	Pro	Ala	Val	Ala	Leu 10	Asp	Thr	Pro	Met	Pro 15	Gln
Ala	Val	Gly	Lys 20	Gln	Ser	Leu	Gly	Glu 25	Val	Ala	Pro	Leu	Gly 30	Ser	Leu
Thr	Leu	Cys 35	Val	Glu	Arg	Gln	Gly 40	Arg	His	Glu	Glu	Gly 45	Arg	Cys	Glu
Trp	Ser 50	Thr	Val	His	Pro	Gly 55	Ile	Ser	Gln	Pro	Glu 60	Ser	Pro	Pro	Ser
Leu 65	Ala	Ala	Pro	Glu	His 70	Ser	Leu	Trp	Pro	Thr 75	Ala	Thr	Glu	Met	Ser 80
Ala	Cys	Gln	Asp	Thr 85	Trp	Arg	Arg	Lys	Lys 90	Thr	Arg	His	Gln	Lys 95	Lys
Leu	Pro	Pro	Gln 100	Glu	Gln	Ile	Glu	Leu 105	Leu	Asp	Gln	Gly	His 110	Thr	Arg
Ser	Gly	Arg 115	His	Pro	Ala	Pro	Cys 120	Ala	Gln	Gly	Lys	Glu 125	Thr	Gln	Phe
Asn 130	Val	Trp	Leu	Leu	Cys	Ser 135	Arg	Glu	Thr	Ala	Thr 140	Leu	Pro		

<210> 411  
 <211> 244  
 <212> PRT  
 <213> homo sapiens

<400> 411

Lys 1	Arg	Arg	Gly	Val 5	Arg	Gln	Phe	Arg	Trp 10	Leu	Val	Cys	Thr	Arg 15	Arg
Ala	Ser	Pro	Gly 20	Ala	Ala	Arg	Ser	Ala 25	Pro	Ile	Ala	Pro	Ala 30	Thr	Gly
Ser	Gly	Arg 35	Arg	Pro	Asn	Met	Asp 40	Ser	Ala	Gly	Gln	Asp 45	Ile	Asn	Leu
Asn 50	Ser	Pro	Asn	Lys	Gly	Leu 55	Leu	Ser	Asp	Ser	Met 60	Thr	Asp	Val	Pro
Val 65	Asp	Thr	Gly	Val	Ala 70	Ala	Arg	Thr	Pro	Ala 75	Val	Glu	Gly	Leu	Thr 80
Glu	Ala	Glu	Glu	Glu 85	Glu	Leu	Arg	Ala	Glu 90	Leu	Thr	Lys	Val	Glu 95	Glu
Glu	Ile	Val	Thr 100	Leu	Arg	Gln	Val	Leu 105	Ala	Ala	Lys	Glu	Arg 110	His	Cys



<210> 413  
 <211> 143  
 <212> PRT  
 <213> homo sapiens

<400> 413

Ala 1	Leu	Glu	Thr	Cys 5	Thr	Ser	Cys	Gln	Leu 10	Leu	Asp	Arg	Phe	Cys 15	Phe
Ser	Ser	Pro	Arg 20	Val	Glu	Arg	Pro	Ser 25	Leu	Leu	Leu	Ser	Ser 30	Pro	Gln
Cys	Leu	Ser 35	Leu	Ala	Ala	Arg	Thr 40	Trp	Arg	Arg	Val	Thr 45	Ile	Ser	Ser
Ser	Thr 50	Leu	Val	Ser	Ser	Ala 55	Leu	Ser	Ser	Ser	Ser 60	Ser	Ala	Ser	Val
Arg 65	Pro	Ser	Thr	Ala	Gly 70	Val	Arg	Ala	Ala	Thr 75	Pro	Val	Ser	Thr	Gly 80
Thr	Ser	Val	Met	Glu 85	Ser	Asp	Ser	Arg	Pro 90	Leu	Leu	Gly	Glu	Phe 95	Arg
Leu	Ile	Ser	Trp 100	Pro	Ala	Glu	Ser	Met 105	Phe	Gly	Arg	Arg	Pro 110	Asp	Pro
Val	Ala	Gly 115	Ala	Met	Gly	Ala	Glu 120	Arg	Ala	Ala	Pro	Gly 125	Glu	Ala	Arg
Arg	Val 130	His	Thr	Ser	Gln	Arg 135	Asn	Cys	Leu	Thr	Pro 140	Arg	Arg	Phe	

<210> 414  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 414

Arg 1	Gly	Arg	Gly	Ala 5	Leu	Trp	Trp	Ala	Ala 10	Lys	Glu	Leu	Arg	Arg 15	Thr
Lys	Lys	Leu	Ser 20	Asp	Tyr	Val	Gly	Lys 25	Asn	Glu	Lys	Thr	Lys 30	Ile	Ile
Ala	Lys	Ile 35	Gln	Gln	Arg	Gly	Gln 40	Gly	Ala	Pro	Ala	Arg 45	Glu	Pro	Ile
Ile	Ser 50	Ser	Glu	Glu	Gln	Lys 55	Gln	Leu	Met	Leu	Tyr 60	Tyr	His	Arg	Arg
Gln 65	Glu	Glu	Leu	Lys	Arg 70	Leu	Glu	Glu	Asn	Asp 75	Asp	Asp	Ala	Tyr	Leu 80
Asn	Ser	Pro	Trp	Ala 85	Asp	Asn	Thr	Ala	Leu 90	Lys	Arg	His	Phe	His 95	Gly
Val	Lys	Asp	Ile 100	Lys	Trp	Arg	Pro	Arg 105							

<210> 415  
 <211> 386  
 <212> PRT  
 <213> homo sapiens

<400> 415

Ala 1	Ala	Glu	Leu	Arg 5	Asp	Cys	Gly	Ser	Arg 10	Arg	Ile	Ser	Arg	Ser 15	Pro
Ser	Ser	Asn 20	Ser	His	Leu	Ser	Pro	Arg 25	Ile	Ser	Leu	Ser	Gly 30	Asn	Leu
Gly	Pro	Gln 35	Thr	Ser	Arg	Leu	Gly 40	Gly	Pro	Pro	Ser	Pro 45	Ser	Ala	Thr
Trp	Ser 50	Val	Phe	Trp	Gln	Leu 55	Pro	Arg	Gln	Gln	Ser 60	Leu	Pro	Gly	Arg
Gly 65	Ser	Ala	Asn	Leu	Leu 70	Pro	Ser	Val	Arg	Ser 75	Glu	Ser	Ala	Val	Leu 80
Ser	Asp	Cys	Val	Gly 85	Gly	Phe	Pro	Gly	Arg 90	Ser	Ser	Val	Arg	Ala 95	Trp
Ile	Ala	Gly	Pro 100	Arg	Cys	Thr	Pro	Ala 105	Ser	Pro	Thr	Arg	Val 110	Leu	Ser
Leu	Ser	Trp 115	Arg	Leu	Phe	Asn	Ser 120	Ala	Ser	Leu	Leu 125	Leu	Leu	Ala	Thr
Ser	Thr 130	Ser	Gly	Ser	Glu	Cys 135	Arg	Phe	Pro	Arg	Ser 140	Pro	Arg	Ala	Arg
Glu 145	Arg	Gly	Ile	Pro	Asp 150	Cys	Glu	Arg	Leu	Leu 155	Val	Arg	Arg	Ser	Cys 160
Trp	Arg	Ser	Gly	Asp 165	Pro	Arg	Pro	Ala	Gly 170	Pro	Ala	Gly	His	Ala 175	Ala
Gly	Ala	Phe	Ser 180	Thr	Pro	Gln	Tyr	Leu 185	Gly	Gly	Thr	Ala	Met 190	Val	Leu
Leu	His	Val 195	Lys	Arg	Gly	Asp	Glu 200	Ser	Gln	Phe	Leu	Leu 205	Gln	Ala	Pro
Gly	Ser 210	Thr	Glu	Leu	Glu	Glu 215	Leu	Thr	Val	Gln	Val 220	Ala	Arg	Val	Tyr
Asn 225	Gly	Arg	Leu	Lys	Val 230	Gln	Arg	Leu	Cys	Ser 235	Glu	Met	Glu	Glu	Leu 240
Ala	Glu	His	Gly	Ile 245	Phe	Leu	Pro	Pro	Asn 250	Met	Gln	Gly	Leu	Thr 255	Asp
Asp	Gln	Ile	Glu 260	Glu	Leu	Lys	Leu	Lys 265	Asp	Glu	Trp	Gly	Glu 270	Lys	Cys
Val	Pro	Ser 275	Gly	Gly	Ala	Val	Phe 280	Lys	Lys	Asp	Asp	Ile 285	Gly	Arg	Arg
Asn	Gly 290	Gln	Ala	Pro	Asn	Glu 295	Lys	Met	Lys	Gln	Val 300	Leu	Lys	Lys	Thr

Ile 305	Glu	Glu	Ala	Lys	Ala 310	Ile	Ile	Ser	Lys	Lys 315	Gln	Val	Glu	Ala	Gly 320
Val	Cys	Val	Thr	Met 325	Glu	Met	Val	Lys	Asp 330	Ala	Leu	Asp	Gln	Leu 335	Arg
Gly	Ala	Val	Met 340	Ile	Val	Tyr	Pro	Met 345	Gly	Leu	Pro	Pro	Tyr 350	Asp	Pro
Ile	Arg	Met 355	Glu	Phe	Glu	Asn	Lys 360	Glu	Asp	Leu	Ser	Gly 365	Thr	Gln	Ala
Gly	Leu 370	Asn	Val	Ile	Lys	Glu 375	Ala	Glu	Ala	His	Cys 380	Gly	Gly	Gln	Pro
Arg 385	Ser														

<210> 416  
 <211> 182  
 <212> PRT  
 <213> homo sapiens

<400> 416

Gly 1	Val	Glu	Lys	Ala 5	Pro	Ala	Ala	Trp	Pro 10	Ala	Gly	Pro	Ala	Gly 15	Arg
Gly	Ser	Pro	Asp 20	Arg	Gln	Gln	Leu	Arg 25	Arg	Thr	Asn	Ser	Arg 30	Ser	Gln
Ser	Gly	Ile 35	Pro	Arg	Ser	Leu	Ala 40	Arg	Gly	Glu	Arg	Gly 45	Lys	Arg	His
Ser	Leu 50	Pro	Glu	Val	Asp	Val 55	Ala	Lys	Ser	Asn	Ser 60	Glu	Ala	Glu	Leu
Lys 65	Ser	Arg	Gln	Leu	Lys 70	Leu	Arg	Thr	Arg	Val 75	Gly	Glu	Ala	Gly	Val 80
His	Arg	Gly	Pro	Ala 85	Ile	Gln	Ala	Arg	Thr 90	Glu	Leu	Arg	Pro	Gly 95	Lys
Pro	Pro	Thr	Gln 100	Ser	Glu	Arg	Thr	Ala 105	Asp	Ser	Glu	Arg	Thr 110	Asp	Gly
Arg	Arg	Phe 115	Ala	Asp	Pro	Leu	Pro 120	Gly	Ser	Asp	Cys	Cys 125	Arg	Gly	Asn
Cys	Gln 130	Asn	Thr	Asp	Gln	Val 135	Ala	Glu	Gly	Glu	Gly 140	Gly	Pro	Pro	Asn
Arg 145	Leu	Val	Trp	Gly	Pro 150	Arg	Phe	Pro	Leu	Arg 155	Glu	Ile	Arg	Gly	Leu 160
Arg	Trp	Glu	Leu	Leu 165	Asp	Gly	Glu	Arg	Glu 170	Ile	Arg	Arg	Glu	Pro 175	Gln
Ser	Arg	Ser	Ser 180	Ala	Ala										

<210> 417



<211> 467  
 <212> PRT  
 <213> homo sapiens

<400> 417

His 1	Thr	Leu	Ser	Arg 5	Trp	Thr	Lys	His	Ser 10	Ile	Pro	Arg	Trp	Asn 15	Asp
Ala	Arg	Thr	Asp 20	Asp	Thr	Trp	His	Ser 25	Glu	Leu	Asp	Met	Arg 30	Lys	Ile
Gly	Gln	Ala 35	Arg	Asn	Thr	Leu	Met 40	Asp	Met	Arg	Leu	Ser 45	Gln	Val	Ser
Asp	Ser 50	Val	Ser	Gly	Gln	Thr 55	Val	Val	Asp	Pro	Lys 60	Gly	Tyr	Leu	Thr
Asp 65	Leu	Asn	Ser	Met	Ile 70	Pro	Thr	His	Gly	Gly 75	Asp	Ile	Asn	Asp	Ile 80
Lys	Lys	Ala	Arg	Leu 85	Leu	Leu	Lys	Ser	Val 90	Arg	Glu	Thr	Asn	Pro 95	His
His	Pro	Pro	Ala 100	Trp	Ile	Ala	Ser	Ala 105	Arg	Leu	Glu	Glu	Val 110	Thr	Gly
Lys	Leu	Gln 115	Val	Ala	Arg	Asn	Leu 120	Ile	Met	Lys	Gly	Thr 125	Glu	Met	Cys
Pro	Lys 130	Ser	Glu	Asp	Val	Trp 135	Leu	Glu	Ala	Ala	Arg 140	Leu	Gln	Pro	Gly
Asp 145	Thr	Ala	Lys	Ala	Val 150	Val	Ala	Gln	Ala	Val 155	Arg	His	Leu	Pro	Gln 160
Ser	Val	Arg	Ile	Tyr 165	Ile	Arg	Ala	Ala	Glu 170	Leu	Glu	Thr	Asp	Ile 175	Arg
Ala	Lys	Lys	Arg 180	Val	Leu	Arg	Lys	Ala 185	Leu	Glu	His	Val	Pro 190	Asn	Ser
Val	Arg	Leu 195	Trp	Lys	Ala	Ala	Val 200	Glu	Leu	Glu	Glu	Pro 205	Glu	Asp	Ala
Arg	Ile 210	Met	Leu	Ser	Arg	Ala 215	Val	Glu	Cys	Cys	Pro 220	Thr	Ser	Val	Glu
Leu 225	Trp	Leu	Ala	Leu	Ala 230	Arg	Leu	Glu	Thr	Tyr 235	Glu	Asn	Ala	Arg	Lys 240
Val	Leu	Asn	Lys	Ala 245	Arg	Glu	Asn	Ile	Pro 250	Thr	Asp	Arg	His	Ile 255	Trp
Ile	Thr	Ala	Ala 260	Lys	Leu	Glu	Glu	Ala 265	Asn	Gly	Asn	Thr	Gln 270	Met	Val
Glu	Lys	Ile 275	Ile	Asp	Arg	Ala	Ile 280	Thr	Ser	Leu	Arg	Ala 285	Asn	Gly	Val
Glu	Ile 290	Asn	Arg	Glu	Gln	Trp 295	Ile	Gln	Asp	Ala	Glu 300	Glu	Cys	Asp	Arg

Ala 305	Gly	Ser	Val	Ala	Thr 310	Cys	Gln	Ala	Val	Met 315	Arg	Ala	Val	Ile	Gly 320
Ile	Gly	Ile	Glu	Glu 325	Glu	Asp	Arg	Lys	His 330	Thr	Trp	Met	Glu	Asp 335	Ala
Asp	Ser	Cys	Val 340	Ala	His	Asn	Ala	Leu 345	Glu	Cys	Ala	Arg	Ala 350	Ile	Tyr
Ala	Tyr	Ala 355	Leu	Gln	Val	Phe	Pro 360	Ser	Lys	Lys	Ser	Val 365	Trp	Leu	Arg
Ala 370	Ala	Tyr	Phe	Glu	Lys	Asn 375	His	Gly	Thr	Arg	Glu 380	Ser	Leu	Glu	Ala
Leu 385	Leu	Gln	Arg	Ala	Val 390	Ala	His	Cys	Pro	Lys 395	Ala	Glu	Val	Leu	Trp 400
Leu	Met	Gly	Ala	Lys 405	Ser	Lys	Trp	Leu	Ala 410	Gly	Asp	Val	Pro	Ala 415	Ala
Arg	Ser	Ile	Leu 420	Ala	Leu	Ala	Phe	Gln 425	Ala	Asn	Pro	Asn	Ser 430	Glu	Glu
Ile	Trp	Leu 435	Ala	Ala	Val	Lys	Leu 440	Glu	Ser	Glu	Asn	Asp 445	Glu	Tyr	Glu
Arg	Ala 450	Arg	Arg	Leu	Leu	Ala 455	Lys	Ala	Arg	Thr	Val 460	Pro	Pro	Pro	Pro
Gly 465	Cys	Ser													

<210> 418

<211> 352

<212> PRT

<213> homo sapiens

<400> 418

Thr 1	Pro	Gly	Arg	Trp 5	Gly	His	Cys	Pro	Arg 10	Leu	Gly	Gln	Gln	Pro 15	Pro
Gly	Pro	Leu	Val 20	Leu	Ile	Ile	Leu	Gly 25	Leu	Gln	Leu	His	Gly 30	Cys	Gln
Pro	Asp	Leu 35	Leu	Thr	Val	Gly	Val 40	Gly	Leu	Glu	Gly	Gln 45	Gly	Gln	Asp
Ala 50	Pro	Cys	Cys	Arg	His	Ile 55	Pro	Cys	Gln	Pro	Leu 60	Gly	Leu	Gly	Ala
His 65	Glu	Pro	Gln	His	Leu 70	Cys	Phe	Gly	Ala	Val 75	Gly	His	Ser	Pro	Leu 80
Gln	Glu	Cys	Phe	Gln 85	Gly	Leu	Pro	Ser	Ala 90	Met	Val	Leu	Leu	Glu 95	Val
Arg	Gly	Ala	Gln 100	Pro	His	Thr	Leu	Leu 105	Ala	Gly	Glu	His	Leu 110	Gln	Gly
Val	Gly	Val 115	Asp	Gly	Ser	Cys	Thr 120	Leu	Gln	Gly	Ile	Val 125	Gly	Tyr	Thr

Thr	Val	Ser	Ile	Leu	His	Pro	Gly	Met	Leu	Pro	Ile	Phe	Leu	Leu	Asn
	130					135					140				
Pro	Asn	Pro	Asn	His	Gly	Thr	His	Asp	Gly	Leu	Ala	Gly	Gly	His	Thr
145					150					155					160
Pro	Ser	Pro	Val	Thr	Phe	Leu	Gly	Ile	Leu	Asp	Pro	Leu	Leu	Thr	Val
				165					170					175	
Asp	Leu	His	Thr	Val	Gly	Pro	Gln	Arg	Gly	Asp	Gly	Ser	Val	Asp	Asp
			180					185					190		
Leu	Leu	His	His	Leu	Arg	Val	Pro	Ile	Gly	Phe	Leu	Gln	Leu	Ser	Ser
		195					200					205			
Arg	Asp	Pro	Asp	Met	Ser	Val	Cys	Arg	Asn	Val	Leu	Pro	Arg	Leu	Val
	210					215					220				
Gln	Asp	Leu	Ala	Gly	Ile	Phe	Ile	Gly	Leu	Gln	Pro	Cys	Gln	Ser	Lys
225					230					235					240
Pro	Glu	Leu	His	Ala	Gly	Gly	Ala	Ala	Leu	His	Ser	Ser	Ala	Gln	His
				245					250					255	
Asp	Ser	Ser	Ile	Phe	Arg	Phe	Phe	Gln	Leu	Asn	Gly	Cys	Phe	Pro	Gln
			260					265					270		
Ala	Asn	Arg	Val	Trp	Asn	Met	Leu	Glu	Gly	Phe	Pro	Lys	Asn	Pro	Leu
		275					280					285			
Leu	Cys	Thr	Asn	Val	Arg	Phe	Gln	Leu	Cys	Gly	Ser	Asp	Val	Asn	Pro
	290					295					300				
Asp	Arg	Leu	Trp	Glu	Met	Thr	Asp	Ser	Leu	Gly	Tyr	His	Gly	Leu	Gly
305					310					315					320
Cys	Val	Pro	Arg	Leu	Gln	Pro	Gly	Cys	Phe	Gln	Pro	Asp	Ile	Phe	Thr
				325					330					335	
Leu	Gly	Ala	His	Leu	Arg	Pro	Leu	His	Asp	Lys	Val	Pro	Ser	Tyr	Leu
			340					345					350		

<210> 419

<211> 424

<212> PRT

<213> homo sapiens

<400> 419

Pro	Pro	Gly	Ala	Pro	Phe	Phe	Leu	Phe	Phe	Phe	Phe	Leu	Thr	Arg	Asp
1				5					10					15	
Ile	Lys	Thr	Phe	Asn	Glu	Gly	Gly	His	Ser	Ser	Glu	Pro	Phe	His	Met
			20					25					30		
Arg	Pro	Asn	Pro	Ala	Pro	Arg	Arg	Pro	Ala	Met	Ala	Thr	Ala	Gln	Ser
		35					40					45			
Glu	Gly	Val	Leu	Asp	Ala	Ala	Gly	His	Gln	Pro	Lys	Asp	Val	Pro	Asp
	50					55					60				
Leu	Leu	Leu	Pro	Val	Gly	Asp	Val	Leu	Gly	His	Gly	Ala	Pro	Gln	Leu

65					70					75					80	
Pro	Met	Pro	Arg	Leu 85	Cys	Thr	Leu	Thr	Ala 90	Leu	Pro	His	Leu	Leu 95	Leu	
Leu	Leu	Leu	Ser 100	Ala	Met	Leu	Gln	Leu 105	Lys	Leu	Val	Glu	Glu 110	Gly	Pro	
Gly	Ile	Pro 115	Gln	Val	Arg	Val	Asn 120	Leu	His	Ser	Ala	Val 125	Glu	Pro	Leu	
Pro	Gly 130	Leu	Gly	Asp	Leu	Pro 135	Leu	Thr	Pro	Lys	Gln 140	Leu	Gly	His	Gly	
Gln 145	Glu	His	Met	Gly	Val 150	Met	Leu	Thr	Leu	Leu 155	Gln	Gly	Ile	His	Ala 160	
Leu	Gly	Pro	Pro	Leu 165	Gly	Pro	Cys	Leu	Glu 170	Glu	Asp	Gly	Leu	Arg 175	Pro	
Gln	Asp	Thr	Gly 180	Val	Gly	Ala	Leu	Leu 185	Gln	Arg	Leu	Gly	His 190	Glu	Cys	
Ile	Cys	Asp 195	Val	Leu	Gln	Pro	Arg 200	Thr	Val	Leu	Gln	Pro 205	His	Gly	Leu	
Gln	Pro 210	Gln	Pro	Arg	Val	Leu 215	Trp	Val	Leu	Gln	Thr 220	Arg	Leu	Phe	Gln	
Asn 225	Gly	Pro	Cys	Ser	Ser 230	Lys	Leu	Pro	Asn	Leu 235	Leu	Leu	Gln	Pro	Arg 240	
Glu	Gln	Lys	Pro	Gln 245	Gly	Cys	Gly	Val	Gly 250	Thr	Leu	Leu	Gln	Pro 255	Leu	
Val	Ile	Gly	Phe 260	Pro	Arg	Leu	Leu	His 265	His	Leu	Leu	Leu	Leu 270	Leu	Asp	
Leu	Pro	Leu 275	His	His	Pro	Gln	Leu 280	Gly	Glu	Val	Leu	Ile 285	Val	Pro	Gln	
Gly	Leu 290	Leu	Ala	Gln	Ile	Leu 295	Gly	Cys	Pro	Asp	Val 300	Val	Leu	His	Pro	
Leu 305	Gln	Leu	His	Arg	Leu 310	His	Glu	His	Pro	Gly 315	Gly	Gly	Gly	Thr	Val 320	
Arg	Ala	Leu	Ala	Ser 325	Ser	Leu	Arg	Ala	Arg 330	Ser	Tyr	Ser	Ser	Phe 335	Ser	
Asp	Ser	Ser	Phe 340	Thr	Ala	Ala	Ser	Gln 345	Ile	Ser	Ser	Leu	Leu 350	Gly	Leu	
Ala	Trp	Lys 355	Ala	Arg	Ala	Arg	Met 360	Leu	Leu	Ala	Ala	Gly 365	Thr	Ser	Pro	
Ala	Ser 370	His	Leu	Asp	Leu	Ala 375	Pro	Met	Ser	His	Ser 380	Thr	Ser	Ala	Leu	
Gly 385	Gln	Trp	Ala	Thr	Ala 390	Leu	Cys	Arg	Ser	Ala 395	Ser	Arg	Asp	Ser	Arg 400	
Val	Pro	Trp	Phe	Phe	Ser	Lys	Tyr	Ala	Ala	Arg	Ser	His	Thr	Leu	Phe	

	405								410				415			
	Leu	Leu	Gly	Asn	Thr	Cys	Arg	Ala								
				420												
<210>	420															
<211>	109															
<212>	PRT															
<213>	homo sapiens															
<400>	420															
	Gly	Arg	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Thr	Val	Trp	Val	Gln	Gly	His
	1				5					10					15	
	Gly	Leu	Glu	Gly	Trp	Trp	Ala	Ala	Leu	Ser	Gly	Ser	Gly	Phe	Pro	Ala
				20					25					30		
	Val	Gly	Phe	Leu	Phe	Trp	Leu	Leu	Arg	Leu	Val	Tyr	Phe	Leu	Ser	Leu
			35					40					45			
	Leu	Pro	Val	Thr	Pro	Gly	Ala	Pro	Glu	Tyr	Arg	Leu	Phe	Ser	Pro	Trp
		50					55					60				
	Ala	Val	Ser	Leu	Ser	Cys	Phe	Leu	Thr	Leu	Leu	Pro	Gly	Leu	Leu	Cys
	65					70					75					80
	Val	His	Leu	Arg	Leu	Ala	Trp	Ser	Lys	Gln	Val	Arg	Pro	Leu	Leu	Leu
					85					90					95	
	Tyr	Ser	Leu	Val	Leu	Phe	Trp	His	Leu	Val	Lys	Leu	Ala			
				100					105							
<210>	421															
<211>	177															
<212>	PRT															
<213>	homo sapiens															
<400>	421															
	Val	Ser	Val	Pro	Ser	Ser	Ser	Ala	Ala	Gly	Thr	Leu	Phe	Gln	Gly	Leu
	1				5					10					15	
	Cys	Gly	Ala	Pro	Asp	Ala	Pro	His	Pro	Leu	Ser	Lys	Ile	Pro	Gly	Gly
				20					25					30		
	Arg	Gly	Gly	Gly	Arg	Asp	Pro	Ser	Leu	Ser	Ala	Leu	Ile	Tyr	Lys	Asp
			35					40					45			
	Glu	Lys	Leu	Thr	Val	Thr	Gln	Asp	Leu	Pro	Val	Asn	Asp	Gly	Lys	Pro
		50					55					60				
	His	Ile	Val	His	Phe	Gln	Tyr	Glu	Val	Thr	Glu	Val	Lys	Val	Ser	Ser
	65					70					75					80
	Trp	Asp	Ala	Val	Leu	Ser	Ser	Gln	Ser	Leu	Phe	Val	Glu	Ile	Pro	Asp
					85					90					95	
	Gly	Leu	Leu	Ala	Asp	Gly	Ser	Lys	Glu	Gly	Leu	Leu	Ala	Leu	Leu	Glu
				100					105					110		
	Phe	Ala	Glu	Glu	Lys	Met	Lys	Val	Asn	Tyr	Val	Phe	Ile	Cys	Phe	Arg
			115					120					125			

Lys	Gly	Arg	Glu	Asp	Arg	Ala	Pro	Leu	Leu	Lys	Thr	Phe	Ser	Phe	Leu
	130					135					140				
Gly	Phe	Glu	Ile	Val	Arg	Pro	Gly	His	Pro	Cys	Val	Pro	Ser	Arg	Pro
145					150					155					160
Asp	Val	Met	Phe	Met	Val	Tyr	Pro	Leu	Asp	Gln	Asn	Leu	Ser	Asp	Glu
				165					170					175	

Asp

<210> 422  
 <211> 114  
 <212> PRT  
 <213> homo sapiens

<400> 422

Ala	Ser	Arg	Pro	Tyr	Ile	Leu	Glu	Leu	Arg	Glu	Lys	Asp	Pro	Cys	Arg
1				5					10					15	
Pro	Leu	Ala	His	Arg	Gly	Ser	Ser	Thr	Val	Gly	Glu	Gly	His	Gln	Glu
			20					25					30		
His	His	Arg	Gly	Pro	Gly	Thr	Met	Cys	Leu	Gln	His	Trp	Ser	Trp	Gly
		35					40					45			
His	Leu	Leu	Asn	Gly	Lys	Ile	Leu	Leu	Ser	Trp	Val	Phe	Ile	Ile	Leu
	50					55					60				
Gly	Gly	Ser	Ala	Gln	Gly	Gly	Arg	Arg	Arg	Arg	Gly	Glu	Trp	Val	Gly
65					70				75						80
Gly	Arg	Val	Gly	Gly	Cys	Gly	Val	Ala	Arg	Ala	Gly	Arg	Ser	Leu	Trp
				85					90					95	
Ala	Lys	Ser	Leu	Ser	Gly	Arg	Gly	Arg	Val	Pro	Ser	Ser	Cys	Leu	Ser
			100					105					110		

Glu Arg

<210> 423  
 <400> 423  
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<210> 424  
 <400> 424  
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<210> 425  
 <400> 425  
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<210> 426  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 426

Pro	Phe	Cys	Ser	Ser	Leu	Ala	Lys	Leu	Gln	Gly	Ile	Trp	Gly	Met	Trp
1				5					10					15	

Asp	Leu	Gln	Phe	Pro	Ala	Pro	Ala	Ser	Ala	Leu	Ser	Gln	Val	Leu	Thr
			20					25					30		
Pro	Ala	Pro	Ala	Ser	Ala	Pro	Ala	Pro	Gly	Arg	Ala	Pro	Ala	Pro	Ala
		35					40					45			
Ala	Ala														
	50														

<210> 427  
 <211> 114  
 <212> PRT  
 <213> homo sapiens

<400> 427

Glu	Asp	Lys	Met	Arg	Pro	Gly	Leu	Ser	Phe	Leu	Leu	Ala	Leu	Leu	Phe
1				5					10					15	
Phe	Leu	Gly	Gln	Ala	Ala	Gly	Asp	Leu	Gly	Asp	Val	Gly	Pro	Pro	Ile
			20					25					30		
Pro	Ser	Pro	Gly	Phe	Ser	Ser	Phe	Pro	Gly	Val	Asp	Ser	Ser	Ser	Ser
		35					40					45			
Phe	Ser	Ser	Ser	Ser	Arg	Ser	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Leu	Gly
	50					55						60			
Ser	Gly	Gly	Ser	Val	Ser	Gln	Leu	Phe	Ser	Asn	Phe	Thr	Gly	Ser	Val
65					70					75					80
Asp	Asp	Arg	Gly	Thr	Cys	Gln	Cys	Ser	Val	Ser	Leu	Pro	Asp	Asn	Asn
				85					90					95	
Phe	Pro	Val	Asp	Arg	Val	Glu	Arg	Trp	Asn	Ser	Gln	Leu	Ile	Val	Ile
			100					105					110		

Ser Gln

<210> 428  
 <211> 113  
 <212> PRT  
 <213> homo sapiens

<400> 428

Glu	Ile	Thr	Met	Ser	Cys	Glu	Phe	Gln	Arg	Ser	Thr	Leu	Ser	Thr	Gly
1				5					10					15	
Lys	Leu	Leu	Ser	Gly	Arg	Glu	Thr	Glu	His	Trp	Gln	Val	Pro	Arg	Ser
			20					25					30		
Ser	Thr	Glu	Pro	Val	Lys	Leu	Glu	Asn	Asn	Trp	Asp	Thr	Glu	Pro	Pro
		35					40					45			
Leu	Pro	Lys	Leu	Arg	Leu	Glu	Leu	Glu	Pro	Asp	Leu	Glu	Leu	Glu	Leu
	50					55					60				
Lys	Leu	Glu	Leu	Glu	Ser	Thr	Pro	Gly	Lys	Glu	Leu	Lys	Pro	Gly	Leu
65					70					75					80
Gly	Ile	Gly	Gly	Pro	Thr	Ser	Pro	Lys	Ser	Pro	Ala	Ala	Trp	Pro	Arg

				85						90					95	
Lys	Asn	Arg	Arg	Ala	Arg	Arg	Asn	Glu	Arg	Pro	Gly	Leu	Ile	Leu	Ser	
			100					105					110			

Ser

<210> 429  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 429

Ala	Ala	Ala	Gly	Ala	Gly	Ala	Arg	Pro	Gly	Ala	Gly	Ala	Glu	Ala	Gly	
1				5					10					15		
Ala	Gly	Val	Asn	Thr	Trp	Glu	Arg	Ala	Glu	Ala	Gly	Ala	Gly	Asn	Trp	
			20					25					30			
Arg	Ser	His	Ile	Pro	Gln	Ile	Pro	Cys	Ser	Leu	Ala	Lys	Glu	Glu	Gln	
		35					40					45				

Lys Gly  
 50

<210> 430  
 <211> 224  
 <212> PRT  
 <213> homo sapiens

<400> 430

Gln	Thr	Gln	Lys	Val	Val	Thr	Ser	Pro	Pro	Arg	Ile	Thr	Leu	His	Trp	
1				5					10					15		
Leu	Leu	Pro	Cys	Ala	Ala	His	Pro	Pro	Asp	Leu	His	Lys	Lys	Gly	Gln	
			20					25					30			
Glu	Asn	Ser	Gly	Cys	Ala	Pro	Ala	Thr	Ala	His	Ser	Ala	Pro	Pro	Gly	
		35					40					45				
Arg	Ser	Pro	Pro	Glu	Leu	Arg	Ala	Gly	Leu	Gln	Arg	Leu	Ala	Arg	Ala	
	50					55					60					
Val	Leu	Pro	Val	Ser	Arg	Phe	Ser	Ala	Pro	Gln	Pro	Pro	Ala	Ala	Ser	
	65				70					75					80	
Phe	Ser	Gly	Pro	Arg	Val	Ala	Pro	Ser	Glu	Glu	Ser	Gly	Pro	Gly	Thr	
				85					90					95		
Ser	Ser	Asn	Ser	Gly	Arg	Leu	Ala	Leu	Pro	Arg	Leu	Arg	Ser	Leu	Cys	
			100					105					110			
Pro	Leu	Gly	Val	Ala	Arg	Pro	Arg	Cys	Cys	Arg	Ala	Leu	Ala	Arg	Cys	
		115					120					125				
Cys	Cys	Ser	Ser	Ser	Pro	Arg	Thr	Ala	Ala	Trp	Ala	Arg	Arg	Ala	Gly	
	130					135					140					
Ser	Ser	Ser	Leu	Ala	Ser	Pro	Thr	Ser	Pro	Thr	Ser	Ala	Glu	Leu	Gln	
					150					155					160	



Ala	His	Pro	Gly	Gln	Pro	Ala	Ala	Val	Pro	Arg	His	Arg	Ile	Pro	Glu
				165					170					175	
His	Ala	Ala	Ala	Gln	Pro	Ala	Gly	Pro	Arg	Asp	His	Glu	Gly	Gly	Ala
			180					185					190		
Gly	Ala	Gly	Arg	Arg	Leu	Asp	Pro	Ala	Gly	His	Glu	Ala	Val	Pro	Pro
		195				200						205			
Gly	His	Gln	Glu	Val	Pro	Val	Leu	Ala	Leu	Arg	Pro	Arg	Leu	Pro	Arg
	210					215					220				

<210> 431

<211> 408

<212> PRT

<213> homo sapiens

<400> 431

Pro	Ala	Leu	Leu	Gly	Leu	Pro	Phe	Ile	Gly	Ser	Ser	Leu	Ala	Pro	Pro
1				5					10					15	
Thr	Leu	Gln	Ile	Cys	Ile	Lys	Lys	Ala	Lys	Lys	Thr	Leu	Ala	Val	Pro
			20					25					30		
Gln	Gln	Arg	Leu	Ile	Leu	Leu	Pro	Arg	Val	Gly	Ala	Pro	Arg	Ser	Cys
		35					40					45			
Ala	Arg	Ala	Cys	Ser	Ala	Ser	Pro	Ala	Leu	Ser	Ser	Arg	Cys	Pro	Ala
	50					55					60				
Ser	Pro	Arg	Pro	Ser	Arg	Arg	Leu	Pro	Ala	Phe	Arg	Gly	Pro	Glu	Ser
65					70					75				80	
His	Pro	Ala	Lys	Arg	Ala	Gly	Pro	Gly	Gln	Ala	Arg	Thr	Pro	Ala	Ala
				85					90					95	
Ser	Pro	Phe	Pro	Gly	Ser	Ala	Pro	Ser	Ala	Pro	Ser	Gly	Ser	Arg	Ala
			100					105					110		
His	Asp	Ala	Ala	Gly	Pro	Trp	Leu	Ala	Ala	Ala	Ala	Leu	Pro	Arg	Leu
		115					120					125			
Ala	Leu	Leu	Pro	Gly	Leu	Gly	Ala	Arg	Ala	Leu	Pro	Leu	Trp	Pro	Ala
	130					135					140				
Arg	Leu	Leu	Leu	Gln	Ala	Gln	Asn	Cys	Lys	Pro	Ile	Pro	Ala	Asn	Leu
145				150						155					160
Gln	Leu	Cys	His	Gly	Ile	Glu	Tyr	Gln	Asn	Met	Arg	Leu	Pro	Asn	Leu
				165					170					175	
Leu	Gly	His	Glu	Thr	Met	Lys	Glu	Val	Leu	Glu	Gln	Ala	Gly	Ala	Trp
			180					185					190		
Ile	Pro	Leu	Val	Met	Lys	Gln	Cys	His	Pro	Asp	Thr	Lys	Lys	Phe	Leu
		195				200						205			
Cys	Ser	Leu	Phe	Ala	Pro	Val	Cys	Leu	Asp	Asp	Leu	Asp	Glu	Thr	Ile
	210					215					220				
Gln	Pro	Cys	His	Ser	Leu	Cys	Val	Gln	Val	Lys	Asp	Arg	Cys	Ala	Pro
225					230					235					240

Val	Met	Ser	Ala	Phe 245	Gly	Phe	Pro	Trp	Pro 250	Asp	Met	Leu	Glu	Cys 255	Asp
Arg	Phe	Pro	Gln 260	Asp	Asn	Asp	Leu	Cys 265	Ile	Pro	Leu	Ala	Ser 270	Ser	Asp
His	Leu	Leu 275	Pro	Ala	Thr	Glu	Glu 280	Ala	Pro	Lys	Val	Cys 285	Glu	Ala	Cys
Lys	Asn 290	Lys	Asn	Asp	Asp	Asp 295	Asn	Asp	Ile	Met	Glu 300	Thr	Leu	Cys	Lys
Asn 305	Asp	Phe	Ala	Leu	Lys 310	Ile	Lys	Val	Lys	Glu 315	Ile	Thr	Tyr	Ile	Asn 320
Arg	Asp	Thr	Lys	Ile 325	Ile	Leu	Glu	Thr	Lys 330	Ser	Lys	Thr	Ile	Tyr 335	Lys
Leu	Asn	Gly	Val 340	Ser	Glu	Arg	Asp	Leu 345	Lys	Lys	Ser	Val	Leu 350	Trp	Leu
Lys	Asp	Ser 355	Leu	Gln	Cys	Thr	Cys 360	Glu	Glu	Met	Asn	Asp 365	Ile	Asn	Ala
Pro	Tyr 370	Leu	Val	Met	Gly	Gln 375	Lys	Gln	Gly	Gly	Glu 380	Leu	Val	Ile	Thr
Ser 385	Val	Lys	Arg	Trp	Gln 390	Lys	Gly	Gln	Arg	Glu 395	Phe	Lys	Arg	Ile	Ser 400
Arg	Ser	Ile	Arg	Lys 405	Leu	Gln	Cys								

<210> 432

<211> 323

<212> PRT

<213> homo sapiens

<400> 432

Val 1	Ile	Ser	Phe	Thr 5	Phe	Ile	Phe	Ser	Ala 10	Lys	Ser	Phe	Leu	Gln 15	Ser
Val	Ser	Ile	Met 20	Ser	Leu	Ser	Ser	Ser 25	Phe	Leu	Phe	Leu	Gln 30	Ala	Ser
His	Thr	Phe 35	Gly	Ala	Ser	Ser	Val 40	Ala	Gly	Arg	Arg	Trp 45	Ser	Leu	Leu
Ala	Arg 50	Gly	Met	Gln	Arg	Ser 55	Leu	Ser	Trp	Gly	Lys 60	Arg	Ser	His	Ser
Ser 65	Met	Ser	Gly	Gln	Gly 70	Lys	Pro	Lys	Ala	Asp 75	Met	Thr	Gly	Ala	Gln 80
Arg	Ser	Phe	Thr	Cys 85	Thr	Gln	Ser	Glu	Trp 90	His	Gly	Trp	Met	Val 95	Ser
Ser	Arg	Ser	Ser 100	Arg	Gln	Thr	Gly	Ala 105	Lys	Ser	Glu	His	Arg 110	Asn	Phe
Leu	Val	Ser	Gly	Trp	His	Cys	Phe	Met	Thr	Ser	Gly	Ile	Gln	Ala	Pro

	115						120					125				
Ala	Cys 130	Ser	Ser	Thr	Ser	Phe 135	Met	Val	Ser	Trp	Pro 140	Ser	Arg	Leu	Gly	
Ser 145	Arg	Met	Phe	Trp	Tyr 150	Ser	Met	Pro	Trp	His 155	Ser	Cys	Arg	Leu	Ala 160	
Gly	Met	Gly	Leu	Gln 165	Phe	Cys	Ala	Cys	Arg 170	Arg	Ser	Arg	Ala	Gly 175	Gln	
Arg	Gly	Arg	Ala 180	Arg	Ala	Pro	Ser	Pro 185	Gly	Ser	Ser	Ala	Arg 190	Arg	Gly	
Arg	Ala	Ala 195	Ala	Ala	Ser	Gln	Gly 200	Pro	Ala	Ala	Ser	Trp 205	Ala	Arg	Asp	
Pro	Glu 210	Gly	Ala	Glu	Gly	Ala 215	Glu	Pro	Gly	Lys	Gly 220	Glu	Ala	Ala	Gly	
Val 225	Arg	Ala	Cys	Pro	Gly 230	Pro	Ala	Leu	Phe	Ala 235	Gly	Cys	Asp	Ser	Gly 240	
Pro	Arg	Lys	Ala	Gly 245	Ser	Arg	Arg	Leu	Gly 250	Arg	Gly	Glu	Ala	Gly 255	His	
Arg	Glu	Asp	Ser 260	Ala	Gly	Glu	Ala	Leu 265	Gln	Ala	Arg	Ala	Gln 270	Leu	Arg	
Gly	Ala	Pro 275	Thr	Arg	Gly	Ser	Arg 280	Met	Ser	Arg	Cys	Trp 285	Gly	Thr	Ala	
Arg	Val 290	Phe	Leu	Ala	Phe	Phe 295	Met	Gln	Ile	Trp	Arg 300	Val	Gly	Gly	Ala	
Arg 305	Glu	Glu	Pro	Met	Lys 310	Gly	Asn	Pro	Arg	Arg 315	Ala	Gly	His	Tyr	Phe 320	
Leu	Gly	Leu														

<210> 433

<211> 333

<212> PRT

<213> homo sapiens

<400> 433

Arg 1	Gly	Arg	Thr	Trp 5	Glu	Leu	Phe	Leu	Ala 10	Gly	Arg	Arg	Val	Leu 15	Val
Thr	Gly	Ala	Gly 20	Lys	Gly	Ile	Gly	Arg 25	Gly	Thr	Val	Gln	Ala 30	Leu	His
Ala	Thr	Gly 35	Ala	Arg	Val	Val	Ala 40	Val	Ser	Arg	Thr	Gln 45	Ala	Asp	Leu
Asp	Ser 50	Leu	Val	Arg	Glu	Cys 55	Pro	Gly	Ile	Glu	Pro 60	Val	Cys	Val	Asp
Leu 65	Gly	Asp	Trp	Glu	Ala 70	Thr	Glu	Arg	Ala	Leu 75	Gly	Ser	Val	Gly	Pro 80
Val	Asp	Leu	Arg	Gly	Asp	Cys	Ala	Asp	Met	Glu	Leu	Phe	Leu	Ala	Gly

85								90				95			
Arg	Arg	Val	Leu 100	Val	Thr	Gly	Ala	Gly 105	Lys	Gly	Ile	Gly	Arg 110	Gly	Thr
Val	Gln	Ala 115	Leu	His	Ala	Thr	Gly 120	Ala	Arg	Val	Val	Ala 125	Val	Ser	Arg
Thr	Gln 130	Ala	Asp	Leu	Asp	Ser 135	Leu	Val	Arg	Glu	Cys 140	Pro	Gly	Ile	Glu
Pro 145	Val	Cys	Val	Asp	Leu 150	Gly	Asp	Trp	Glu	Ala 155	Thr	Glu	Arg	Ala	Leu 160
Gly	Ser	Val	Gly	Pro 165	Val	Asp	Leu	Leu	Val 170	Asn	Asn	Ala	Ala	Val 175	Ala
Leu	Leu	Gln	Pro 180	Phe	Leu	Glu	Val	Thr 185	Lys	Glu	Ala	Phe	Asp 190	Arg	Ser
Phe	Glu	Val 195	Asn	Leu	Arg	Ala	Val 200	Ile	Gln	Val	Ser	Gln 205	Ile	Val	Ala
Arg	Gly 210	Leu	Ile	Ala	Arg	Gly 215	Val	Pro	Gly	Ala	Ile 220	Val	Asn	Val	Ser
Ser 225	Gln	Cys	Ser	Gln	Arg 230	Ala	Val	Thr	Asn	His 235	Ser	Val	Tyr	Cys	Ser 240
Thr	Lys	Gly	Ala	Leu 245	Asp	Met	Leu	Thr	Lys 250	Val	Met	Ala	Leu	Glu 255	Leu
Gly	Pro	His	Lys 260	Ile	Arg	Val	Asn	Ala 265	Val	Asn	Pro	Thr	Val 270	Val	Met
Thr	Ser	Met 275	Gly	Gln	Ala	Thr	Trp 280	Ser	Asp	Pro	His	Lys 285	Ala	Lys	Thr
Met	Leu 290	Asn	Arg	Ile	Pro	Leu 295	Gly	Lys	Phe	Ala	Glu 300	Val	Glu	His	Val
Val 305	Asn	Ala	Ile	Leu	Phe 310	Leu	Leu	Ser	Asp	Arg 315	Ser	Gly	Met	Thr	Thr 320
Gly	Ser	Thr	Leu	Pro 325	Val	Glu	Gly	Gly	Phe 330	Trp	Ala	Cys			

<210> 434

<211> 210

<212> PRT

<213> homo sapiens

<400> 434

Ala 1	Pro	Gly	His	Asn 5	Leu	Arg	His	Leu	Asp 10	Asp	Arg	Thr	Gln	Val 15	His
Leu	Lys	Gly	Ser 20	Val	Lys	Gly	Leu	Leu 25	Gly	Asp	Leu	Gln	Glu 30	Gly	Leu
Gln	Gln	Gly 35	Asp	Ser	Gly	Val	Val 40	His	Gln	Gln	Val	His 45	Gly	Ala	His

Ala	Ala	Gln	Arg	Pro	Leu	Gly	Gly	Leu	Pro	Val	Thr	Gln	Val	His	Ala
	50					55					60				
His	Gly	Phe	Tyr	Pro	Arg	Ala	Leu	Ala	Asp	Lys	Ala	Val	Lys	Ile	Arg
65					70					75					80
Leu	Ser	Pro	Ala	His	Ser	His	His	Pro	Arg	Ala	Arg	Arg	Val	Gln	Arg
				85					90					95	
Leu	Asp	Arg	Ala	Ala	Pro	Tyr	Thr	Phe	Ala	Cys	Pro	Gly	Asp	Gln	His
			100					105					110		
Pro	Ala	Ala	Arg	Glu	Glu	Gln	Leu	His	Val	Gly	Ala	Val	Ser	Ala	Gln
		115					120					125			
Val	His	Gly	Ala	His	Ala	Ala	Gln	Arg	Pro	Leu	Gly	Gly	Leu	Pro	Val
	130					135					140				
Thr	Gln	Val	His	Ala	His	Gly	Phe	Tyr	Pro	Arg	Ala	Leu	Ala	Asp	Lys
145					150					155					160
Ala	Val	Lys	Ile	Arg	Leu	Ser	Pro	Ala	His	Ser	His	His	Pro	Arg	Ala
				165					170					175	
Arg	Arg	Val	Gln	Arg	Leu	Asp	Arg	Ala	Ala	Pro	Tyr	Thr	Phe	Ala	Cys
			180					185					190		
Pro	Gly	Asp	Gln	His	Pro	Ala	Ala	Arg	Glu	Glu	Gln	Leu	Pro	Cys	Ser
		195					200					205			
Pro	Thr														
	210														

<210> 435

<211> 132

<212> PRT

<213> homo sapiens

<400> 435

Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Gly	Ser	Arg	Ile	Arg	Phe
1				5					10					15	
Ile	Gly	Gly	Ile	Gly	Gly	Arg	Met	Ser	Thr	Ala	Trp	Gly	Leu	Arg	Cys
			20					25					30		
Val	Glu	Gly	Ala	Gln	Gln	Ala	Gln	Lys	Pro	Pro	Ser	Thr	Gly	Lys	Val
		35					40					45			
Glu	Pro	Val	Val	Met	Pro	Leu	Arg	Ser	Leu	Ser	Arg	Lys	Arg	Met	Ala
	50					55					60				
Phe	Thr	Thr	Cys	Ser	Thr	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Ile	Arg	Phe
65					70					75					80
Ser	Ile	Val	Leu	Ala	Leu	Trp	Gly	Ser	Leu	Gln	Val	Ala	Trp	Pro	Met
				85					90					95	
Asp	Val	Ile	Thr	Thr	Val	Gly	Phe	Thr	Ala	Phe	Thr	Arg	Ile	Leu	Trp
			100					105					110		
Gly	Pro	Ser	Ser	Arg	Ala	Ile	Thr	Leu	Val	Ser	Met	Ser	Arg	Ala	Pro
		115					120					125			

Leu Val Glu Gln  
130

<210> 436

<211> 94

<212> PRT

<213> homo sapiens

<400> 436

Lys 1	Ala	Lys	Ser	Trp 5	Val	Pro	Ser	Asp	Phe 10	Arg	Phe	Gln	Glu	Leu 15	Pro
Glu	Asn	Thr	Arg 20	Ser	Gln	Arg	Val	Ile 25	Phe	Trp	Ser	Leu	Phe 30	Cys	Arg
Asp	Ser	Trp 35	Glu	Tyr	Gly	His	Pro 40	Ala	Pro	Arg	Cys	Gly 45	Asn	Glu	Ser
Ser	Arg 50	Ser	Gly	Glu	Ala	Ala 55	Leu	Ala	Asp	Val	Gln 60	Leu	Ala	Ala	Pro
Val 65	Ser	Asn	Gln	Leu	His 70	Pro	Asp	Gly	Val	Glu 75	Asp	Arg	Gly	Val	Gly 80
Gly	Leu	Leu	Pro	Glu 85	Leu	His	His	Ala	Glu 90	Pro	Tyr	Leu	Val		

<210> 437

<211> 70

<212> PRT

<213> homo sapiens

<400> 437

Phe 1	Ser	Gly	Val	Cys 5	Phe	Ala	Gly	Ile	Ala 10	Gly	Ser	Met	Ala	Thr 15	Leu
Leu	His	Asp	Ala 20	Val	Met	Asn	Pro	Ala 25	Glu	Val	Val	Lys	Gln 30	Arg	Leu
Gln	Met	Tyr 35	Asn	Ser	Gln	His	Arg 40	Ser	Ala	Ile	Ser	Cys 45	Ile	Arg	Thr
Val	Trp 50	Arg	Thr	Glu	Gly	Leu 55	Gly	Ala	Phe	Tyr	Arg 60	Ser	Tyr	Thr	Thr
Pro 65	Ser	Pro	Ile	Ser	Cys 70										

<210> 438

<211> 98

<212> PRT

<213> homo sapiens

<400> 438

Lys 1	Ala	Pro	Asn	Pro 5	Ser	Val	Leu	His	Thr 10	Val	Arg	Met	Gln	Leu 15	Ile
Ala	Asp	Arg	Cys 20	Cys	Glu	Leu	Tyr	Ile 25	Cys	Lys	Arg	Cys	Phe 30	Thr	Thr

Ser	Ala	Gly	Phe	Ile	Thr	Ala	Ser	Trp	Ser	Arg	Val	Ala	Ile	Leu	Pro
		35					40					45			
Ala	Ile	Pro	Ala	Lys	Gln	Thr	Pro	Glu	Asn	Tyr	Pro	Leu	Arg	Ser	Gly
	50					55					60				
Val	Leu	Arg	Lys	Phe	Leu	Glu	Pro	Lys	Ile	Arg	Arg	Asn	Pro	Gly	Leu
	65				70					75					80
Ser	Phe	Leu	Arg	Ser	Lys	Met	Tyr	Tyr	Gln	Ser	Ala	Gln	Val	Ser	Thr
				85					90					95	

Asp Ser

<210> 439  
 <211> 270  
 <212> PRT  
 <213> homo sapiens

<400> 439

Arg	Ser	Val	Val	Arg	Arg	Cys	Leu	Lys	Met	Ala	Ala	Glu	Glu	Pro	Gln
1				5					10					15	
Gln	Gln	Lys	Gln	Glu	Pro	Leu	Gly	Ser	Asp	Ser	Glu	Gly	Val	Asn	Cys
			20					25					30		
Leu	Ala	Tyr	Asp	Glu	Ala	Ile	Met	Ala	Gln	Gln	Asp	Arg	Ile	Gln	Gln
		35					40					45			
Glu	Ile	Ala	Val	Gln	Asn	Pro	Leu	Val	Ser	Glu	Arg	Leu	Glu	Leu	Ser
	50					55					60				
Val	Leu	Tyr	Lys	Glu	Tyr	Ala	Glu	Asp	Asp	Asn	Ile	Tyr	Gln	Gln	Lys
	65				70					75					80
Ile	Lys	Asp	Leu	His	Lys	Lys	Tyr	Ser	Tyr	Ile	Arg	Lys	Thr	Arg	Pro
				85					90					95	
Asp	Gly	Asn	Cys	Phe	Tyr	Arg	Ala	Phe	Gly	Phe	Ser	His	Leu	Glu	Ala
			100					105					110		
Leu	Leu	Asp	Asp	Ser	Lys	Glu	Leu	Gln	Arg	Phe	Lys	Ala	Val	Ser	Ala
		115					120					125			
Lys	Ser	Lys	Glu	Asp	Leu	Val	Ser	Gln	Gly	Phe	Thr	Glu	Phe	Thr	Ile
	130					135					140				
Glu	Asp	Phe	His	Asn	Thr	Phe	Met	Asp	Leu	Ile	Glu	Gln	Val	Glu	Lys
	145				150					155					160
Gln	Thr	Ser	Val	Ala	Asp	Leu	Leu	Ala	Ser	Phe	Asn	Asp	Gln	Ser	Thr
				165					170					175	
Ser	Asp	Tyr	Leu	Val	Val	Tyr	Leu	Arg	Leu	Leu	Thr	Ser	Gly	Tyr	Leu
			180					185					190		
Gln	Arg	Glu	Ser	Lys	Phe	Phe	Glu	His	Phe	Ile	Glu	Gly	Gly	Arg	Thr
		195					200					205			
Val	Lys	Glu	Phe	Cys	Gln	Gln	Glu	Val	Glu	Pro	Met	Cys	Lys	Glu	Ser
	210					215					220				

Asp 225	His	Ile	His	Ile	Ile 230	Ala	Leu	Ala	Gln	Ala 235	Leu	Ser	Val	Ser	Ile 240
Gln	Val	Glu	Tyr	Met 245	Asp	Arg	Gly	Glu	Gly 250	Gly	Thr	Thr	Asn	Pro 255	His
Ile	Phe	Pro	Glu 260	Gly	Phe	Arg	Ala	Gln 265	Gly	Leu	Thr	Leu	Phe 270		

<210> 440  
 <211> 145  
 <212> PRT  
 <213> homo sapiens

<400> 440

Arg 1	Trp	Arg	Arg	Arg 5	Asn	Leu	Ser	Ser	Arg 10	Ser	Arg	Ser	Arg	Trp 15	Ala
Ala	Thr	Pro	Lys 20	Val	Leu	Thr	Val	Trp 25	Pro	Met	Met	Lys	Pro 30	Ser	Trp
Leu	Ser	Arg 35	Thr	Glu	Phe	Ser	Lys 40	Arg	Leu	Leu	Cys	Arg 45	Thr	Leu	Trp
Cys	Gln 50	Ser	Gly	Trp	Ser	Ser 55	Arg	Ser	Tyr	Thr	Arg 60	Ser	Met	Leu	Lys
Met 65	Thr	Thr	Ser	Ile	Asn 70	Arg	Arg	Ser	Arg	Thr 75	Ser	Thr	Lys	Ser	Thr 80
Arg	Thr	Ser	Ala	Arg 85	Pro	Gly	Leu	Thr	Ala 90	Thr	Val	Ser	Ile	Gly 95	Leu
Ser	Asp	Ser	Pro 100	Thr	Trp	Arg	His	Cys 105	Trp	Met	Thr	Ala	Arg 110	Ser	Cys
Ser	Gly	Ser 115	Arg	Leu	Cys	Leu	Pro 120	Arg	Ala	Arg	Lys	Thr 125	Trp	Cys	Pro
Arg	Ala 130	Ser	Leu	Asn	Ser	Gln 135	Leu	Arg	Ile	Ser	Thr 140	Thr	Arg	Ser	Trp
Thr 145															

<210> 441  
 <211> 210  
 <212> PRT  
 <213> homo sapiens

<400> 441

Ile 1	Ala	Pro	Ser	Arg 5	Leu	Lys	Gln	Gly	Lys 10	Thr	Leu	Gly	Ser	Glu 15	Ala
Leu	Arg	Glu	Asp 20	Val	Arg	Ile	Gly	Gly 25	Ala	Ala	Leu	Ala	Ala 30	Val	His
Val	Leu	His 35	Leu	Asp	Gly	His	Ala 40	Glu	Gly	Leu	Gly	Gln 45	Arg	Asn	Asp



Val	Asp	Val	Val	Ala	Leu	Leu	Ala	His	Gly	Leu	His	Leu	Leu	Leu	Ala
	50					55					60				
Glu	Leu	Leu	Asp	Ser	Pro	Ser	Thr	Leu	Asp	Glu	Val	Leu	Glu	Glu	Leu
65					70					75					80
Ala	Leu	Ala	Leu	Gln	Val	Ala	Arg	Gly	Glu	Gln	Pro	Gln	Val	Asp	His
				85					90					95	
Lys	Val	Val	Gly	Gly	Ala	Leu	Val	Ile	Glu	Gly	Gly	Gln	Gln	Val	Gly
			100					105					110		
Asp	Arg	Gly	Leu	Leu	Leu	His	Leu	Leu	Asn	Gln	Val	His	Glu	Arg	Val
		115					120					125			
Val	Glu	Ile	Leu	Asn	Cys	Glu	Phe	Ser	Glu	Ala	Leu	Gly	His	Gln	Val
	130					135					140				
Phe	Leu	Ala	Leu	Gly	Arg	His	Ser	Leu	Glu	Pro	Leu	Gln	Leu	Leu	Ala
145					150					155					160
Val	Ile	Gln	Gln	Cys	Leu	Gln	Val	Gly	Glu	Ser	Glu	Ser	Pro	Ile	Glu
				165					170					175	
Thr	Val	Ala	Val	Arg	Pro	Gly	Leu	Ala	Asp	Val	Arg	Val	Leu	Phe	Val
			180					185					190		
Glu	Val	Leu	Asp	Leu	Leu	Leu	Ile	Asp	Val	Val	Ile	Phe	Ser	Ile	Leu
		195					200					205			
Leu	Val														
	210														

<210> 442

<211> 322

<212> PRT

<213> homo sapiens

<400> 442

Asn	Ser	Glu	Arg	Gly	Arg	Leu	Gln	Ala	Met	Met	Thr	His	Leu	His	Val
1				5					10					15	
Lys	Ser	Thr	Glu	Pro	Lys	Ala	Ala	Pro	Gln	Pro	Leu	Asn	Leu	Val	Ser
			20					25					30		
Ser	Val	Thr	Leu	Ser	Lys	Ser	Ala	Ser	Glu	Ala	Ser	Pro	Gln	Ser	Leu
		35					40					45			
Pro	His	Thr	Pro	Thr	Thr	Pro	Thr	Ala	Pro	Leu	Thr	Pro	Val	Thr	Gln
	50					55					60				
Gly	Pro	Ser	Val	Ile	Thr	Thr	Thr	Ser	Met	His	Thr	Val	Gly	Pro	Ile
65					70					75					80
Arg	Arg	Arg	Tyr	Ser	Asp	Lys	Tyr	Asn	Val	Pro	Ile	Ser	Ser	Ala	Asp
				85					90					95	
Ile	Ala	Gln	Asn	Gln	Glu	Phe	Tyr	Lys	Asn	Ala	Glu	Val	Arg	Pro	Pro
			100					105					110		
Phe	Thr	Tyr	Ala	Ser	Leu	Ile	Arg	Gln	Ala	Ile	Leu	Glu	Ser	Pro	Glu
		115					120					125			

Lys	Gln	Leu	Thr	Leu	Asn	Glu	Ile	Tyr	Asn	Trp	Phe	Thr	Arg	Met	Phe
	130					135					140				
Ala	Tyr	Phe	Arg	Arg	Asn	Ala	Ala	Thr	Trp	Lys	Asn	Ala	Val	Arg	His
145					150					155					160
Asn	Leu	Ser	Leu	His	Lys	Cys	Phe	Val	Arg	Val	Glu	Asn	Val	Lys	Gly
				165					170					175	
Ala	Val	Trp	Thr	Val	Asp	Glu	Val	Glu	Phe	Gln	Lys	Arg	Arg	Pro	Gln
			180					185					190		
Lys	Ile	Ser	Gly	Asn	Pro	Ser	Leu	Ile	Lys	Asn	Met	Gln	Ser	Ser	His
		195					200					205			
Ala	Tyr	Cys	Thr	Pro	Leu	Asn	Ala	Ala	Leu	Gln	Ala	Ser	Met	Ala	Glu
	210					215					220				
Asn	Ser	Ile	Pro	Leu	Tyr	Thr	Thr	Ala	Ser	Met	Gly	Asn	Pro	Thr	Leu
225					230					235					240
Gly	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Glu	Glu	Leu	Asn	Gly	Ala	Met	Glu
				245					250					255	
His	Thr	Asn	Ser	Asn	Glu	Ser	Asp	Ser	Ser	Pro	Gly	Arg	Ser	Pro	Met
			260					265					270		
Gln	Ala	Val	His	Pro	Val	His	Val	Lys	Glu	Glu	Pro	Leu	Asp	Pro	Glu
		275					280					285			
Glu	Ala	Glu	Gly	Pro	Leu	Ser	Leu	Val	Thr	Thr	Ala	Asn	His	Ser	Pro
	290					295					300				
Asp	Phe	Asp	His	Asp	Arg	Asp	Tyr	Glu	Asp	Glu	Pro	Val	Asn	Glu	Asp
305					310					315					320
Met	Glu														

<210> 443

<211> 103

<212> PRT

<213> homo sapiens

<400> 443

Phe	Gly	Thr	Arg	Ala	Pro	Ala	Ser	His	Asp	Asp	Pro	Pro	Ala	Cys	Glu
1				5					10					15	
Val	Tyr	Arg	Thr	Gln	Ser	Cys	Pro	Ser	Ala	Pro	Glu	Ser	Gly	Ile	Lys
			20					25					30		
Cys	His	Pro	Leu	Gln	Val	Arg	Ile	Gly	Gly	Phe	Ser	Thr	Glu	Leu	Thr
		35					40					45			
Ser	Tyr	Ser	Asn	Asp	Pro	Asn	Arg	Pro	Pro	Asp	Ser	Arg	His	Pro	Arg
	50					55					60				
Pro	Leu	Cys	His	His	Asn	His	Gln	His	Ala	His	Gly	Gly	Thr	His	Pro
65					70					75					80
Gln	Ala	Val	Leu	Arg	Gln	Ile	Gln	Arg	Ala	His	Phe	Val	Ser	Arg	Tyr
				85					90					95	

Cys Ala Glu Pro Arg Ile Leu  
100

<210> 444  
<211> 101  
<212> PRT  
<213> homo sapiens

<400> 444

Ser 1	Leu	Ser	Trp	Ser 5	Lys	Ser	Gly	Leu	Trp 10	Leu	Ala	Val	Val	Thr 15	Lys
Asp	Arg	Gly	Pro 20	Ser	Ala	Ser	Ser	Gly 25	Ser	Arg	Gly	Ser	Ser 30	Leu	Thr
Cys	Thr	Gly 35	Cys	Thr	Ala	Cys	Ile 40	Gly	Asp	Leu	Pro	Gly 45	Leu	Leu	Ser
Leu	Ser 50	Leu	Leu	Leu	Val	Cys 55	Ser	Ile	Ala	Pro	Phe 60	Ser	Ser	Ser	Arg
Ile 65	Ala	Leu	Ala	Lys	Leu 70	Pro	Arg	Val	Gly	Phe 75	Pro	Met	Glu	Ala	Val 80
Val	Tyr	Arg	Gly	Ile 85	Leu	Phe	Ser	Ala	Ile 90	Glu	Ala	Cys	Lys	Ala 95	Ala
Leu	Arg	Gly	Val 100	Gln											

<210> 445  
<211> 539  
<212> PRT  
<213> homo sapiens

<400> 445

Leu 1	Asp	Val	Gln	Val 5	Lys	Asp	Asp	Ser	Arg 10	Ala	Leu	Thr	Leu	Gly 15	Ala
Leu	Thr	Leu	Pro 20	Leu	Ala	Arg	Leu	Leu 25	Thr	Ala	Pro	Glu	Leu 30	Ile	Leu
Asp	Gln	Trp 35	Phe	Gln	Leu	Ser	Ser 40	Ser	Gly	Pro	Asn	Ser 45	Arg	Leu	Tyr
Met	Lys 50	Leu	Val	Met	Arg	Ile 55	Leu	Tyr	Leu	Asp	Ser 60	Ser	Glu	Ile	Cys
Phe 65	Pro	Thr	Val	Pro	Gly 70	Cys	Pro	Gly	Ala	Trp 75	Asp	Val	Asp	Ser	Glu 80
Asn	Pro	Gln	Arg	Gly 85	Ser	Ser	Val	Asp	Ala 90	Pro	Pro	Arg	Pro	Cys 95	His
Thr	Thr	Pro	Asp 100	Ser	Gln	Phe	Gly	Thr 105	Glu	His	Val	Leu	Arg 110	Ile	His
Val	Leu	Glu 115	Ala	Gln	Asp	Leu	Ile 120	Ala	Lys	Asp	Arg	Phe 125	Leu	Gly	Gly

Leu	Val	Lys	Gly	Lys	Ser	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ala	Gly
	130					135					140				
Arg	Ser	Phe	Arg	Ser	His	Val	Val	Arg	Glu	Asp	Leu	Asn	Pro	Arg	Trp
145					150					155					160
Asn	Glu	Val	Phe	Glu	Val	Ile	Val	Thr	Ser	Val	Pro	Gly	Gln	Glu	Leu
				165					170					175	
Glu	Val	Glu	Val	Phe	Asp	Lys	Asp	Leu	Asp	Lys	Asp	Asp	Phe	Leu	Gly
			180					185					190		
Arg	Cys	Lys	Val	Arg	Leu	Thr	Thr	Val	Leu	Asn	Ser	Gly	Phe	Leu	Asp
		195					200					205			
Glu	Trp	Leu	Thr	Leu	Glu	Asp	Val	Pro	Ser	Gly	Arg	Leu	His	Leu	Arg
	210					215					220				
Leu	Glu	Arg	Leu	Thr	Pro	Arg	Pro	Thr	Ala	Ala	Glu	Leu	Glu	Glu	Val
225					230					235					240
Leu	Gln	Val	Asn	Ser	Leu	Ile	Gln	Thr	Gln	Lys	Ser	Ala	Glu	Leu	Ala
				245					250					255	
Ala	Ala	Leu	Leu	Ser	Ile	Tyr	Met	Glu	Arg	Ala	Glu	Asp	Leu	Pro	Leu
			260					265					270		
Arg	Lys	Gly	Thr	Lys	His	Leu	Ser	Pro	Tyr	Ala	Thr	Leu	Thr	Val	Gly
		275					280					285			
Asp	Ser	Ser	His	Lys	Thr	Lys	Thr	Ile	Ser	Gln	Thr	Ser	Ala	Pro	Val
	290					295					300				
Trp	Asp	Glu	Ser	Ala	Ser	Phe	Leu	Ile	Arg	Lys	Pro	His	Thr	Glu	Ser
305					310					315					320
Leu	Glu	Leu	Gln	Val	Arg	Gly	Glu	Gly	Thr	Gly	Val	Leu	Gly	Ser	Leu
				325					330					335	
Ser	Leu	Pro	Leu	Ser	Glu	Leu	Leu	Val	Ala	Asp	Gln	Leu	Cys	Leu	Asp
			340					345					350		
Arg	Trp	Phe	Thr	Leu	Ser	Ser	Gly	Gln	Gly	Gln	Val	Leu	Leu	Arg	Ala
		355					360					365			
Gln	Leu	Gly	Ile	Leu	Val	Ser	Gln	His	Ser	Gly	Val	Glu	Ala	His	Ser
	370					375					380				
His	Ser	Tyr	Ser	His	Ser	Ser	Ser	Ser	Leu	Ser	Glu	Glu	Pro	Glu	Leu
385					390					395					400
Ser	Gly	Gly	Pro	Pro	His	Ile	Thr	Ser	Ser	Ala	Pro	Glu	Leu	Arg	Gln
				405					410					415	
Arg	Leu	Thr	His	Val	Asp	Ser	Pro	Leu	Glu	Ala	Pro	Ala	Gly	Pro	Leu
			420					425					430		
Gly	Gln	Val	Lys	Leu	Thr	Leu	Trp	Tyr	Tyr	Ser	Glu	Glu	Arg	Lys	Leu
		435					440					445			
Val	Ser	Ile	Val	His	Gly	Cys	Arg	Ser	Leu	Arg	Gln	Asn	Gly	Arg	Asp
	450					455					460				

Pro 465	Pro	Asp	Pro	Tyr	Val 470	Ser	Leu	Leu	Leu	Leu 475	Pro	Asp	Lys	Asn	Arg 480
Gly	Thr	Lys	Arg	Arg 485	Thr	Ser	Gln	Lys	Lys 490	Arg	Thr	Leu	Ser	Pro 495	Glu
Phe	Asn	Glu	Arg 500	Phe	Glu	Trp	Glu	Leu 505	Pro	Leu	Asp	Glu	Ala 510	Gln	Arg
Arg	Lys	Leu 515	Asp	Val	Ser	Val	Lys 520	Ser	Asn	Ser	Ser	Phe 525	Met	Ser	Arg
Glu	Arg 530	Asp	Cys	Trp	Gly	Arg 535	Cys	Ser	Trp	Thr					

<210> 446

<211> 99

<212> PRT

<213> homo sapiens

<400> 446

Leu 1	Leu	Cys	Leu	Pro 5	Ala	Phe	Val	Ser	Leu 10	His	His	Arg	Leu	Asn 15	Val
Met	Ser	Leu	Lys 20	Leu	Gly	Ser	Lys	Gly 25	Arg	Ala	Cys	Ala	Leu 30	Gln	Pro
Phe	His	Leu 35	Thr	Gly	Pro	Tyr	Ser 40	Gly	Leu	Cys	Leu	Thr 45	Lys	Glu	Lys
Asn	Arg 50	Met	Phe	Pro	Leu	Leu 55	His	Gly	Leu	Tyr	Pro 60	Ser	Gly	Pro	Leu
Gly 65	Arg	Gly	Pro	Glu	Leu 70	Ala	Val	Ser	Cys	Phe 75	Ala	Cys	Thr	Leu	Phe 80
Ser	Leu	Pro	Pro	Asn 85	Ser	Ser	Gly	Pro	Ser 90	Val	Ser	Val	Pro	Gly 95	Gln
Trp	Gln	His													

<210> 447

<211> 112

<212> PRT

<213> homo sapiens

<400> 447

Val 1	Trp	Ile	Lys	Leu 5	Phe	Thr	Cys	Ser	Thr 10	Ser	Ser	Asn	Ser	Ala 15	Ala
Val	Gly	Arg	Gly 20	Val	Arg	Arg	Ser	Arg 25	Arg	Lys	Cys	Arg	Arg 30	Pro	Asp
Gly	Thr	Ser 35	Ser	Arg	Val	Ser	His 40	Ser	Ser	Arg	Lys	Pro 45	Leu	Phe	Lys
Thr 50	Val	Val	Arg	Arg	Thr	Leu 55	His	Leu	Pro	Arg	Lys 60	Ser	Ser	Leu	Ser
Lys 65	Ser	Leu	Ser	Lys	Thr 70	Ser	Thr	Ser	Ser	Ser 75	Trp	Pro	Gly	Thr	Asp 80

Val	Thr	Ile	Thr	Ser 85	Lys	Thr	Ser	Phe	Gln 90	Arg	Gly	Leu	Arg	Ser 95	Ser
-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Arg	Thr	Thr	Trp 100	Leu	Arg	Lys	Leu	Arg 105	Pro	Ala	Asn	Phe	Ser 110	Leu	Thr
-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----	-----	-----	------------	-----	-----

<210> 448

<400> 448

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<210> 449

<400> 449

000

<210> 450

<400> 450

000

<210> 451

<211> 56

<212> PRT

<213> homo sapiens

<400> 451

Phe 1	Phe	Phe	Phe	Phe 5	Val	Glu	Thr	Gly	Phe 10	Arg	His	Val	Asp	Glu 15	Thr
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Gly	Leu	Glu	Leu 20	Leu	Ala	Ser	Ser	Asp 25	Leu	Pro	Pro	Gln	Leu 30	Leu	Lys
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

Val	Leu	Gly 35	Leu	Tyr	Arg	His	Glu 40	Pro	Leu	Ser	Leu	Ala 45	Leu	Lys	Arg
-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----

Phe	Ser 50	Gln	Arg	Pro	Ser	Val 55	Arg
-----	-----------	-----	-----	-----	-----	-----------	-----

<210> 452

<211> 56

<212> PRT

<213> homo sapiens

<400> 452

Ile 1	Arg	Phe	Gly	Ile 5	Ser	Cys	Pro	Gly	Pro 10	Gly	Ile	Ser	Leu	Gln 15	Glu
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Pro	Leu	Pro	Leu 20	Cys	Trp	Arg	His	Ser 25	Phe	Arg	Ile	Arg	Arg 30	Arg	Arg
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

Glu	Lys	Arg 35	Lys	Cys	Lys	Gly	Gly 40	Arg	Ser	Phe	Pro	Gly 45	Arg	Thr	Ile
-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----

Ser	Val 50	Thr	His	Met	Asp	Pro 55	Arg
-----	-----------	-----	-----	-----	-----	-----------	-----

<210> 453

<211> 57

<212> PRT

<213> homo sapiens

<400> 453

Val 1	Thr	Glu	Met	Val 5	Arg	Pro	Gly	Lys	Asp 10	Leu	Pro	Pro	Leu	His 15	Phe
Leu	Phe	Ser	Leu 20	Leu	Leu	Leu	Ile	Leu 25	Lys	Leu	Cys	Leu	Gln 30	Gln	Arg
Gly	Arg	Gly 35	Ser	Cys	Arg	Glu	Ile 40	Pro	Gly	Pro	Gly	Gln 45	Glu	Met	Pro
Asn	Leu 50	Ile	Tyr	Leu	Thr	Glu 55	Gly	Leu							

<210> 454

<211> 80

<212> PRT

<213> homo sapiens

<400> 454

Ile 1	Leu	Ala	Phe	Trp 5	Arg	Ala	Ala	Pro	Leu 10	Trp	His	His	Gln	Thr 15	Leu
Leu	Cys	Phe	Pro 20	Ser	Thr	Trp	Asn	Ser 25	Ser	Asn	Ile	Arg	Gly 30	Cys	Glu
Gly	Leu	Ala 35	Ile	Leu	Leu	Ser	Trp 40	Val	His	Val	Ser	Asp 45	Arg	Asn	Gly
Ala	Ala 50	Trp	Glu	Arg	Ser	Pro 55	Ser	Phe	Thr	Phe	Ser 60	Leu	Leu	Pro	Pro
Pro 65	Pro	Tyr	Ser	Lys	Thr 70	Val	Pro	Pro	Thr	Glu 75	Gly	Gln	Gly	Leu	Leu 80

<210> 455

<211> 182

<212> PRT

<213> homo sapiens

<400> 455

Ala 1	Arg	Leu	Pro	Leu 5	Leu	Ala	Ala	Glu	Asp 10	Arg	Gly	Gln	Pro	Gly 15	Ser
Val	Lys	Asp	Pro 20	Lys	Met	Ala	Gly	Arg 25	Lys	Leu	Ala	Leu	Lys 30	Thr	Ile
Asp	Trp	Val 35	Ala	Phe	Ala	Glu	Ile 40	Ile	Pro	Gln	Asn	Gln 45	Lys	Ala	Ile
Ala	Ser 50	Ser	Leu	Lys	Ser	Trp 55	Asn	Glu	Thr	Leu	Thr 60	Ser	Arg	Leu	Ala
Ala 65	Leu	Pro	Glu	Asn	Pro 70	Pro	Ala	Ile	Asp	Trp 75	Ala	Tyr	Tyr	Lys	Ala 80
Asn	Val	Ala	Lys	Ala 85	Gly	Leu	Val	Asp	Asp 90	Phe	Glu	Lys	Lys	Phe 95	Asn
Ala	Leu	Lys	Val 100	Pro	Val	Pro	Glu	Asp 105	Lys	Tyr	Thr	Ala	Gln 110	Val	Asp

Ala	Glu	Glu	Lys	Glu	Asp	Val	Lys	Ser	Cys	Ala	Glu	Trp	Val	Ser	Leu
		115					120					125			
Ser	Lys	Ala	Arg	Ile	Val	Glu	Tyr	Glu	Lys	Glu	Met	Glu	Lys	Met	Lys
	130					135					140				
Asn	Leu	Ile	Pro	Phe	Asp	Gln	Met	Thr	Ile	Glu	Asp	Leu	Asn	Glu	Ala
145					150					155					160
Phe	Pro	Glu	Thr	Lys	Leu	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Trp	Pro	His
				165					170					175	
Gln	Pro	Ile	Glu	Asn	Leu										
			180												

<210> 456  
 <211> 76  
 <212> PRT  
 <213> homo sapiens

<400> 456

Ala	Gln	Ser	Ile	Ala	Gly	Gly	Phe	Ser	Gly	Lys	Ala	Ala	Asn	Leu	Glu
1				5					10					15	
Val	Arg	Val	Ser	Phe	Gln	Asp	Phe	Arg	Glu	Leu	Ala	Met	Ala	Phe	Trp
			20					25					30		
Phe	Trp	Gly	Met	Ile	Ser	Ala	Lys	Ala	Thr	Gln	Ser	Met	Val	Phe	Arg
		35					40					45			
Ala	Ser	Phe	Arg	Pro	Ala	Ile	Leu	Gly	Ser	Phe	Thr	Asp	Pro	Gly	Cys
	50					55					60				
Pro	Arg	Ser	Ser	Ala	Ala	Ser	Asn	Gly	Ser	Arg	Ala				
65					70					75					

<210> 457  
 <211> 104  
 <212> PRT  
 <213> homo sapiens

<400> 457

Cys	Pro	Glu	Cys	Val	Ile	Gln	Gly	Pro	Glu	Leu	Pro	Pro	Gly	Leu	Asn
1				5					10					15	
Phe	Ile	Asn	Ser	Gln	Leu	Val	Gly	Glu	Ala	Asn	Arg	Asp	Thr	Phe	Ser
			20					25					30		
Cys	Leu	Ile	Trp	Phe	Leu	Gly	Lys	Leu	His	Ser	Ser	Pro	Gln	Trp	Ser
		35					40					45			
Ser	Asp	Gln	Met	Glu	Leu	Ser	Ser	Ser	Ser	Ser	Pro	Ser	Leu	Ser	His
	50					55					60				
Ile	Leu	Gln	Ser	Trp	Pro	Leu	Arg	Glu	Thr	Pro	Thr	Gln	His	Lys	Ile
65					70					75					80
Ser	His	Leu	Leu	Phe	Leu	Arg	His	Pro	Pro	Gly	Gln	Tyr	Ile	Tyr	Pro
				85					90					95	
Leu	Ala	Arg	Glu	Pro	Ser	Ala	His								



<210> 458  
 <211> 223  
 <212> PRT  
 <213> homo sapiens

<400> 458

Arg 1	Gly	Ala	Gly	Gly 5	His	Gln	Gly	Glu	Ser 10	Gly	Arg	Pro	Glu	Gly 15	Trp
Pro	Pro	Pro	Phe 20	Leu	His	Pro	Arg	Gly 25	Arg	Phe	Gln	Val	Pro 30	Trp	Leu
Glu	Ser	Val 35	Leu	Ile	Val	Val	Ser 40	Asn	Asn	Ile	Asp	Glu 45	Glu	Ala	Leu
Ala	Arg 50	Leu	Ala	Gln	Glu	Gly 55	Ser	Glu	Val	Asn	Val 60	Ile	Gly	Ile	Gly
Thr 65	Ser	Val	Val	Thr	Cys 70	Pro	Gln	Gln	Pro	Ser 75	Leu	Gly	Gly	Val	Tyr 80
Lys	Leu	Val	Ala	Val 85	Gly	Gly	Gln	Pro	Arg 90	Met	Lys	Leu	Thr	Glu 95	Asp
Pro	Glu	Lys	Gln 100	Thr	Leu	Pro	Gly	Ser 105	Lys	Ala	Ala	Phe	Arg 110	Leu	Leu
Gly	Ser	Asp 115	Gly	Ser	Pro	Leu	Met 120	Asp	Met	Leu	Gln	Leu 125	Ala	Glu	Glu
Pro	Val 130	Pro	Gln	Ala	Gly	Gln 135	Glu	Leu	Arg	Val	Trp 140	Pro	Pro	Gly	Ala
Gln 145	Glu	Pro	Cys	Thr	Val 150	Arg	Pro	Ala	Gln	Val 155	Glu	Pro	Leu	Leu	Arg 160
Leu	Cys	Leu	Gln	Gln 165	Gly	Gln	Leu	Cys	Glu 170	Pro	Leu	Pro	Ser	Leu 175	Ala
Glu	Ser	Arg	Ala 180	Leu	Ala	Gln	Leu	Ser 185	Leu	Ser	Arg	Leu	Ser 190	Pro	Glu
His	Arg	Arg 195	Leu	Arg	Ser	Pro	Ala 200	Gln	Tyr	Gln	Val	Val 205	Leu	Ser	Glu
Arg	Leu 210	Gln	Ala	Leu	Val	Asn 215	Ser	Leu	Cys	Ala	Gly 220	Gln	Ser	Pro	

<210> 459  
 <211> 157  
 <212> PRT  
 <213> homo sapiens

<400> 459

Val 1	Ile	Arg	Val	Val 5	Ser	Ser	Gln	Pro	Arg 10	Ser	Glu	Ser	Gln	Gly 15	Asp
Cys	Pro	Ala	His 20	Arg	Leu	Phe	Thr	Arg 25	Ala	Cys	Ser	Leu	Ser 30	Asp	Ser

Thr	Thr	Trp	Tyr	Cys	Ala	Gly	Leu	Arg	Ser	Arg	Leu	Cys	Ser	Gly	Leu
		35					40					45			
Ser	Arg	Leu	Arg	Asp	Ser	Trp	Ala	Lys	Ala	Leu	Asp	Ser	Ala	Arg	Asp
	50					55					60				
Gly	Ser	Gly	Ser	His	Ser	Cys	Pro	Cys	Trp	Arg	Gln	Ser	Arg	Ser	Ser
65					70					75					80
Gly	Ser	Thr	Trp	Ala	Gly	Leu	Thr	Val	Gln	Gly	Ser	Trp	Ala	Pro	Gly
				85					90					95	
Gly	His	Thr	Leu	Ser	Ser	Cys	Pro	Ala	Cys	Gly	Thr	Gly	Ser	Ser	Ala
			100					105					110		
Asn	Cys	Ser	Met	Ser	Met	Ser	Gly	Asp	Pro	Ser	Glu	Pro	Arg	Ser	Arg
		115					120					125			
Lys	Ala	Ala	Leu	Leu	Pro	Gly	Asn	Val	Cys	Phe	Ser	Gly	Ser	Ser	Val
	130					135					140				
Ser	Phe	Ile	Arg	Gly	Trp	Pro	Pro	Thr	Ala	Thr	Ser	Leu			
145					150					155					

<210> 460  
 <211> 93  
 <212> PRT  
 <213> homo sapiens

<400> 460

Pro	Pro	Leu	Phe	Pro	His	Leu	Leu	Phe	Leu	Trp	Gly	Lys	Val	Ser	Asp
1				5					10					15	
Ser	Cys	Cys	Phe	Gln	Ser	Ala	Pro	Leu	Arg	Val	Ser	Gly	Gly	Leu	Pro
			20					25					30		
Arg	Thr	Gln	Thr	Val	His	Gln	Gly	Leu	Gln	Pro	Leu	Gly	Gln	His	His
		35					40					45			
Leu	Val	Leu	Cys	Arg	Ala	Pro	Gln	Pro	Pro	Val	Leu	Arg	Ala	Glu	Ser
	50					55					60				
Ala	Gln	Gly	Gln	Leu	Gly	Gln	Gly	Ser	Arg	Leu	Cys	Gln	Gly	Trp	Glu
65					70					75					80
Arg	Leu	Thr	Gln	Leu	Ser	Leu	Leu	Glu	Ala	Glu	Pro	Gln			
				85					90						

<210> 461  
 <211> 328  
 <212> PRT  
 <213> homo sapiens

<400> 461

Phe	Ser	Leu	Ile	Leu	Cys	Lys	His	Ser	Ile	Gly	Asp	Arg	Lys	Asn	Tyr
1				5					10					15	
Ala	Ser	Ala	Lys	Leu	Ser	Glu	Leu	Leu	Pro	Glu	Glu	Val	Glu	Ala	Glu
			20					25					30		

Val	Lys	Ala	Ala	Ala	Glu	Ile	Ser	Met	Gly	Thr	Glu	Val	Ser	Glu	Glu
		35					40					45			
Asp	Ile	Cys	Asn	Ile	Leu	His	Leu	Cys	Thr	Gln	Val	Ile	Glu	Ile	Ser
	50					55					60				
Glu	Tyr	Arg	Thr	Gln	Leu	Tyr	Glu	Tyr	Leu	Gln	Asn	Arg	Met	Met	Ala
65					70					75					80
Ile	Ala	Pro	Asn	Val	Thr	Val	Met	Val	Gly	Glu	Leu	Val	Gly	Ala	Arg
				85					90					95	
Leu	Ile	Ala	His	Ala	Gly	Ser	Leu	Leu	Asn	Leu	Ala	Lys	His	Ala	Ala
			100					105					110		
Ser	Thr	Val	Gln	Ile	Leu	Gly	Ala	Glu	Lys	Ala	Leu	Phe	Arg	Ala	Leu
		115					120					125			
Lys	Ser	Arg	Arg	Asp	Thr	Pro	Lys	Tyr	Gly	Leu	Ile	Tyr	His	Ala	Ser
	130					135					140				
Leu	Val	Gly	Gln	Thr	Ser	Pro	Lys	His	Lys	Gly	Lys	Ile	Ser	Arg	Met
145					150					155					160
Leu	Ala	Ala	Lys	Thr	Val	Leu	Ala	Ile	Arg	Tyr	Asp	Ala	Phe	Gly	Glu
				165					170					175	
Asp	Ser	Ser	Ser	Ala	Met	Gly	Val	Glu	Asn	Arg	Ala	Lys	Leu	Glu	Ala
			180					185					190		
Arg	Leu	Arg	Thr	Leu	Glu	Asp	Arg	Gly	Ile	Arg	Lys	Ile	Ser	Gly	Thr
		195					200					205			
Gly	Lys	Ala	Leu	Ala	Lys	Thr	Glu	Lys	Tyr	Glu	His	Lys	Ser	Glu	Val
	210					215					220				
Lys	Thr	Tyr	Asp	Pro	Ser	Gly	Asp	Ser	Thr	Leu	Pro	Thr	Cys	Ser	Lys
225					230					235					240
Lys	Arg	Lys	Ile	Glu	Gln	Val	Asp	Lys	Glu	Asp	Glu	Ile	Thr	Glu	Lys
				245					250					255	
Lys	Ala	Lys	Lys	Ala	Lys	Ile	Lys	Val	Lys	Val	Glu	Glu	Glu	Glu	Glu
			260					265					270		
Glu	Lys	Val	Ala	Glu	Glu	Glu	Glu	Thr	Ser	Val	Lys	Lys	Lys	Lys	Lys
		275					280					285			
Arg	Gly	Lys	Lys	Lys	His	Ile	Lys	Glu	Glu	Pro	Leu	Ser	Glu	Glu	Glu
	290					295					300				
Pro	Cys	Thr	Ser	Thr	Ala	Ile	Ala	Ser	Pro	Glu	Lys	Lys	Lys	Lys	Lys
305					310					315					320
Lys	Lys	Lys	Arg	Glu	Asn	Glu	Asp								
				325											

<210> 462

<211> 124

<212> PRT

<213> homo sapiens

<400> 462

Tyr 1	Asn	Arg	Asn	Ser 5	Phe	Leu	Leu	Ile	Leu 10	Val	Leu	Ser	Leu	Phe 15	Phe
Leu	Phe	Leu	Leu 20	Phe	Leu	Trp	Thr	Ser 25	Asn	Cys	Cys	Ala	Gly 30	Thr	Trp
Phe	Phe	Leu 35	Arg	Lys	Trp	Phe	Phe 40	Leu	Asn	Val	Phe	Leu 45	Phe	Thr	Pro
Phe	Leu 50	Leu	Leu	Leu	His	Arg 55	Cys	Phe	Phe	Phe	Phe 60	Cys	His	Phe	Phe
Phe 65	Phe	Leu	Phe	Phe	Asn 70	Phe	Asn	Phe	Asn	Leu 75	Gly	Phe	Phe	Gly	Phe 80
Leu	Phe	Ser	Asn	Phe 85	Ile	Leu	Phe	Ile	Tyr 90	Leu	Phe	Tyr	Phe	Ala 95	Phe
Phe	Arg	Thr	Gly 100	Trp	Lys	Cys	Gly	Val 105	Thr	Arg	Arg	Ile	Val 110	Ser	Leu
His	Phe	Thr 115	Phe	Val	Phe	Ile	Phe 120	Phe	Cys	Phe	Cys				

<210> 463  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 463

Ser 1	Ser	Phe	Ser	Leu 5	Phe	Phe	Phe	Phe	Phe 10	Phe	Phe	Phe	Ser	Gly 15	Leu
Ala	Ile	Ala	Val 20	Leu	Val	His	Gly	Ser 25	Ser	Ser	Glu	Ser	Gly 30	Ser	Ser
Leu	Met	Cys 35	Phe	Phe	Leu	Pro	Leu 40	Phe	Phe	Phe	Phe	Phe 45	Thr	Asp	Val
Ser 50	Ser	Ser	Ser	Ala	Thr	Phe 55	Ser	Ser	Ser	Ser	Ser 60	Ser	Thr	Leu	Thr
Leu 65	Ile	Leu	Ala	Phe	Leu 70	Ala	Phe	Phe	Ser	Val 75	Ile	Ser	Ser	Ser	Leu 80
Ser	Thr	Cys	Ser	Ile 85	Leu	Arg	Phe	Leu	Glu 90	Gln	Val	Gly	Ser	Val 95	Glu
Ser	Pro	Glu	Gly 100	Ser											

<210> 464  
 <211> 427  
 <212> PRT  
 <213> homo sapiens

<400> 464

Gly 1	Gly	Ser	Ser	Arg 5	Arg	His	Gly	Gly	Gly 10	Tyr	Ala	Ala	Val	Ala 15	Leu
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Leu	Val	Leu	Leu 20	Leu	Leu	Gly	Pro	Gly 25	Gly	Trp	Cys	Leu	Ala 30	Glu	Pro
Pro	Arg	Asp 35	Ser	Leu	Arg	Glu	Glu 40	Leu	Val	Ile	Thr	Pro 45	Leu	Pro	Ser
Gly	Asp 50	Val	Ala	Ala	Thr	Phe 55	Gln	Phe	Arg	Thr	Arg 60	Trp	Asp	Ser	Glu
Leu 65	Gln	Arg	Glu	Gly	Val 70	Ser	His	Tyr	Arg	Leu 75	Phe	Pro	Lys	Ala	Leu 80
Gly	Gln	Leu	Ile	Ser 85	Lys	Tyr	Ser	Leu	Arg 90	Glu	Leu	His	Leu	Ser 95	Phe
Thr	Gln	Gly	Phe 100	Trp	Arg	Thr	Arg	Tyr 105	Trp	Gly	Pro	Pro	Phe 110	Leu	Gln
Ala	Pro	Ser 115	Gly	Ala	Glu	Leu	Trp 120	Val	Trp	Phe	Gln	Asp 125	Thr	Val	Thr
Asp	Val 130	Asp	Lys	Ser	Trp	Lys 135	Glu	Leu	Ser	Asn	Val 140	Leu	Ser	Gly	Ile
Phe 145	Cys	Ala	Ser	Leu	Asn 150	Phe	Ile	Asp	Ser	Thr 155	Asn	Thr	Val	Thr	Pro 160
Thr	Ala	Ser	Phe	Lys 165	Pro	Leu	Gly	Leu	Ala 170	Asn	Asp	Thr	Asp	His 175	Tyr
Phe	Leu	Arg	Tyr 180	Ala	Val	Leu	Pro	Arg 185	Glu	Val	Val	Cys	Thr 190	Glu	Asn
Leu	Thr	Pro 195	Trp	Lys	Lys	Leu	Leu 200	Pro	Cys	Ser	Ser	Lys 205	Ala	Gly	Leu
Ser	Val 210	Leu	Leu	Lys	Ala	Asp 215	Arg	Leu	Phe	His	Thr 220	Ser	Tyr	His	Ser
Gln 225	Ala	Val	His	Ile	Arg 230	Pro	Val	Cys	Arg	Asn 235	Ala	Arg	Cys	Thr	Ser 240
Ile	Ser	Trp	Glu	Leu 245	Arg	Gln	Thr	Leu	Ser 250	Val	Val	Phe	Asp	Ala 255	Phe
Ile	Thr	Gly	Gln 260	Gly	Lys	Lys	Asp	Trp 265	Ser	Leu	Phe	Arg	Met 270	Phe	Ser
Arg	Thr	Leu 275	Thr	Glu	Pro	Cys	Pro 280	Leu	Ala	Ser	Glu	Ser 285	Arg	Val	Tyr
Val	Asp 290	Ile	Thr	Thr	Tyr	Asn 295	Gln	Asp	Asn	Glu	Thr 300	Leu	Glu	Val	His
Pro 305	Pro	Pro	Thr	Thr	Thr 310	Tyr	Gln	Asp	Val	Ile 315	Leu	Gly	Thr	Arg	Lys 320
Thr	Tyr	Ala	Ile	Tyr 325	Asp	Leu	Leu	Asp	Thr 330	Ala	Met	Ile	Asn	Asn 335	Ser
Arg	Asn	Leu	Asn 340	Ile	Gln	Leu	Lys	Trp 345	Lys	Arg	Pro	Pro	Glu 350	Asn	Glu

Ala	Pro	Pro	Val	Pro	Phe	Leu	His	Ala	Gln	Arg	Tyr	Val	Ser	Gly	Tyr
		355					360					365			
Gly	Leu	Gln	Lys	Gly	Glu	Leu	Ser	Thr	Leu	Leu	Tyr	Asn	Thr	His	Pro
	370					375					380				
Tyr	Arg	Ala	Phe	Pro	Val	Leu	Leu	Leu	Asp	Thr	Val	Pro	Trp	Tyr	Leu
385					390					395					400
Arg	Leu	Leu	His	Pro	Leu	Pro	Ala	Cys	Pro	Gly	Pro	Ala	Ala	Thr	Pro
				405					410					415	
Pro	Pro	Gly	Asp	Ala	Asp	Ser	Ala	Ala	Gly	Gln					
			420					425							

<210> 465

<211> 128

<212> PRT

<213> homo sapiens

<400> 465

Ser	Pro	Ser	Ile	Leu	Tyr	Gly	Ser	Cys	Thr	Cys	His	Ser	His	Lys	Ala
1				5					10					15	
Phe	Gly	Gly	Pro	Asp	Thr	Gly	Gly	His	Pro	Ser	Cys	Arg	Pro	His	Gln
			20					25					30		
Val	Gln	Ser	Cys	Gly	Ser	Gly	Ser	Lys	Thr	Leu	Ser	Leu	Met	Trp	Ile
		35					40					45			
Asn	Leu	Gly	Arg	Ser	Ser	Val	Met	Ser	Ser	Gln	Gly	Ser	Ser	Ala	Pro
	50					55					60				
Leu	Ser	Thr	Ser	Ser	Thr	Pro	Pro	Thr	Gln	Ser	Leu	Pro	Leu	Pro	Pro
					70					75					80
Ser	Asn	Pro	Trp	Val	Trp	Pro	Met	Thr	Leu	Thr	Thr	Thr	Phe	Cys	Ala
				85					90					95	
Met	Leu	Cys	Cys	Arg	Gly	Arg	Trp	Ser	Ala	Pro	Lys	Thr	Ser	Pro	Pro
			100					105					110		
Gly	Arg	Ser	Ser	Cys	Pro	Val	Val	Pro	Arg	Gln	Ala	Ser	Leu	Cys	Cys
		115					120					125			

<210> 466

<211> 124

<212> PRT

<213> homo sapiens

<400> 466

Pro	Gln	Ala	Trp	Arg	Arg	Leu	Cys	Arg	Cys	Cys	Ser	Ala	Arg	Pro	Val
1				5					10					15	
Ala	Pro	Gly	Ala	Arg	Arg	Leu	Val	Pro	Cys	Arg	Thr	Pro	Thr	Arg	Gln
			20					25					30		
Pro	Ala	Gly	Gly	Thr	Cys	His	His	Pro	Ala	Ala	Phe	Arg	Gly	Arg	Ser
		35					40					45			
Arg	His	Ile	Pro	Val	Pro	His	Ala	Leu	Gly	Phe	Gly	Ala	Ser	Ala	Gly

50					55					60					
Arg 65	Ser	Val	Pro	Leu	Gln 70	Ala	Leu	Ser	Gln	Ser 75	Pro	Gly	Ala	Ala	Asp 80
Leu	Gln	Val	Phe	Ser 85	Thr	Gly	Ala	Ala	Pro 90	Val	Ile	His	Thr	Arg 95	Leu
Leu	Glu	Asp	Pro 100	Ile	Leu	Gly	Ala	Thr 105	Leu	Pro	Ala	Gly	Pro 110	Ile	Arg
Cys	Arg	Ala 115	Val	Gly	Leu	Val	Pro 120	Arg	His	Cys	His				

<210> 467  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

<400> 467

Phe 1	Leu	His	Lys	Thr 5	His	Asn	Arg	Ala	Val 10	Glu	Glu	Ala	Lys	Glu 15	Pro
Phe	Leu	Cys	Leu 20	Cys	Ser	Arg	Thr	Glu 25	Arg	Gly	Pro	Leu	Ala 30	Ser	Val
Ser	Leu	Leu 35	Val	Leu	Pro	Gly	Leu 40	Tyr	Gln	Ala	Leu	Arg 45	Arg	Gly	Met
Glu	Thr 50	Pro	His	Ser	Gly	Ala 55	Trp	Leu	Gly	Glu	Gly 60	Glu	Ala	Ala	Gly
Val 65	Leu	Trp	Ala	Ser	Arg 70	Gly	Tyr	Asn	Leu	Ser 75	Ser	Leu	Gly	Asn	Val 80
Cys	Pro	Phe	Val	Gly 85	Ser	Ser	Pro	Thr	Arg 90	Arg	Gly	Thr	Gln	Leu 95	Tyr
Thr	Gly	Thr	Ile 100	Cys	Val	Trp	Ser	Val 105	Leu						

<210> 468  
 <211> 164  
 <212> PRT  
 <213> homo sapiens

<400> 468

Ile 1	Ser	Thr	Lys	Gln 5	Thr	Thr	His	Arg	Leu 10	Ser	Gln	Cys	Lys	Val 15	Glu
Ser	Pro	Asp	Val 20	Ser	Asp	Tyr	Cys	Leu 25	Gln	Met	Asp	Thr	Arg 30	Ser	Pro
Glu	Ser	Ser 35	Asp	Tyr	Thr	Leu	Glu 40	Lys	Pro	Lys	Glu	Pro 45	Leu	Pro	Pro
Pro	Leu 50	Pro	Gln	Ala	Arg	Pro 55	Gln	Ser	Gly	Ala	Phe 60	Pro	Tyr	Pro	Ala
Ser 65	Arg	Pro	Gly	Thr	Val 70	Arg	Glu	Glu	Pro	Ala 75	Gly	Ser	Arg	Trp	Pro 80

Glu	Gly	Leu	Ser	Gln	Ser	Tyr	Tyr	Arg	Gly	Ile	Lys	Arg	Ala	Pro	Leu
				85					90					95	
Leu	Pro	Pro	Gln	Pro	Cys	Cys	Glu	Ser	Cys	Ala	Gly	Ile	Asn	Leu	Arg
			100					105					110		
Asn	Ser	Pro	Glu	Ala	Glu	Thr	Gly	Leu	Met	Pro	Trp	Glu	Arg	Ser	Glu
		115					120					125			
Cys	Glu	Pro	Met	Ala	Pro	Ser	Leu	Leu	Gly	Thr	Asn	Leu	Pro	Lys	Tyr
	130					135					140				
Val	Lys	Ala	Glu	Gly	Asp	Arg	Asp	Leu	Ala	Glu	Gly	Arg	Lys	Ser	Phe
145					150					155					160
Ser	Ser	Arg	Asn												

<210> 469  
 <211> 108  
 <212> PRT  
 <213> homo sapiens

<400> 469

Glu	Ile	Arg	Gly	Arg	Pro	Pro	Leu	Phe	Met	Pro	Pro	Leu	Ser	Cys	Val
1				5					10					15	
Asp	Glu	Phe	Leu	Gln	Asn	Arg	Pro	His	Thr	Asp	Cys	Pro	Ser	Val	Lys
			20					25					30		
Leu	Ser	Pro	Pro	Thr	Cys	Arg	Thr	Thr	Ala	Tyr	Lys	Trp	Thr	His	Val
		35					40					45			
Pro	Gln	Arg	Ala	Gln	Ile	Ile	Pro	Ser	Arg	Ser	Pro	Lys	Asn	Pro	Cys
	50					55					60				
Arg	Leu	Pro	Phe	Pro	Lys	Pro	Gly	Pro	Arg	Val	Gly	Arg	Phe	His	Thr
65					70					75					80
Pro	Pro	Gln	Gly	Leu	Val	Gln	Ser	Gly	Lys	Asn	Gln	Gln	Ala	His	Ala
				85					90					95	
Gly	Gln	Arg	Ala	Ser	Leu	Ser	Pro	Thr	Thr	Glu	Ala				
			100					105							

<210> 470  
 <211> 317  
 <212> PRT  
 <213> homo sapiens

<400> 470

Asn	Met	Val	Asp	Tyr	Tyr	Glu	Val	Leu	Gly	Val	Gln	Arg	His	Ala	Ser
1				5					10					15	
Pro	Glu	Asp	Ile	Lys	Lys	Ala	Tyr	Arg	Lys	Leu	Ala	Leu	Lys	Trp	His
			20					25					30		
Pro	Asp	Lys	Asn	Pro	Glu	Asn	Lys	Glu	Glu	Ala	Glu	Arg	Lys	Phe	Lys
		35					40					45			
Gln	Val	Ala	Glu	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ala	Lys	Lys	Arg	Asp



	50					55					60					
Ile 65	Tyr	Asp	Lys	Tyr	Gly 70	Lys	Glu	Gly	Leu	Asn 75	Gly	Gly	Gly	Gly	Gly 80	
Gly	Ser	His	Phe	Asp 85	Ser	Pro	Phe	Glu	Phe 90	Gly	Phe	Thr	Phe	Arg 95	Asn	
Pro	Asp	Asp	Val 100	Phe	Arg	Glu	Phe	Phe 105	Gly	Gly	Arg	Asp	Pro 110	Phe	Ser	
Phe	Asp	Phe 115	Phe	Glu	Asp	Pro	Phe 120	Glu	Asp	Phe	Phe	Gly 125	Asn	Arg	Arg	
Gly	Pro 130	Arg	Gly	Ser	Arg	Ser 135	Arg	Gly	Thr	Gly	Ser 140	Phe	Phe	Ser	Ala	
Phe 145	Ser	Gly	Phe	Pro	Ser 150	Phe	Gly	Ser	Gly	Phe 155	Ser	Ser	Phe	Asp	Thr 160	
Gly	Phe	Thr	Ser	Phe 165	Gly	Ser	Leu	Gly	His 170	Gly	Gly	Leu	Thr	Ser 175	Phe	
Ser	Ser	Thr	Ser 180	Phe	Gly	Gly	Ser	Gly 185	Met	Gly	Asn	Phe	Lys 190	Ser	Ile	
Ser	Thr	Ser 195	Thr	Lys	Met	Val	Asn 200	Gly	Arg	Lys	Ile	Thr 205	Thr	Lys	Arg	
Ile	Val 210	Glu	Asn	Gly	Gln	Glu 215	Arg	Val	Glu	Val	Glu 220	Glu	Asp	Gly	Gln	
Leu 225	Lys	Ser	Leu	Thr	Ile 230	Asn	Gly	Val	Ala	Asp 235	Asp	Asp	Ala	Leu	Ala 240	
Glu	Glu	Arg	Met 245	Arg	Arg	Gly	Gln	Asn	Ala 250	Leu	Pro	Ala	Gln	Pro 255	Ala	
Gly	Leu	Arg	Pro 260	Pro	Lys	Pro	Pro	Arg 265	Pro	Ala	Ser	Leu	Leu 270	Arg	His	
Ala	Pro	His 275	Cys	Leu	Ser	Glu	Glu 280	Glu	Gly	Glu	Gln	Asp 285	Arg	Pro	Gly	
Ala	Pro 290	Gly	Pro	Trp	Asp	Pro 295	Leu	Gly	Val	Arg	Ser 300	Arg	Ile	Glu	Arg	
Arg 305	Trp	Gln	Glu	Glu	Glu 310	Ala	Glu	Ala	Glu	Arg 315	Gly	Val				

<210> 471

<211> 123

<212> PRT

<213> homo sapiens

<400> 471

Ser 1	Met	Pro	Leu	Val 5	Gln	Leu	Pro	Ser	Ser 10	Phe	Lys	Leu	Leu	Ser 15	Leu
Leu	Leu	Leu	Leu 20	Pro	Leu	Ala	Thr	Phe 25	Phe	Gln	Ser	Cys	Cys 30	Gly	Arg

Arg	Gly	Gly	Pro	Arg	Ala	Arg	Val	Pro	Gln	Val	Gly	Pro	Ala	Arg	Pro
		35					40					45			
Pro	Pro	Gln	Arg	Asp	Ser	Glu	Ala	Arg	Val	Ser	Ala	Ala	Arg	Gln	Ala
	50					55					60				
Gly	Ala	Ala	Ser	Ala	Gly	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Ala	Gly	Arg
65					70					75					80
Ser	Gly	Leu	Ser	Ala	Cys	Ala	Pro	Gln	Arg	Gly	His	Arg	Arg	Arg	Pro
				85					90					95	
His	His	Leu	Leu	Leu	Arg	Thr	Leu	Thr	Gly	His	Leu	Leu	Gln	Leu	Leu
			100					105					110		
Leu	Phe	Leu	Asp	Arg	Ser	Arg	Gln	Phe	Ser	Leu					
		115					120								

<210> 472  
 <211> 105  
 <212> PRT  
 <213> homo sapiens

<400> 472

Lys	Ile	Arg	Ser	Asn	Gln	Cys	Leu	Trp	Ser	Asn	Phe	Leu	Pro	Pro	Ser
1				5					10					15	
Asn	Ser	Ser	Leu	Cys	Phe	Cys	Phe	Phe	Leu	Leu	Pro	Pro	Ser	Phe	Asn
			20					25					30		
Pro	Ala	Ala	Asp	Ala	Glu	Gly	Val	Pro	Gly	Pro	Gly	Cys	Pro	Arg	Ser
		35					40					45			
Val	Leu	Leu	Ala	Leu	Leu	Leu	Arg	Glu	Thr	Val	Arg	Arg	Val	Ser	Gln
	50					55					60				
Gln	Arg	Gly	Arg	Pro	Gly	Arg	Leu	Arg	Arg	Ala	Glu	Ala	Gly	Arg	Leu
65					70					75					80
Gly	Trp	Gln	Gly	Val	Leu	Ala	Ser	Pro	His	Ala	Leu	Leu	Ser	Glu	Gly
				85					90					95	
Ile	Val	Val	Gly	His	Thr	Ile	Tyr	Cys							
			100					105							

<210> 473  
 <211> 159  
 <212> PRT  
 <213> homo sapiens

<400> 473

Ile	Val	Ser	Glu	Arg	Ser	Leu	Arg	Ser	Leu	Trp	Thr	Ala	His	Trp	Ala
1				5					10					15	
Leu	Pro	Glu	Met	Asp	Ser	Arg	Ile	Pro	Tyr	Asp	Asp	Tyr	Pro	Val	Val
			20					25					30		
Phe	Leu	Pro	Ala	Tyr	Glu	Asn	Pro	Pro	Ala	Trp	Ile	Pro	Pro	His	Glu
		35					40					45			
Arg	Val	His	His	Pro	Asp	Tyr	Asn	Asn	Glu	Leu	Thr	Gln	Phe	Leu	Pro

50					55					60					
Arg 65	Thr	Ile	Thr	Leu	Lys 70	Lys	Pro	Pro	Gly	Ala 75	Gln	Leu	Gly	Phe	Asn 80
Ile	Arg	Gly	Gly	Lys 85	Ala	Ser	Gln	Leu	Gly 90	Ile	Phe	Ile	Ser	Lys 95	Val
Ile	Pro	Asp	Ser 100	Asp	Ala	His	Arg	Ala 105	Gly	Leu	Gln	Glu	Gly 110	Asp	Gln
Val	Leu	Ala 115	Val	Asn	Asp	Val	Asp 120	Phe	Gln	Asp	Ile	Glu 125	His	Ser	Lys
Ala	Val 130	Glu	Ile	Leu	Lys	Thr 135	Ala	Arg	Glu	Ile	Ser 140	Met	Arg	Val	Arg
Phe 145	Phe	Pro	Tyr	Asn	Tyr 150	His	Arg	Gln	Lys	Glu 155	Arg	Thr	Val	His	

<210> 474  
 <211> 75  
 <212> PRT  
 <213> homo sapiens

<400> 474

Pro 1	Pro	Thr	Gly	Arg 5	Pro	Pro	Pro	Phe	Phe 10	Phe	Phe	Phe	Phe	Phe 15	Phe
Phe	Ser	Ile	Val 20	Phe	Tyr	Phe	Leu	Gly 25	Glu	Arg	Leu	Gly	Gly 30	Gly	Arg
Gly	Glu	Asn 35	Ser	Val	Ser	Leu	Glu 40	Ser	Gln	Lys	Cys	Met 45	Asn	Leu	Leu
Val	Val 50	Gln	Gly	Trp	Asp	Lys 55	Met	Ala	Arg	Glu	Val 60	Arg	Trp	Lys	Ile
Pro 65	Lys	Ile	Leu	Phe	Ala 70	Thr	Asp	Phe	Tyr	Asn 75					

<210> 475  
 <211> 97  
 <212> PRT  
 <213> homo sapiens

<400> 475

Leu 1	Gly	Gly	Leu	Ser 5	Ser	Ser	Asp	Val	Lys 10	Ser	Gln	Leu	Ser	Ser 15	Arg
Arg	Leu	Leu	Gln 20	Cys	Asp	Gly	Ser	Gly 25	Gln	Lys	Leu	Gly	Gln 30	Leu	Ile
Val	Val	Val 35	Arg	Val	Val	Tyr	Pro 40	Leu	Met	Arg	Arg	Asn 45	Pro	Cys	Trp
Arg	Ile 50	Leu	Ile	Gly	Arg	Gln 55	Glu	Asn	His	Arg	Val 60	Val	Ile	Ile	Arg
Asn 65	Pro	Ala	Val	His	Leu 70	Gly	Gln	Gly	Pro	Val 75	Gly	Ser	Pro	Gln	Arg 80

Pro	Gln	Thr	Pro	Leu 85	Thr	Asp	Asn	Ser	Val 90	Trp	Glu	Pro	Glu	Ala 95	Asp
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Ala

<210> 476

<211> 274

<212> PRT

<213> homo sapiens

<400> 476

Gly 1	His	Leu	Trp	Arg 5	Pro	Ala	Gly	Gly	Arg 10	Leu	Pro	Arg	His	His 15	Asp
Gln	Val	Cys	Arg 20	Ala	Ala	Glu	Pro	His 25	Arg	Gly	Gly	Gly	Leu 30	Cys	Gly
His	Gln	Arg 35	Arg	Leu	Pro	His	Arg 40	Pro	Arg	Val	Gln	Glu 45	Gly	Trp	Gly
Leu	Cys 50	Pro	His	Glu	Ser	Leu 55	His	Gln	Val	Pro	Ala 60	Asp	Arg	Pro	Trp
His 65	Glu	Pro	Gly	Ala	Gly 70	Cys	Ala	Ala	Asp	Cys 75	Glu	Asp	Pro	His	Arg 80
Arg	Pro	Gly	Ala	Cys 85	Glu	Pro	Gly	Ala	Pro 90	Pro	Ala	Ala	Arg	Ala 95	Ala
Gly	Leu	Gly	Arg 100	Gly	Thr	Arg	His	Gly 105	Asn	Gly	Asp	Ile	Leu 110	Ser	Phe
Glu	Asp	Ala 115	Asn	Arg	Ala	Met	Gln 120	Thr	Gly	Val	Thr	Gly 125	Ile	Met	Ile
Ala	Arg 130	Gly	Ala	Leu	Leu	Lys 135	Pro	Trp	Leu	Phe	Thr 140	Glu	Ile	Lys	Glu
Gln 145	Arg	His	Trp	Asp	Ile 150	Ser	Ser	Ser	Glu	Arg 155	Leu	Asp	Ile	Leu	Arg 160
Asp	Phe	Thr	Asn	Tyr 165	Gly	Leu	Glu	His	Trp 170	Gly	Ser	Asp	Thr	Gln 175	Gly
Val	Glu	Lys	Thr 180	Arg	Arg	Phe	Leu	Leu 185	Glu	Trp	Leu	Ser	Phe 190	Leu	Cys
Arg	Tyr	Asp 195	Pro	Val	Gly	Leu	Leu 200	Glu	Arg	Leu	Pro	Gln 205	Arg	Ile	Asn
Glu	Arg 210	Pro	Pro	Tyr	Tyr	Leu 215	Gly	Arg	Asp	Tyr	Leu 220	Glu	Thr	Leu	Met
Ala 225	Ser	Gln	Lys	Ala	Ala 230	Asp	Trp	Ile	Arg	Ile 235	Ser	Glu	Met	Leu	Leu 240
Gly	Pro	Val	Pro	Pro 245	Thr	Ser	Pro	Ser	Cys 250	Arg	Ser	Thr	Arg	Pro 255	Thr
Arg	Thr	Ser	Ser 260	Leu	Arg	Leu	Ser	Gln 265	Gly	His	Pro	Gly	Ala 270	Arg	Arg

Val Gln

<210> 477

<211> 256

<212> PRT

<213> homo sapiens

<400> 477

Ala 1	Gly	Pro	Ala	Pro 5	Val	Gln	Pro	Gly	Pro 10	His	Thr	Arg	Cys	Arg 15	Cys
Pro	Arg	Gly	His 20	Gly	Ser	Arg	Gly	Arg 25	Ser	Gln	Ala	Gly	Lys 30	Leu	Trp
Cys	Pro	Ala 35	Gly	Pro	Arg	Arg	Pro 40	Gly	Thr	Ser	Thr	Pro 45	Pro	Ser	Ser
Pro	Val 50	Arg	Thr	Cys	Gly	Pro 55	Leu	Thr	Asp	Glu	Asp 60	Val	Val	Arg	Leu
Arg 65	Pro	Cys	Glu	Lys	Lys 70	Arg	Leu	Asp	Ile	Arg 75	Gly	Lys	Leu	Tyr	Leu 80
Ala	Pro	Leu	Thr	Thr 85	Cys	Gly	Asn	Leu	Pro 90	Phe	Arg	Arg	Ile	Cys 95	Lys
Arg	Phe	Gly	Ala 100	Asp	Val	Thr	Cys	Gly 105	Glu	Met	Ala	Val	Cys 110	Thr	Asn
Leu	Leu	Gln 115	Gly	Gln	Met	Ser	Glu 120	Trp	Ala	Leu	Leu	Lys 125	Arg	His	Gln
Cys	Glu 130	Asp	Ile	Phe	Gly	Val 135	Gln	Leu	Glu	Gly	Ala 140	Phe	Pro	Asp	Thr
Met 145	Thr	Lys	Cys	Ala	Glu 150	Leu	Leu	Ser	Arg	Thr 155	Val	Glu	Val	Asp	Phe 160
Val	Asp	Ile	Asn	Val 165	Gly	Cys	Pro	Ile	Asp 170	Leu	Val	Tyr	Lys	Lys 175	Gly
Gly	Gly	Cys	Ala 180	Leu	Met	Asn	Arg	Ser 185	Thr	Lys	Phe	Gln	Gln 190	Ile	Val
Arg	Gly	Met 195	Asn	Gln	Val	Leu	Asp 200	Val	Pro	Leu	Thr	Val 205	Lys	Ile	Arg
Thr	Gly 210	Val	Gln	Glu	Arg	Val 215	Asn	Leu	Ala	His	Arg 220	Leu	Leu	Pro	Glu
Leu 225	Arg	Asp	Trp	Gly	Val 230	Ala	Leu	Val	Thr	Glu 235	Met	Gly	Thr	Ser	Cys 240
His	Leu	Arg	Met	Pro 245	Thr	Ala	Pro	Cys	Arg 250	Leu	Val	Ser	Pro	Gly 255	Ser

<210> 478

<211> 165

<212> PRT

<213> homo sapiens

<400> 478

Asn 1	Leu	Leu	Tyr	Ser 5	Pro	Arg	Pro	Arg	Val 10	Pro	Leu	Gly	Lys	Pro 15	Glu
Ala	Thr	Cys	Thr 20	Arg	Trp	Pro	Cys	Ala 25	Ser	Ala	Arg	Arg	Arg 30	Gly	Gly
Gly	His	Trp 35	Pro	Lys	Glu	His	Leu 40	Ala	Asp	Ala	Asp	Pro 45	Val	Gly	Cys
Leu	Leu 50	Ala	Gly	His	Gln	Arg 55	Leu	Gln	Val	Val	Ala 60	Ala	Gln	Val	Val
Gly 65	Arg	Pro	Leu	Val	Asp 70	Pro	Leu	Trp	Glu	Pro 75	Leu	Gln	Gln	Pro	His 80
Gly	Ile	Val	Pro	Ala 85	Gln	Glu	Gly	Gln	Pro 90	Leu	Glu	Gln	Lys	Ala 95	Pro
Gly	Leu	Leu	His 100	Ala	Leu	Arg	Val	Arg 105	Ala	Pro	Val	Leu	Gln 110	Ala	Val
Val	Gly	Glu 115	Val	Pro	Gln	Asp	Val 120	Gln	Ala	Leu	Gly	Arg 125	Arg	Asp	Val
Pro	Val 130	Pro	Leu	Leu	Leu	Asp 135	Leu	Arg	Glu	Glu	Pro 140	Arg	Leu	Glu	Gln
Gly 145	Ala	Thr	Gly	Asn	His 150	Asp	Pro	Gly	Asp	Thr 155	Ser	Leu	His	Gly	Ala 160
Val	Gly	Ile	Leu	Lys 165											

<210> 479

<211> 262

<212> PRT

<213> homo sapiens

<400> 479

Gly 1	Ser	Pro	Met	Ser 5	Pro	Ala	Arg	Ala	Met 10	Gln	Thr	Leu	Phe	Val 15	Pro
Glu	His	Gly	Asp 20	His	Gly	Ala	Gly	Val 25	Cys	Ser	Asp	His	His 30	His	Arg
Gly	Gly	His 35	Val	Pro	Ala	Glu	Pro 40	Leu	Gln	Ala	Val	Cys 45	Thr	Val	Leu
His	Gln 50	Pro	Ala	Gln	Pro	Gly 55	Ala	Glu	Glu	Arg	Arg 60	Cys	Pro	Val	Leu
Arg 65	Arg	Met	Pro	Val	Ala 70	Ser	Glu	Thr	Gln	Cys 75	Gln	Ala	Thr	Glu	Ser 80
Gln	Ser	Arg	Ser	Leu 85	Thr	Pro	Arg	Leu	Gly 90	Pro	Pro	Thr	Ala	Trp 95	Pro
Cys	Ala	Leu	Arg 100	Pro	Ala	Glu	Arg	Phe 105	Pro	Pro	Leu	Pro	Ala 110	Gln	Cys

Leu	Leu	His 115	Val	Gln	Leu	Gln	Thr 120	Leu	Phe	Val	Pro	Glu 125	His	Gly	Asp
His	Gly 130	Ala	Gly	Val	Cys	Ser 135	Asp	His	His	His	Arg 140	Gly	Gly	His	Val
Pro 145	Ala	Glu	Pro	Leu	Gln 150	Ala	Val	Cys	Thr	Val 155	Leu	His	Gln	Pro	Ala 160
Gln	Pro	Gly	Ala	Glu 165	Glu	Arg	Arg	Cys	Pro 170	Val	Leu	Arg	Arg	Met 175	Pro
Val	Ala	Leu	Gly 180	Glu	His	Ser	Val	Arg 185	Gln	Arg	Asn	Pro	Arg 190	Ala	Ala
Gly	Leu	Arg 195	Pro	Ala	Ser	Ala	His 200	Arg	Pro	Pro	Gly	Arg 205	Ala	Ala	Leu
Arg	Pro 210	Ala	Gly	Ala	Leu	Pro 215	Pro	Leu	Pro	Ala	His 220	Leu	Ser	Val	Pro
Ala 225	Ala	Arg	Asp	Arg	Pro 230	Ala	Ala	His	His	Leu 235	Ala	Val	Arg	Arg	Gly 240
Gly	Ala	Pro	Thr	Leu 245	Pro	Gly	Pro	Leu	Asp 250	Leu	Gln	Gly	Ser	Gly 255	Pro
Arg	Gly	Gly	Val 260	Gly	Asn										

<210> 480

<211> 270

<212> PRT

<213> homo sapiens

<400> 480

Ala 1	Ala	Gln	Cys	Leu 5	Leu	His	Val	Gln	Cys 10	Lys	Arg	Ser	Leu	Phe 15	Gln
Ser	Met	Glu	Ile 20	Thr	Glu	Leu	Glu	Phe 25	Val	Gln	Ile	Ile	Ile 30	Ile	Val
Val	Val	Thr 35	Cys	Leu	Leu	Ser	His 40	Tyr	Lys	Leu	Ser	Ala 45	Arg	Ser	Phe
Ile	Ser 50	Arg	His	Ser	Gln	Gly 55	Arg	Arg	Arg	Glu	Asp 60	Ala	Leu	Ser	Ser
Glu 65	Gly	Cys	Leu	Trp	Pro 70	Arg	Arg	His	Ser	Val 75	Arg	Gln	Arg	Asn	Pro 80
Arg	Ala	Ala	Val	Leu 85	Arg	Pro	Ala	Ser	Ala 90	His	Arg	Pro	Pro	Gly 95	Arg
Ala	Pro	Phe	Ala 100	Gln	Arg	Ser	Val	Phe 105	His	Arg	Cys	Gln	Pro 110	Asn	Val
Ser	Cys	Thr 115	Cys	Asn	Cys	Lys	Arg 120	Ser	Leu	Phe	Gln	Ser 125	Met	Glu	Ile
Thr	Glu 130	Leu	Glu	Phe	Val	Gln 135	Ile	Ile	Ile	Ile	Val 140	Val	Val	Thr	Cys

Leu 145	Leu	Ser	His	Tyr	Lys 150	Leu	Ser	Ala	Arg	Ser 155	Phe	Ile	Ser	Arg	His 160
Ser	Gln	Gly	Arg	Arg 165	Arg	Glu	Asp	Ala	Leu 170	Ser	Ser	Glu	Gly	Cys 175	Leu
Trp	Pro	Ser	Glu 180	Ser	Thr	Val	Ser	Gly 185	Asn	Gly	Ile	Pro	Glu 190	Pro	Gln
Val	Tyr	Ala 195	Pro	Pro	Arg	Pro	Thr 200	Asp	Arg	Leu	Ala	Val 205	Pro	Pro	Phe
Ala	Gln 210	Arg	Glu	Arg	Phe	His 215	Arg	Phe	Gln	Pro	Thr 220	Tyr	Pro	Tyr	Leu
Gln 225	His	Glu	Ile	Asp	Leu 230	Pro	Pro	Thr	Ile	Ser 235	Leu	Ser	Asp	Gly	Glu 240
Glu	Pro	Pro	Pro	Tyr 245	Gln	Gly	Pro	Trp	Thr 250	Phe	Lys	Val	Arg	Asp 255	Pro
Glu	Glu	Glu	Leu 260	Glu	Ile	Glu	Arg	Gly 265	Leu	Gly	Ala	Glu	Thr 270		

<210> 481  
 <211> 124  
 <212> PRT  
 <213> homo sapiens

<400> 481

Ala 1	Thr	Thr	Ser	Cys 5	Leu	His	Gly	Pro	Ser 10	Ser	Ala	Gly	Thr	Ala 15	Arg
Gly	Gly	Gly	Glu 20	Lys	Met	Pro	Cys	Pro 25	Gln	Lys	Asp	Ala	Cys 30	Gly	Pro
Arg	Arg	Ala 35	Gln	Cys	Gln	Ala	Thr 40	Glu	Ser	Gln	Ser	Arg 45	Arg	Ser	Thr
Pro	Arg 50	Leu	Gly	Pro	Pro	Thr 55	Ala	Trp	Pro	Cys	Arg 60	Pro	Ser	Pro	Ser
Gly 65	Ser	Ala	Ser	Thr	Ala 70	Ser	Ser	Pro	Pro	Ile 75	Arg	Thr	Cys	Ser	Thr 80
Arg	Ser	Thr	Cys	Arg 85	Pro	Pro	Ser	Arg	Cys 90	Gln	Thr	Gly	Arg	Ser 95	Pro
His	Pro	Thr	Arg 100	Ala	Pro	Gly	Pro	Ser 105	Arg	Phe	Gly	Thr	Pro 110	Arg	Arg
Ser	Trp	Lys 115	Leu	Asn	Gly	Asp	Trp 120	Val	Arg	Arg	Pro				

<210> 482  
 <211> 99  
 <212> PRT  
 <213> homo sapiens

<400> 482



Arg 1	Val	Leu	Val	Ser 5	Pro	Leu	Ser	Leu	Ser 10	Met	Trp	Arg	Trp	Lys 15	Val
Glu	Lys	Asp	Thr 20	Val	Ser	Ile	Leu	Lys 25	Leu	Leu	Arg	Phe	Ser 30	Glu	Arg
Gly	Arg	His 35	Leu	Asn	Arg	Gln	Val 40	Gly	Phe	Ser	Val	Leu 45	Ser	Ala	Leu
Gly	Ile 50	Trp	Arg	Glu	Met	Gly 55	Leu	Leu	Ser	Leu	Cys 60	Thr	Gln	Glu	Gly
His 65	Ala	Leu	Lys	Thr	Val 70	Phe	Val	Asp	Gln	Arg 75	Arg	Leu	Tyr	Ser	Thr 80
Gly	Gly	Ile	Gln	Met 85	Ser	Leu	Arg	Gly	Arg 90	Glu	Glu	Thr	Trp	Gln 95	Ala

Asp Tyr Ile

<210> 483  
 <211> 104  
 <212> PRT  
 <213> homo sapiens

<400> 483

Val 1	Leu	Glu	Glu	Glu 5	Lys	Lys	His	Gly	Lys 10	Gln	Ile	Thr	Ser	Glu 15	Pro
Phe	Glu	Leu	Cys 20	Phe	Ser	Phe	Phe	Pro 25	Cys	Leu	Phe	Ser	Lys 30	Ile	Tyr
Leu	Asn	Leu 35	Glu	Thr	Gln	Asp	Ile 40	Phe	Leu	Gly	Asn 45	Leu	Leu	Pro	Met
Ser	Glu 50	Val	Ala	Ser	Ala	Ala 55	Ser	Arg	Gln	Ile	Pro 60	Gly	Asn	Pro	Glu
Pro 65	Gln	Asn	Val	Ile	Pro 70	Pro	Gly	Ser	Ala	Trp 75	Pro	Asp	Pro	Val	Leu 80
Ser	Ala	Gly	Phe	Thr 85	Tyr	Gln	Ser	His	Ser 90	Ser	Phe	Ser	Ile	Asn 95	Thr
Pro	Lys	Ser	Ser 100	Pro	Asn	His	His								

<210> 484  
 <211> 123  
 <212> PRT  
 <213> homo sapiens

<400> 484

Lys 1	Leu	Asp	Ser	Thr 5	Gln	Cys	Arg	Pro	Ser 10	Leu	His	Thr	Asn	Met 15	Tyr
Val	Leu	Leu	Ser 20	Glu	Cys	His	Leu	Leu 25	Cys	Thr	Gln	Cys	His 30	Asp	Ser
Lys	Ile	Lys 35	Ile	Ser	Val	Ser	Asn 40	Gln	Asn	Ile	Asn	Gln 45	Ala	Arg	Asn

Ser	Trp	Ala	Gln	Arg	Gly	Val	Arg	Gly	Leu	Ser	Tyr	Thr	Ala	Val	Lys
	50					55					60				
Gln	Pro	Thr	Cys	Ser	Ala	His	Ser	Gln	Ala	Glu	Ser	Asp	Trp	Ser	Cys
65					70					75					80
Arg	Gln	Arg	Gly	Gly	Gly	Arg	Val	Leu	Cys	Cys	Pro	Leu	Leu	Cys	Met
				85					90					95	
Val	Ser	Trp	Val	Phe	Gln	Gly	Gly	Gln	Leu	Leu	Ser	Pro	Asn	Lys	Thr
			100					105					110		
Val	Asn	Ser	Leu	Arg	Thr	Gly	Pro	Leu	Pro	His					
		115					120								

<210> 485

<211> 303

<212> PRT

<213> homo sapiens

<400> 485

Leu	Gly	Arg	Lys	Pro	Ser	Trp	Val	Gly	Gly	Ala	Gly	Leu	Glu	Pro	Ser
1				5					10					15	
Gln	Gly	Ser	Gly	Leu	Ser	His	His	Pro	Ala	Pro	Gln	Ser	Asp	Ser	Ala
			20					25					30		
Pro	Thr	Ser	Pro	Pro	Ile	Pro	Gly	Glu	Pro	Gly	Pro	Gln	Arg	Glu	Val
		35					40					45			
Asp	Lys	Trp	Gly	Gly	Ser	Leu	Gly	Arg	Pro	Glu	Ser	Ser	Gly	His	Pro
	50					55					60				
Gly	Arg	Thr	Pro	Ala	Thr	Cys	Cys	His	Cys	Ala	Ala	Val	Met	Ala	Arg
65					70					75					80
Ser	Gly	Ser	Ala	Thr	Pro	Pro	Ala	Arg	Ala	Pro	Gly	Ala	Pro	Pro	Arg
				85					90					95	
Ser	Pro	Pro	Gln	Arg	Leu	Val	Gln	Asp	Val	Ser	Gly	Pro	Leu	Arg	Glu
			100					105					110		
Leu	Arg	Pro	Arg	Leu	Cys	His	Leu	Arg	Lys	Gly	Pro	Gln	Gly	Tyr	Gly
		115					120					125			
Phe	Asn	Leu	His	Ser	Asp	Lys	Ser	Arg	Pro	Gly	Gln	Tyr	Ile	Arg	Ser
	130					135					140				
Val	Asp	Pro	Gly	Ser	Pro	Ala	Ala	Arg	Ser	Gly	Leu	Arg	Ala	Gln	Asp
145					150					155					160
Arg	Leu	Ile	Glu	Val	Asn	Gly	Gln	Asn	Val	Glu	Gly	Leu	Arg	His	Ala
				165					170					175	
Glu	Val	Val	Ala	Ser	Ile	Lys	Ala	Arg	Glu	Asp	Glu	Ala	Arg	Leu	Leu
			180					185					190		
Val	Val	Asp	Pro	Glu	Thr	Asp	Glu	His	Phe	Lys	Arg	Leu	Arg	Val	Thr
		195					200					205			
Pro	Thr	Glu	Glu	His	Val	Glu	Gly	Pro	Leu	Pro	Ser	Pro	Val	Thr	Asn

210					215					220					
Gly 225	Thr	Ser	Pro	Ala	Gln 230	Leu	Asn	Gly	Gly	Ser 235	Ala	Cys	Ser	Ser	Arg 240
Ser	Asp	Leu	Pro	Gly 245	Ser	Asp	Lys	Asp	Thr 250	Glu	Asp	Gly	Ser	Ala 255	Trp
Lys	Gln	Asp	Pro 260	Phe	Gln	Glu	Ser	Gly 265	Leu	His	Leu	Ser	Pro 270	Thr	Ala
Ala	Glu	Ala 275	Lys	Glu	Lys	Ala	Arg 280	Ala	Met	Arg	Val	Asn 285	Lys	Arg	Ala
Pro	Gln 290	Met	Asp	Trp	Asn	Arg 295	Lys	Arg	Glu	Ile	Phe 300	Ser	Asn	Phe	

<210> 486

<211> 149

<212> PRT

<213> homo sapiens

<400> 486

Ala 1	Pro	Arg	Arg	Pro 5	Arg	Pro	Arg	Arg	Arg 10	Leu	Glu	Pro	Cys	Glu 15	Ser
Thr	Ser	Ala	Arg 20	His	Arg	Trp	Thr	Gly 25	Thr	Gly	Ser	Val	Lys 30	Ser	Ser
Ala	Thr	Ser 35	Glu	Pro	Leu	Pro	Ala 40	Cys	Leu	Gly	Thr	Leu 45	Gly	Pro	Leu
Pro	His 50	Gly	Pro	Trp	Ala	Ser 55	Ala	Cys	Pro	Glu	Leu 60	Pro	Gln	Pro	Gln
Trp 65	Thr	Gly	Gly	Trp	Ser 70	Cys	His	Cys	Pro	Glu 75	Ile	Ser	Pro	Ser	Pro 80
Gly	Glu	Pro	Pro	Ser 85	Cys	Pro	Cys	Pro	Pro 90	Gly	Thr	Gly	Gly	Leu 95	Trp
Gln	Gln	Asp	Arg 100	Gly	Arg	Glu	Thr	Gln 105	Arg	Cys	Glu	Arg	Glu 110	Ser	Glu
Thr	Glu	Thr 115	Glu	Arg	Glu	Arg	Glu 120	Arg	His	Arg	Glu	Arg 125	Gln	Arg	Glu
Ser	Glu 130	Arg	Ala	Arg	Gly	Ser 135	Arg	Gly	Ala	Arg	Ala 140	Phe	Ala	Ala	Leu
Pro 145	Gly	Pro	Ala	Asp											

<210> 487

<211> 217

<212> PRT

<213> homo sapiens

<400> 487

Phe 1	Leu	Gly	Asn	Gly 5	Arg	Thr	Thr	Leu	Gln 10	Ser	Thr	Glu	Ala	Gly 15	Gly
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Ala	Arg	Gly	Arg 20	Leu	Arg	Pro	Lys	Val 25	Arg	Ala	Gly	Gly	Val 30	Pro	Gly
Ser	Arg	Asp 35	Arg	Gln	Glu	Gly	Ala 40	Gln	Lys	Leu	Leu	Lys 45	Ile	Ser	Arg
Phe	Leu 50	Phe	Gln	Ser	Ile	Cys 55	Gly	Ala	Arg	Leu	Leu 60	Thr	Arg	Met	Ala
Arg 65	Ala	Phe	Ser	Leu	Ala 70	Ser	Ala	Ala	Val	Gly 75	Leu	Arg	Trp	Arg	Pro 80
Leu	Ser	Trp	Lys	Gly 85	Ser	Cys	Phe	Gln	Ala 90	Leu	Pro	Ser	Ser	Val 95	Ser
Leu	Ser	Glu	Pro 100	Gly	Arg	Ser	Leu	Arg 105	Asp	Glu	His	Ala	Glu 110	Pro	Pro
Leu	Ser	Trp 115	Ala	Gly	Leu	Val	Pro 120	Leu	Val	Thr	Gly	Asp 125	Gly	Arg	Gly
Pro	Ser 130	Thr	Cys	Ser	Ser	Val 135	Gly	Val	Thr	Arg	Ser 140	Arg	Leu	Lys	Cys
Ser 145	Ser	Val	Ser	Gly	Ser 150	Thr	Thr	Ser	Ser	Arg 155	Ala	Ser	Ser	Ser	Arg 160
Ala	Leu	Met	Leu	Ala 165	Thr	Thr	Ser	Ala	Trp 170	Arg	Ser	Pro	Ser	Thr 175	Phe
Cys	Pro	Phe	Thr 180	Ser	Met	Ser	Arg	Ser 185	Trp	Ala	Arg	Arg	Pro 190	Glu	Arg
Ala	Ala	Gly 195	Glu	Pro	Gly	Ser	Thr 200	Glu	Arg	Met	Tyr	Trp 205	Pro	Gly	Arg
Asp	Leu 210	Ser	Leu	Cys	Arg	Leu 215	Asn	Pro							

<210> 488

<211> 298

<212> PRT

<213> homo sapiens

<400> 488

Glu 1	Ile	Arg	Ala	Val 5	Gly	Gly	Gly	Val	Cys 10	Val	Asp	Gly	Met	Gly 15	Thr
Pro	Gly	Glu	Gly 20	Leu	Gly	Arg	Cys	Ser 25	His	Ala	Leu	Ile	Arg 30	Gly	Val
Pro	Glu	Ser 35	Leu	Ala	Ser	Gly	Glu 40	Gly	Ala	Gly	Ala	Gly 45	Leu	Pro	Ala
Leu	Asp 50	Leu	Ala	Lys	Ala	Gln 55	Arg	Glu	His	Gly	Val 60	Leu	Gly	Gly	Lys
Leu 65	Arg	Gln	Arg	Leu	Gly 70	Leu	Gln	Leu	Leu	Glu 75	Leu	Pro	Pro	Glu	Glu 80
Ser	Leu	Pro	Leu	Gly	Pro	Leu	Leu	Gly	Asp	Thr	Ala	Val	Ile	Gln	Gly

85								90				95			
Asp	Thr	Ala	Leu 100	Ile	Thr	Arg	Pro	Trp 105	Ser	Pro	Ala	Arg	Arg 110	Pro	Glu
Val	Asp	Gly 115	Val	Arg	Lys	Ala	Leu 120	Gln	Asp	Leu	Gly	Leu 125	Arg	Ile	Val
Glu	Ile 130	Gly	Asp	Glu	Asn	Ala 135	Thr	Leu	Asp	Gly	Thr 140	Asp	Val	Leu	Phe
Thr 145	Gly	Arg	Glu	Phe	Phe 150	Val	Gly	Leu	Ser	Lys 155	Trp	Thr	Asn	His	Arg 160
Gly	Ala	Glu	Ile	Val 165	Ala	Asp	Thr	Phe	Arg 170	Asp	Phe	Ala	Val	Ser 175	Thr
Val	Pro	Val	Ser 180	Gly	Pro	Ser	His	Leu 185	Arg	Gly	Leu	Cys	Gly 190	Met	Gly
Gly	Pro	Arg 195	Thr	Val	Val	Ala	Gly 200	Ser	Ser	Asp	Ala	Ala 205	Gln	Lys	Ala
Val	Arg 210	Ala	Met	Ala	Val	Leu 215	Thr	Asp	His	Pro	Tyr 220	Ala	Ser	Leu	Thr
Leu 225	Pro	Asp	Asp	Ala	Ala 230	Ala	Asp	Cys	Leu	Phe 235	Leu	Arg	Pro	Gly	Leu 240
Pro	Gly	Val	Pro	Pro 245	Phe	Leu	Leu	His	Arg 250	Gly	Gly	Gly	Asp	Leu 255	Pro
Asn	Ser	Gln	Glu 260	Ala	Leu	Gln	Lys	Leu 265	Ser	Asp	Val	Thr	Leu 270	Val	Pro
Val	Ser	Cys 275	Ser	Glu	Leu	Glu	Lys 280	Ala	Gly	Ala	Gly	Leu 285	Ser	Ser	Leu
Cys 290	Leu	Val	Leu	Ser	Thr	Arg 295	Pro	His	Ser						

<210> 489

<211> 175

<212> PRT

<213> homo sapiens

<400> 489

Ala 1	Gly	His	Arg	Tyr 5	Gln	Gly	Asp	Ile	Arg 10	Glu	Leu	Leu	Gln	Cys 15	Leu
Leu	Ala	Val	Gly 20	Gln	Ile	Pro	Thr	Ser 25	Thr	Val	Gln	Glu	Glu 30	Arg	Gly
His	Thr	Arg 35	Gln	Pro	Arg	Thr	Lys 40	Lys	Glu	Thr	Val	Ser 45	Ser	Cys	Val
Ile	Trp 50	Glu	Gly	Gln	Gly	Gly 55	Ile	Trp	Val	Ile	Cys 60	Gln	His	Cys	His
Cys 65	Pro	Asp	Ser	Leu	Leu 70	Gly	Ser	Val	Ala	Ala 75	Ala	Cys	His	Asn	Ser 80

Ala	Arg	Ser	Pro	His 85	Ala	Ala	Glu	Thr	Ala 90	Gln	Val	Gly	Gly	Thr 95	Arg
Asp	Trp	His	Ser 100	Gly	Asp	Gly	Glu	Val 105	Pro	Glu	Arg	Val	Arg 110	His	Asp
Leu	Ser	Ser 115	Ser	Val	Ile	Gly	Pro 120	Phe	Gly	Glu	Ala	Tyr 125	Glu	Lys	Leu
Pro	Ala 130	Gly	Glu	Glu	Asn	Val 135	Ser	Ala	Ile	Gln	Arg 140	Arg	Val	Leu	Val
Ser 145	Tyr	Phe	His	Asn	Ser 150	Glu	Pro	Gln	Val	Leu 155	Gln	Gly	Phe	Ala	Asp 160
Ser	Ile	Asp	Leu	Trp 165	Pro	Thr	Ser	Gly	Ala 170	Pro	Gly	Pro	Arg	Asp 175	

<210> 490

<211> 150

<212> PRT

<213> homo sapiens

<400> 490

Leu 1	Gly	Pro	Cys	Pro 5	Leu	Gly	Ser	Arg	Pro 10	Cys	Arg	Gln	Ala	Ala 15	Val
Pro	Ala	Ala	Met 20	Thr	Pro	Gln	Val	Ala 25	Val	Leu	Ala	Ala	Val 30	Ala	Pro
Val	Val	Ala 35	Ser	Val	Tyr	Leu	Pro 40	Ala	Pro	Arg	Ala	Pro 45	Phe	Glu	Leu
Trp	Pro 50	Asp	Pro	Glu	Arg	Glu 55	Gly	Gln	Pro	Pro	His 60	Leu	Pro	Pro	Thr
Pro 65	Gly	Ser	Leu	Gly	Leu 70	Pro	Gly	Ser	Gly	His 75	Gly	Ser	Ser	Gly	Pro 80
Ala	Pro	Pro	Pro	Ala 85	Ser	Pro	Ser	His	Pro 90	His	Arg	Leu	Pro	Leu 95	Gln
Pro	Leu	Gly	Phe 100	Leu	Ser	Phe	Leu	Val 105	Ser	Ser	Pro	Val	Ser 110	Ser	Gly
His	Pro	His 115	Ser	Cys	Arg	Ala	Val 120	Ile	Ser	Ala	Gly	Ala 125	Pro	Pro	Pro
Glu	Asp 130	Arg	Val	Gly	Gly	Glu 135	Gly	Ser	Pro	Arg	Leu 140	Gln	Ala	Ser	Gly
Thr 145	Gly	Ser	Ser	Gly	Phe 150										

<210> 491

<211> 89

<212> PRT

<213> homo sapiens

<400> 491

Phe	Val	Lys	Arg	Thr	Lys	Gln	Pro	Arg	Gln	Thr	Leu	Asp	Ala	Pro	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1				5					10					15		
Ser	Ala	Leu	Arg 20	Leu	Trp	Gly	Arg	Cys 25	Leu	Leu	Gly	Glu	Ala 30	Val	Ala	
Gln	Gly	Val 35	His	Cys	Glu	Ala	Gly 40	Pro	Val	Asp	Ser	Ala 45	Gly	Gly	Ile	
His	Leu 50	Ala	Ser	Gly	Cys	Leu 55	Val	Ser	Val	Tyr	Ser 60	Asp	Ile	Ala	Phe	
Cys 65	Cys	His	Leu	Ser	Cys 70	Gly	Gln	Arg	Gly	Val 75	Ser	Trp	His	Glu	Asn 80	
Ile	Phe	Phe	Phe	Lys 85	Cys	Gly	Ser	Phe								

<210> 492  
 <211> 63  
 <212> PRT  
 <213> homo sapiens

<400> 492

Leu 1	Thr	His	Leu	Leu 5	Phe	Glu	Lys	Cys	Leu 10	Leu	Pro	Ser	Leu	Gly 15	Leu	
Ile	Thr	Lys	Phe 20	Asp	His	Asp	His	Ile 25	Val	Val	Ser	Gln	Ser 30	Ala	Leu	
Glu	Ile	Val 35	Ser	Gly	Leu	His	Glu 40	Val	Ala	Met	Gly	Val 45	Trp	Ser	Thr	
Leu	Lys 50	Leu	Tyr	Gln	Ser	Cys 55	Thr	Tyr	Phe	Gln	Thr 60	Phe	Leu	Lys		

<210> 493  
 <211> 73  
 <212> PRT  
 <213> homo sapiens

<400> 493

Asp 1	Gly	Ser	Arg	Met 5	Leu	Cys	His	Tyr	Ile 10	Gln	Lys	Gln	Asp	Asn 15	Leu	
Lys	Leu	Asn	Gly 20	Cys	Pro	Leu	Gln	Ser 25	Gln	Gln	Val	Gln	Pro 30	His	Ser	
Ala	Arg	Pro 35	Glu	Leu	Gln	Pro	Leu 40	Pro	Lys	Gly	Ile	Phe 45	Pro	Thr	Ala	
Ser	Thr 50	Pro	Ser	Lys	Glu	His 55	Gln	Gly	Phe	Val	Ser 60	Val	Val	Leu	Phe	
Phe 65	Leu	Gln	Thr	Ile	Asp 70	Ile	Tyr	Ser								

<210> 494  
 <211> 318  
 <212> PRT  
 <213> homo sapiens

<400> 494

Lys 1	Cys	Ala	Thr	Phe 5	Trp	Ser	Phe	Pro	Arg 10	Arg	Gln	Gly	Gly	Leu 15	Gly
Ile	Ala	Ile	Ser 20	Glu	Glu	Asp	Thr	Leu 25	Ser	Gly	Val	Ile	Ile 30	Lys	Ser
Leu	Thr	Glu 35	His	Gly	Val	Ala	Ala 40	Thr	Asp	Gly	Arg	Leu 45	Lys	Val	Gly
Asp	Gln 50	Ile	Leu	Ala	Val	Asp 55	Asp	Glu	Ile	Val	Val 60	Gly	Tyr	Pro	Ile
Glu 65	Lys	Phe	Ile	Ser	Leu 70	Leu	Lys	Thr	Ala	Lys 75	Met	Thr	Val	Lys	Leu 80
Thr	Ile	His	Ala	Glu 85	Asn	Pro	Asp	Ser	Gln 90	Ala	Val	Pro	Ser	Ala 95	Ala
Gly	Ala	Ala	Ser 100	Gly	Glu	Lys	Lys	Asn 105	Ser	Ser	Gln	Ser	Leu 110	Met	Val
Pro	Gln	Ser 115	Gly	Ser	Pro	Glu	Pro 120	Glu	Ser	Ile	Arg	Asn 125	Thr	Ser	Arg
Ser	Ser 130	Thr	Pro	Ala	Ile	Phe 135	Ala	Ser	Asp	Pro	Ala 140	Thr	Cys	Pro	Ile
Ile 145	Pro	Gly	Cys	Glu	Thr 150	Thr	Ile	Glu	Ile	Ser 155	Lys	Gly	Arg	Thr	Gly 160
Leu	Gly	Leu	Ser	Ile 165	Val	Gly	Gly	Ser	Asp 170	Thr	Leu	Leu	Gly	Ala 175	Ile
Ile	Ile	His	Glu 180	Val	Tyr	Glu	Glu	Gly 185	Ala	Ala	Cys	Lys	Asp 190	Gly	Arg
Leu	Trp	Ala 195	Gly	Asp	Gln	Ile	Leu 200	Glu	Val	Asn	Gly	Ile 205	Asp	Leu	Arg
Lys	Ala 210	Thr	His	Asp	Glu	Ala 215	Ile	Asn	Val	Leu	Arg 220	Gln	Thr	Pro	Gln
Arg 225	Val	Arg	Leu	Thr	Leu 230	Tyr	Arg	Asp	Glu	Ala 235	Pro	Tyr	Lys	Glu	Glu 240
Glu	Val	Cys	Asp	Thr 245	Leu	Thr	Ile	Glu	Leu 250	Gln	Lys	Lys	Pro	Gly 255	Lys
Gly	Leu	Gly	Leu 260	Ser	Ile	Val	Gly	Lys 265	Arg	Asn	Asp	Thr	Gly 270	Val	Phe
Val	Ser	Asp 275	Ile	Val	Lys	Gly	Gly 280	Ile	Ala	Asp	Ala	Asp 285	Gly	Arg	Leu
Met	Gln 290	Gly	Asp	Gln	Ile	Leu 295	Met	Val	Asn	Gly	Glu 300	Asp	Val	Arg	Asn
Ala 305	Thr	Gln	Glu	Ala	Val 310	Ala	Val	Trp	Ile	Lys 315	Val	Phe	Pro		

<210> 495



<211> 206  
 <212> PRT  
 <213> homo sapiens

<400> 495

Ser 1	Ala	Phe	Ala	Glu 5	Met	Gly	Ser	Asp	His 10	Thr	Gln	Ser	Ser	Ala 15	Ser
Lys	Ile	Ser	Gln 20	Asp	Val	Asp	Lys	Glu 25	Asp	Glu	Phe	Gly	Tyr 30	Ser	Trp
Lys	Asn	Ile 35	Arg	Glu	Arg	Tyr	Gly 40	Thr	Leu	Thr	Gly	Glu 45	Leu	His	Met
Ile	Glu 50	Leu	Glu	Lys	Gly	His 55	Ser	Gly	Leu	Gly	Leu 60	Ser	Leu	Ala	Gly
Asn 65	Lys	Asp	Arg	Ser	Arg 70	Met	Ser	Val	Phe	Ile 75	Val	Gly	Ile	Asp	Pro 80
Asn	Gly	Ala	Ala	Gly 85	Lys	Asp	Gly	Arg	Leu 90	Gln	Ile	Ala	Asp	Glu 95	Leu
Leu	Glu	Ile	Asn 100	Gly	Gln	Ile	Leu	Tyr 105	Gly	Arg	Ser	His	Gln 110	Asn	Ala
Ser	Ser	Ile 115	Ile	Lys	Cys	Ala	Pro 120	Ser	Lys	Val	Lys	Ile 125	Ile	Phe	Ile
Arg	Asn 130	Lys	Asp	Ala	Val	Asn 135	Gln	Met	Ala	Val	Cys 140	Pro	Gly	Asn	Ala
Val 145	Glu	Pro	Leu	Pro	Ser 150	Asn	Ser	Glu	Asn	Leu 155	Gln	Asn	Lys	Glu	Thr 160
Glu	Pro	Thr	Val	Thr 165	Thr	Ser	Asp	Ala	Ala 170	Val	Asp	Leu	Ser	Ser 175	Phe
Lys	Asn	Val	Gln 180	His	Ser	Gly	Ala	Ser 185	Gln	Gly	Gly	Arg	Gly 190	Val	Trp
Val	Leu	Leu 195	Ser	Ala	Lys	Lys	Ile 200	His	Ser	Val	Glu	Ser 205	Ser		

<210> 496  
 <211> 119  
 <212> PRT  
 <213> homo sapiens

<400> 496

Thr 1	Ser	Trp	Ile	Ile 5	Met	Ala	Pro	Ser	Ser 10	Val	Ser	Glu	Pro	Pro 15	Thr
Met	Leu	Arg	Pro 20	Ser	Pro	Val	Arg	Pro 25	Leu	Glu	Ile	Ser	Met 30	Val	Val
Ser	Gln	Pro 35	Gly	Ile	Met	Gly	Gln 40	Val	Ala	Gly	Ser	Glu 45	Ala	Lys	Ile
Ala	Gly 50	Val	Asp	Asp	Leu	Leu 55	Val	Phe	Arg	Met	Asp 60	Ser	Gly	Ser	Gly

Glu 65	Pro	Asp	Cys	Gly	Thr 70	Ile	Arg	Asp	Trp	Glu 75	Leu	Phe	Phe	Phe	Ser 80
Pro	Leu	Ala	Ala	Pro 85	Ala	Ala	Glu	Gly	Thr 90	Ala	Trp	Glu	Ser	Gly 95	Phe
Ser	Ala	Trp	Met 100	Val	Ser	Phe	Thr	Val 105	Ile	Phe	Ala	Val	Phe 110	Arg	Arg
Leu	Ile	Asn 115	Phe	Ser	Ile	Gly									

<210> 497  
 <211> 71  
 <212> PRT  
 <213> homo sapiens

<400> 497

Ser 1	Ala	Pro	Ser	Leu 5	Thr	Lys	Cys	Arg	Ser 10	Thr	His	Val	Tyr	Pro 15	Leu
Ser	Leu	Ile	Met 20	Phe	Met	Ser	Gly	Gly 25	Ser	Ser	Arg	Ser	Thr 30	Leu	Arg
Arg	Met	Val 35	Pro	Thr	Pro	Ser	Thr 40	Thr	Ser	Leu	Ser	Pro 45	Arg	Ser	Ser
Ser	Ser 50	Thr	Ser	Lys	Leu	Leu 55	Thr	Gln	Ser	Gly	Pro 60	Ser	Leu	Pro	Gln
Pro 65	Pro	Ala	Ser	Arg	Pro 70	Phe									

<210> 498  
 <211> 139  
 <212> PRT  
 <213> homo sapiens

<400> 498

Ser 1	Arg	Ser	Pro	Ala 5	Cys	Gly	Ala	Ser	Glu 10	His	Gly	Asp	Gly	Ala 15	Met
Ser	Leu	Ile	Cys 20	Ser	Ile	Ser	Asn	Glu 25	Val	Pro	Glu	His	Pro 30	Cys	Val
Ser	Pro	Val 35	Ser	Asn	His	Val	Tyr 40	Glu	Arg	Arg	Leu	Ile 45	Glu	Lys	Tyr
Ile	Ala 50	Glu	Asn	Gly	Thr	Asp 55	Pro	Ile	Asn	Asn	Gln 60	Pro	Leu	Ser	Glu
Glu 65	Gln	Leu	Ile	Asp	Ile 70	Lys	Val	Ala	His	Pro 75	Ile	Arg	Pro	Lys	Pro 80
Pro	Ser	Ala	Thr	Ser 85	Ile	Pro	Ala	Ile	Leu 90	Lys	Ala	Leu	Gln	Asp 95	Glu
Trp	Asp	Ala	Val 100	Met	Leu	His	Ser	Phe 105	Thr	Leu	Arg	Gln	Ser 110	Cys	Arg

Gln	Pro	Ala	Lys	Ser	Cys	His	Thr	Leu	Cys	Thr	Ser	Thr	Met	Pro	Pro
		115					120					125			

Ala	Val	Ser	Leu	Pro	Val	Ser	Pro	Arg	Lys	Leu
	130					135				

<210> 499

<211> 74

<212> PRT

<213> homo sapiens

<400> 499

Thr	Thr	Gly	Arg	Glu	Arg	Gly	Cys	Arg	Pro	Cys	Ala	Gly	Leu	Phe	Tyr
1				5					10					15	

Cys	Phe	Leu	Phe	Leu	Met	Lys	Leu	Asp	His	Cys	Leu	Gln	Asn	Pro	Ala
			20					25					30		

Gln	Ala	Leu	Leu	Pro	Ile	Pro	Phe	Thr	Val	Ser	Leu	Val	Arg	Arg	Ala
		35					40					45			

Met	Thr	Arg	Gln	Ala	Ala	Ser	Cys	Trp	Tyr	Arg	Ala	Cys	Asp	Ser	Ser
	50					55					60				

Trp	Arg	Val	Val	Cys	Ser	Ser	Gly	Ala	Glu
65					70				

<210> 500

<211> 71

<212> PRT

<213> homo sapiens

<400> 500

Phe	Ser	Phe	Phe	Asn	Glu	Thr	Arg	Ser	Leu	Leu	Thr	Lys	Pro	Cys	Thr
1				5					10					15	

Ser	Pro	Pro	Ala	His	Pro	Leu	His	Ser	Ser	Leu	Gly	Ser	Ala	Ser	Pro
			20					25					30		

Val	Ser	Gln	Glu	Leu	Gln	Gln	Asn	Gly	Cys	Gly	Thr	Ala	Thr	Thr	Thr
		35					40					45			

Ser	Ile	Glu	Arg	Gln	Glu	Gly	Arg	Gly	Ala	Val	Gly	Leu	Val	Gln	Gly
	50					55					60				

Phe	Phe	Ile	Val	Phe	Phe	Phe
65					70	

<210> 501

<211> 284

<212> PRT

<213> homo sapiens

<400> 501

Glu	Ala	Arg	Gly	Leu	Ala	Thr	Arg	Thr	Arg	Ser	Gly	Ala	Ala	Ala	His
1				5					10					15	

Ala	Gly	Asp	Arg	Phe	Thr	Asp	Ala	Asp	Asp	Val	Ala	Ile	Leu	Thr	Tyr
			20					25					30		

Val	Lys	Glu	Asn	Ala	Arg	Ser	Pro	Ser	Ser	Val	Thr	Gly	Asn	Ala	Leu	
		35					40					45				
Trp	Lys	Ala	Met	Glu	Lys	Ser	Ser	Leu	Thr	Gln	His	Ser	Trp	Gln	Ser	
	50					55					60					
Leu	Lys	Asp	Arg	Tyr	Leu	Lys	His	Leu	Arg	Gly	Gln	Glu	His	Lys	Tyr	
65					70					75					80	
Leu	Leu	Gly	Asp	Ala	Pro	Val	Ser	Pro	Ser	Ser	Gln	Lys	Leu	Lys	Arg	
				85					90					95		
Lys	Ala	Glu	Glu	Asp	Pro	Glu	Ala	Ala	Asp	Ser	Gly	Glu	Pro	Gln	Asn	
			100					105					110			
Lys	Arg	Thr	Pro	Asp	Leu	Pro	Glu	Glu	Glu	Tyr	Val	Lys	Glu	Glu	Ile	
		115					120					125				
Gln	Glu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Met	Leu	Val	Glu	Ala	Thr	Arg	
	130					135					140					
Glu	Phe	Glu	Glu	Val	Val	Val	Asp	Glu	Ser	Pro	Pro	Asp	Phe	Glu	Ile	
145					150					155					160	
His	Ile	Thr	Met	Cys	Asp	Asp	Asp	Pro	Pro	Thr	Pro	Glu	Glu	Asp	Ser	
				165				170						175		
Glu	Thr	Gln	Pro	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Val	Ser	
			180					185					190			
Gln	Pro	Glu	Val	Gly	Ala	Ala	Ile	Lys	Ile	Ile	Arg	Gln	Leu	Met	Glu	
		195					200					205				
Lys	Phe	Asn	Leu	Asp	Leu	Ser	Thr	Val	Thr	Gln	Ala	Phe	Leu	Lys	Asn	
	210					215					220					
Ser	Gly	Glu	Leu	Glu	Ala	Thr	Ser	Ala	Phe	Leu	Ala	Ser	Gly	Gln	Arg	
225					230					235					240	
Ala	Asp	Gly	Tyr	Pro	Ile	Trp	Ser	Arg	Gln	Asp	Asp	Ile	Asp	Leu	Gln	
				245					250					255		
Lys	Asp	Asp	Glu	Asp	Thr	Arg	Glu	Ala	Leu	Val	Lys	Lys	Phe	Gly	Ala	
			260					265					270			
Gln	Asn	Val	Ala	Arg	Arg	Ile	Glu	Phe	Arg	Lys	Lys					
		275					280									

<210> 502

<211> 123

<212> PRT

<213> homo sapiens

<400> 502

Glu	Thr	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Cys	Val	Ser	
1				5					10					15		
Glu	Ser	Ser	Ser	Gly	Val	Gly	Gly	Ser	Ser	Ser	His	Ile	Val	Ile	Cys	
			20					25					30			
Ile	Ser	Lys	Ser	Gly	Gly	Leu	Ser	Ser	Thr	Thr	Thr	Ser	Ser	Asn	Ser	
		35					40					45				

Arg	Val 50	Ala	Ser	Thr	Ser	Ile 55	Phe	Leu	Thr	Ala	Ser 60	Ser	Phe	Ser	Trp
Ile 65	Ser	Ser	Phe	Thr	Tyr 70	Ser	Ser	Ser	Gly	Lys 75	Ser	Gly	Val	Leu	Leu 80
Phe	Cys	Gly	Ser	Pro 85	Leu	Ser	Ala	Ala	Ser 90	Gly	Ser	Ser	Ser	Ala 95	Phe
Arg	Leu	Ser	Phe 100	Trp	Glu	Glu	Gly	Leu 105	Thr	Gly	Ala	Ser	Pro 110	Ser	Arg
Tyr	Leu	Cys 115	Ser	Trp	Pro	Arg	Arg 120	Cys	Leu	Arg					

<210> 503  
 <211> 175  
 <212> PRT  
 <213> homo sapiens

<400> 503

Val 1	Phe	Leu	Arg	Cys 5	Gly	Trp	Ile	Ile	Ile 10	Thr	His	Ser	Tyr	Met 15	Tyr
Phe	Lys	Ile	Arg 20	Arg	Ala	Leu	Ile	His 25	His	Asn	Leu	Leu	Lys 30	Leu	Pro
Gly	Gly	Phe 35	His	Lys	His	Leu	Phe 40	Asp	Cys	Phe	Phe	Ile 45	Leu	Leu	Asp
Phe 50	Phe	Leu	His	Ile	Leu	Phe 55	Phe	Arg	Gln	Ile	Trp 60	Ser	Ser	Leu	Ile
Leu 65	Trp	Phe	Pro	Ala	Ile 70	Arg	Gly	Leu	Arg	Val 75	Leu	Leu	Arg	Leu	Pro 80
Leu	Glu	Leu	Leu	Gly 85	Gly	Gly	Ala	His	Arg 90	Arg	Val	Pro	Gln	Gln 95	Val
Leu	Met	Leu	Leu 100	Ala	Pro	Gln	Val	Leu 105	Glu	Val	Ala	Val	Leu 110	Gln	Gly
Leu	Pro	Arg 115	Val	Leu	Arg	Glu	Arg 120	Ala	Leu	Leu	His	Arg 125	Phe	Pro	Gln
Gly	Val 130	Thr	Gly	Asp	Gly	Ala 135	Gly	Arg	Ala	Gly	Ile 140	Phe	Leu	His	Val
Gly 145	Lys	Asp	Gly	Tyr	Val 150	Val	Arg	Ile	Arg	Glu 155	Ala	Ile	Ala	Arg	Val 160
Arg	Cys	Arg	Ser	Ala 165	Pro	Arg	Ala	Arg	Arg 170	Gln	Ala	Pro	Gly	Phe 175	

<210> 504  
 <211> 78  
 <212> PRT  
 <213> homo sapiens

<400> 504

Cys 1	Pro	Pro	Glu	Lys 5	Ser	Leu	Gln	Met	Phe 10	Gln	Pro	Leu	Ser	Ser 15	Pro
Asp	Ser	His	Arg 20	Lys	Gly	Thr	Gly	Phe 25	Gly	Leu	Gly	Ile	Val 30	Phe	Ser
Leu	Thr	Phe 35	Phe	Lys	Arg	Arg	Met 40	Trp	Pro	Leu	Ala	Phe 45	Gly	Ser	Gly
Met	Gly 50	Leu	Gly	Met	Ala	Tyr 55	Ser	Asn	Cys	Gln	His 60	Asp	Phe	Gln	Ala
Pro 65	Tyr	Leu	Leu	His	Gly 70	Lys	Tyr	Val	Lys	Glu 75	Gln	Glu	Gln		

<210> 505  
 <211> 95  
 <212> PRT  
 <213> homo sapiens

<400> 505

Ser 1	Lys	Thr	Ser	Thr 5	Leu	Pro	Val	Ala	Ile 10	Trp	Thr	Arg	Gln	Arg 15	Leu
Glu	His	Leu	Gln 20	Gly	Phe	Leu	Gly	Trp 25	Thr	Ser	Ile	Thr	Arg 30	Ile	Leu
Ser	Ser	Arg 35	Pro	His	Pro	Pro	Asp 40	Thr	Gly	Pro	Thr	Ser 45	Cys	Arg	Ala
Pro	Thr 50	Gln	Thr	Cys	Ser	Pro 55	Pro	Ala	Pro	Pro	Ala 60	Phe	Leu	Ser	Ala
Gly 65	Pro	Arg	Ala	Pro	Thr 70	Pro	Glu	Ser	Leu	Ala 75	Arg	Ala	Gly	Asn	Lys 80
Ser	Gln	Val	Arg	Lys 85	Ala	Gly	Ala	Asp	Ala 90	Pro	Asp	Ile	Ala	Arg 95	

<210> 506  
 <211> 156  
 <212> PRT  
 <213> homo sapiens

<400> 506

Ala 1	Ile	Pro	Asn	Pro 5	Met	Pro	Glu	Pro	Lys 10	Ala	Asn	Gly	His	Ile 15	Leu
Leu	Leu	Lys	Lys 20	Val	Ser	Glu	Lys	Thr 25	Ile	Pro	Asn	Pro	Lys 30	Pro	Val
Pro	Phe	Leu 35	Trp	Leu	Ser	Gly	Leu 40	Asp	Arg	Gly	Trp	Asn 45	Ile	Cys	Arg
Asp	Phe 50	Ser	Gly	Gly	His	Gln 55	Leu	Pro	Gly	Phe	Tyr 60	Leu	His	Asp	Arg
Ile 65	Arg	Gln	Thr	Pro	Val 70	Pro	Leu	Pro	Ala	Glu 75	Leu	Arg	Leu	Arg	His 80
Val	Pro	His	Pro	Arg	Leu	Gln	Leu	Ser	Ser	Arg	Pro	Ala	Pro	Ala	Leu

				85					90						95	
Arg	Pro	Leu	Lys 100	Val	Ser	Arg	Glu	Leu 105	Glu	Thr	Ser	Pro	Arg 110	Ser	Gly	
Arg	Gln	Ala 115	Gln	Thr	Leu	Gln	Ile 120	Ser	Arg	Asp	Asp	Pro 125	Leu	Leu	Pro	
Ser	Leu 130	Pro	Val	Phe	Ser	Val 135	Gly	Arg	Gln	Gly	Asp 140	Ala	Val	Val	Trp	
Arg 145	Leu	Glu	Val	Thr	Leu 150	Thr	Leu	Gly	Cys	Ala 155	Tyr					

<210> 507  
 <211> 169  
 <212> PRT  
 <213> homo sapiens  
 <400> 507

Ala 1	Ala	Ser	Gly	Met 5	Leu	Gly	Ser	Trp	Pro 10	Ala	Arg	Thr	Phe	His 15	Pro	
Gly	Ala	Cys	Val 20	Ser	Arg	Arg	Pro	Ser 25	Ala	Pro	Trp	Lys	His 30	Thr	Ala	
Ser	Gly	Lys 35	Asp	Ser	Pro	Asp	Leu 40	Arg	Phe	Ser	Glu	His 45	Gly	Val	Ser	
Gln	Glu 50	Phe	Trp	Ala	Gly	Gly 55	Leu	Val	Ala	Val	Leu 60	Glu	Met	Thr	Pro	
Ser 65	Pro	Ser	Pro	Trp	Gly 70	Thr	Gln	Glu	Gly	Pro 75	Ala	Gly	Met	Cys	Ser 80	
Leu	Trp	Val	Val	Gly 85	Trp	Cys	Pro	Cys	Arg 90	Gly	Ala	Gly	Val	Arg 95	Asp	
Leu	Val	Leu	Val 100	His	Ala	Gly	Val	Trp 105	Cys	Lys	His	Val	Cys 110	Ala	Val	
Gln	Arg	Asp 115	Ala	Cys	Gly	Glu	Ser 120	Arg	Thr	Pro	Ala	Pro 125	Pro	Arg	Lys	
Gly	Gly 130	Ala	Val	Thr	Ser	Val 135	Leu	Cys	Leu	Phe	Leu 140	Ile	Lys	Thr	Phe	
Pro 145	Leu	Phe	Ser	Tyr	Lys 150	Phe	Ala	Ser	Cys	Lys 155	Gln	Val	His	Lys	Asp 160	
Pro	Pro	Leu	Val	Lys 165	Ser	Gly	Phe	Glu								

<210> 508  
 <211> 155  
 <212> PRT  
 <213> homo sapiens

<400> 508

Thr 1	Gln	Asn	Thr	Gly 5	Asn	Arg	Ser	Ala	Phe 10	Pro	Gly	Trp	Arg	Trp 15	Cys	
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145

<210> 510  
 <211> 75  
 <212> PRT  
 <213> homo sapiens

<400> 510

Asn 1	Ala	Tyr	Ile	Ser 5	Gly	Tyr	Glu	Arg	Asp 10	Phe	Met	Thr	Ile	Gln 15	Ser
Asn	Ile	Thr	Leu 20	Ala	Asp	Arg	Glu	Thr 25	Glu	Val	Phe	His	Asp 30	Leu	Pro
Ser	Leu	Pro 35	Ala	Ser	Leu	Arg	Gln 40	Asn	Trp	Ile	Pro	Thr 45	Leu	Val	Phe
Phe	Leu 50	Pro	Phe	Thr	Ser	Phe 55	Ser	Leu	Leu	Tyr	Asn 60	Val	Leu	Arg	Asp
Gln 65	Asn	Ser	His	Gln	Asn 70	Arg	Leu	Phe	Leu	Arg 75					

<210> 511  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 511

Phe 1	Arg	Asp	Thr	Glu 5	Gly	Leu	Leu	Ala	Leu 10	Met	Thr	Phe	Trp	Met 15	Gly
Leu	Gln	Leu	Met 20	Thr	Ile	Leu	Ile	Leu 25	Glu	Glu	Arg	Thr	Leu 30	Leu	Ile
Phe	Ser	Pro 35	Ile	Ala	Leu	Leu	Arg 40	Arg	Ser	Thr	Ser	Tyr 45	Ser	Glu	Ser
Leu	His 50	Ile	Pro	Leu	Val	Phe 55	Leu	Gln	Ala	Pro	Glu 60	Pro	Leu	Val	Gln
Met 65	Leu	Tyr													

<210> 512  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 512

Ile 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Phe	Phe	Phe 10	Pro	Leu	Arg	His	Leu 15	Phe
Asn	Asn	Cys	Arg 20	Asn	Pro	Lys	Glu	Leu 25	Ala	Ser	Asn	Leu	Glu 30	Val	Val
Ser	Glu	Ala 35	Ala	Gly	Trp	Leu	Asp 40	Trp	Ala	Gln	Pro	Leu 45	Ser	Cys	Leu
Asn	Arg	Pro	Arg	Asn	Gly	Ile	Met	Met	Thr	Met	Arg	Thr	Ser	Ile	Leu

	50					55				60						
Ser	Ser	Ser	His	Cys	Val	Tyr	Tyr	Val	Phe	Ser	Phe	Asn	Lys	Ala	Phe	
65					70					75					80	
Val	Pro	Met	Ala	Leu	Glu	Leu	Gly	Gly	Arg	Leu	Lys	Glu	Cys	Val	Val	
				85					90					95		
Ile	Leu	Ser	Lys	Met												
			100													

<210> 513  
 <211> 179  
 <212> PRT  
 <213> homo sapiens

<400> 513

Phe	Gly	Thr	Met	Gly	Gly	Ile	Ser	Asp	Pro	Asp	Thr	Leu	His	Ile	Trp	
1				5					10					15		
Lys	Thr	Asn	Ser	Leu	Pro	Leu	Arg	Phe	Trp	Val	Asn	Ile	Leu	Lys	Asn	
			20					25					30			
Pro	Gln	Phe	Val	Phe	Asp	Ile	Asp	Lys	Thr	Asp	His	Ile	Asp	Ala	Cys	
		35					40					45				
Leu	Ser	Val	Ile	Ala	Gln	Ala	Phe	Ile	Asp	Ala	Cys	Ser	Ile	Ser	Asp	
	50					55					60					
Leu	Gln	Leu	Gly	Lys	Asp	Ser	Pro	Thr	Asn	Lys	Leu	Leu	Tyr	Ala	Lys	
65				70						75					80	
Glu	Ile	Pro	Glu	Tyr	Arg	Lys	Ile	Val	Gln	Arg	Tyr	Tyr	Lys	Gln	Ile	
				85					90					95		
Gln	Asp	Met	Thr	Pro	Leu	Ser	Glu	Gln	Glu	Met	Asn	Ala	His	Leu	Ala	
			100					105					110			
Glu	Glu	Ser	Arg	Lys	Tyr	Gln	Asn	Glu	Phe	Asn	Thr	Asn	Val	Ala	Met	
		115					120					125				
Ala	Glu	Ile	Tyr	Lys	Tyr	Ala	Lys	Arg	Tyr	Arg	Pro	Gln	Ile	Met	Ala	
	130					135					140					
Ala	Leu	Glu	Ala	Asn	Pro	Thr	Ala	Arg	Arg	Thr	Gln	Leu	Gln	His	Lys	
145					150					155					160	
Phe	Glu	Gln	Val	Val	Ala	Leu	Met	Glu	Asp	Asn	Ile	Tyr	Glu	Cys	Tyr	
				165					170					175		
Ser	Glu	Ala														

<210> 514  
 <211> 179  
 <212> PRT  
 <213> homo sapiens

<400> 514

Asp	Arg	Gly	Ala	Pro	Ala	Leu	Thr	Pro	Gly	His	Leu	His	Pro	Leu	Pro	
1				5					10					15		

Pro	Val	Pro	Arg 20	Ser	Val	Ser	Gly	Met 25	Glu	Ala	Arg	Glu	Leu 30	Val	Arg	
Leu	Pro	His 35	Leu	Pro	Ser	Thr	Ala 40	Cys	Thr	Val	Pro	Thr 45	His	Leu	Leu	
His	Asn 50	Val	Gln	Leu	Val	Leu 55	Leu	Pro	Arg	Ala	Pro 60	Cys	Ile	Gln	Ala	
Ala 65	Lys	His	Lys	Leu	Gly 70	Glu	Arg	Arg	Pro	Pro 75	Ala	Arg	Arg	Leu	Gln 80	
Pro	Arg	Asn	Ser	Thr 85	Ser	Ser	Thr	Leu	Val 90	Gln	Gly	Ala	Leu	Leu 95	Glu	
Leu	Thr	Phe	Asp 100	Trp	Phe	Leu	Leu	Gln 105	Leu	Pro	Lys	Cys	Tyr 110	Leu	His	
Phe	Pro	Leu 115	Thr	Arg	Arg	Gly	Ser 120	Trp	Pro	Gln	Thr	Val 125	Ser	Ser	Ser	
Val	Arg 130	Phe	Leu	Leu	Leu	Gly 135	Arg	Leu	Leu	Val	Glu 140	Trp	Ala	Val	Pro	
Ala 145	Pro	Trp	Gly	Ala	Leu 150	Trp	Ala	Ser	Pro	Gly 155	Ala	Gly	Arg	Val	Glu 160	
Gly	Arg	Asp	Gly	Gly 165	His	Arg	Ser	Trp	Glu 170	Pro	Arg	Leu	Gln	Glu 175	Lys	
Glu	Arg	Gly														

<210> 515

<211> 200

<212> PRT

<213> homo sapiens

<400> 515

Ser 1	Gly	Asp	Arg	Trp 5	Glu	Gly	Met	Glu	Val 10	Pro	Arg	Gly	Gln	Gly 15	Gly	
Gly	Ala	Pro	Val 20	Ser	Glu	Ser	Ser	Pro 25	Ser	Ser	Cys	Pro	Arg 30	Pro	Ser	
Arg	Leu	Cys 35	Ser	Val	Phe	Pro	Ser 40	Leu	Ser	His	Arg	His 45	Gly	Val	Glu	
Asp	Gln 50	Val	Glu	Ala	Gln	Trp 55	Ala	Ser	Ile	Ser	Pro 60	Ser	Ser	Ser	Leu	
Thr 65	Asn	Ser	Pro	Cys	Val 70	Ser	Gly	Leu	Thr	Val 75	Ala	Leu	Val	Asp	Val 80	
Val	Leu	His	Gln	Ser 85	His	His	Leu	Leu	Lys 90	Leu	Val	Leu	Gln	Leu 95	Cys	
Pro	Pro	Gly	Arg 100	Gly	Val	Gly	Leu	Gln 105	Arg	Gly	His	Asp	Leu 110	Arg	Pro	
Ile	Pro	Leu 115	Gly	Val	Leu	Ile	Asn 120	Leu	Cys	His	Gly	His 125	Ile	Gly	Val	

Glu	Leu	Ile	Leu	Val	Phe	Pro	Arg	Leu	Leu	Gly	Gln	Met	Gly	Ile	His
	130					135					140				
Leu	Leu	Leu	Ala	Glu	Arg	Arg	His	Val	Leu	Asp	Leu	Leu	Val	Val	Ala
145					150					155					160
Leu	His	Asp	Leu	Pro	Val	Leu	Arg	Asn	Leu	Leu	Gly	Val	Glu	Glu	Leu
				165					170					175	
Val	Gly	Trp	Arg	Ile	Leu	Ala	Gln	Leu	Gln	Val	Arg	Asp	Gly	Ala	Gly
			180					185					190		
Val	Asp	Glu	Gly	Leu	Arg	Asp	Asp								
		195					200								

<210> 516  
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 <212> PRT  
 <213> homo sapiens

<400> 516

Thr	Ser	Met	Glu	Ala	Leu	Leu	Phe	Arg	Leu	Phe	Lys	Leu	Pro	Ala	Thr
1				5					10					15	
Thr	Leu	Arg	Cys	Ile	Gly	Leu	Arg	Arg	Pro	Leu	Val	Thr	His	Thr	Leu
			20					25					30		
Arg	Arg	Lys	Cys	Glu	His	Lys	Ala	Ser	Arg	Leu	Cys	His	Gly	Gly	Cys
		35					40					45			
Cys	Cys	Thr	Leu	Glu	Pro	Cys	Val	Gly	Arg	His	Arg	Asp	Trp	Asp	Leu
	50					55					60				
Glu	Arg	Gly	Lys	Ser	Ser	Ala	Lys	Thr	Gly	Gly	Glu	Leu	His	Gly	Arg
65					70					75					80
Arg	Thr	Ala	Ala	Ala	Arg	Gly	Gly	Ser	Glu	Arg	Pro	Val	Leu	Gly	His
				85					90					95	
Arg	Arg	Arg	Asp	Pro	Asp	Ala	Gly	Gly	Leu	Arg	Gly	Gln	Asp	Gly	Glu
			100					105					110		
Ala	Leu	Gln	His	Arg	Gly	Trp	His	Ile	Pro	Gly	Ser	Glu	Thr	Leu	Pro
		115					120					125			
Gly	Arg	Gly	Gly	His	Val	Pro	Trp	Pro	Arg	Pro	Gly	Arg	Arg	His	Pro
	130					135					140				
His	His	Met	Cys	Gly	Phe	Trp	Asp	Ser	Gln	Ser	Leu	Ala			
145					150					155					

<210> 517  
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 <212> PRT  
 <213> homo sapiens

<400> 517

Arg	Thr	Arg	Cys	Ala	Gly	Ser	Val	Asn	Thr	Lys	Pro	Pro	Gly	Phe	Val
1				5					10					15	
Met	Ala	Ala	Ala	Ala	Ala	Arg	Trp	Asn	His	Val	Trp	Val	Gly	Thr	Glu

20							25					30				
Thr	Gly	Ile 35	Leu	Lys	Gly	Val	Asn 40	Leu	Gln	Arg	Lys	Gln 45	Ala	Ala	Asn	
Phe	Thr 50	Ala	Gly	Gly	Gln	Pro 55	Arg	Arg	Glu	Glu	Ala 60	Val	Ser	Ala	Leu	
Cys 65	Trp	Gly	Thr	Gly	Gly 70	Glu	Thr	Gln	Met	Leu 75	Val	Gly	Cys	Ala	Asp 80	
Arg	Thr	Val	Lys	His 85	Phe	Ser	Thr	Glu	Asp 90	Gly	Ile	Phe	Gln	Gly 95	Gln	
Arg	His	Cys	Pro 100	Gly	Gly	Glu	Gly	Met 105	Phe	Arg	Gly	Leu	Ala 110	Gln	Ala	
Asp	Gly	Thr 115	Leu	Ile	Thr	Cys	Val 120	Asp	Ser	Gly	Ile	Leu 125	Arg	Val	Trp	
His	Asp 130	Lys	Asp	Lys	Asp	Thr 135	Ser	Ser	Asp	Pro	Leu 140	Leu	Glu	Leu	Arg	
Val 145	Gly	Pro	Gly	Val	Cys 150	Arg	Met	Arg	Gln	Asp 155	Pro	Ala	His	Pro	His 160	
Val	Val	Ala	Thr	Gly 165	Gly	Lys	Glu	Asn	Ala 170	Leu	Lys	Ile	Trp	Asp 175	Leu	
Gln	Gly	Ser	Glu 180	Glu	Pro	Val	Phe	Arg 185	Ala	Lys	Asn	Val	Arg 190	Asn	Asp	
Trp	Leu	Asp 195	Leu	Arg	Val	Pro	Ile 200	Trp	Asp	Gln	Asp	Ile 205	Gln	Phe	Leu	
Pro	Gly 210	Ser	Gln	Lys	Leu	Val 215	Thr	Cys	Thr	Gly	Tyr 220	His	Gln	Val	Arg	
Val 225	Tyr	Asp	Pro	Ala	Ser 230	Pro	Gln	Arg	Arg	Pro 235	Val	Leu	Glu	Thr	Thr 240	
Tyr	Gly	Glu	Tyr	Pro 245	Leu	Thr	Ala	Met	Thr 250	Leu	Thr	Pro	Gly	Gly 255	Asn	
Ser	Val	Ile	Val 260	Gly	Asn	Thr	His	Gly 265	Gln	Leu	Ala	Glu	Ile 270	Asp	Leu	
Arg	Gln	Gly 275	Arg	Leu	Leu	Gly	Cys 280	Leu	Lys	Gly	Leu	Ala 285	Gly	Ser	Val	
Arg	Gly 290	Leu	Gln	Cys	His	Pro 295	Ser	Lys	Pro	Leu	Leu 300	Ala	Ser	Cys	Gly	
Leu 305	Asp	Arg	Val	Leu	Arg 310	Ile	His	Arg	Ile	Gln 315	Asn	Pro	Arg	Gly	Leu 320	
Glu	His	Lys	Val	Tyr 325	Leu	Lys	Ser	Gln	Leu 330	Asn	Cys	Leu	Leu	Leu 335	Ser	
Gly	Arg	Asp	Asn 340	Trp	Glu	Asp	Glu	Pro 345	Gln	Glu	Pro	Gln	Glu 350	Pro	Asn	
Lys	Val	Pro	Leu	Glu	Asp	Thr	Glu	Thr	Asp	Glu	Leu	Trp	Ala	Ser	Leu	

		355					360					365				
Glu	Ala	Ala	Ala	Lys	Arg	Lys	Leu	Ser	Gly	Leu	Glu	Gln	Pro	Gln	Gly	
	370					375					380					
Ala	Leu	Gln	Thr	Arg	Arg	Arg	Lys	Lys	Lys	Arg	Pro	Gly	Ser	Thr	Ser	
385					390					395					400	

Pro

<210> 518  
 <211> 222  
 <212> PRT  
 <213> homo sapiens

<400> 518

Ser	Trp	Glu	Lys	Leu	Tyr	Val	Leu	Val	Pro	Asp	Gly	Asn	Pro	Gln	Val	
1				5					10					15		
Gln	Pro	Val	Ile	Pro	His	Val	Leu	Gly	Pro	Glu	His	Arg	Phe	Leu	Arg	
			20					25					30			
Ala	Leu	Gln	Val	Pro	Tyr	Leu	Gln	Ser	Ile	Leu	Phe	Pro	Thr	Cys	Gly	
		35					40					45				
Asn	His	Met	Gly	Val	Cys	Trp	Val	Leu	Ala	His	Pro	Thr	His	Pro	Arg	
	50					55					60					
Ala	His	Ser	Gln	Phe	Gln	Glu	Trp	Val	Arg	Gly	Cys	Val	Leu	Val	Leu	
65					70					75					80	
Val	Met	Pro	Asp	Ser	Glu	Asn	Pro	Arg	Ile	His	Thr	Cys	Asp	Glu	Gly	
				85					90					95		
Ala	Val	Gly	Leu	Gly	Glu	Ala	Thr	Glu	His	Ala	Leu	Pro	Ala	Arg	Ala	
			100					105					110			
Val	Ser	Leu	Thr	Leu	Glu	Tyr	Ala	Ile	Leu	Gly	Ala	Glu	Val	Leu	His	
		115					120					125				
Arg	Pro	Val	Arg	Ala	Ala	His	Gln	His	Leu	Gly	Leu	Ala	Ala	Gly	Ala	
	130					135					140					
Pro	Thr	Gln	Gly	Ala	His	Cys	Leu	Leu	Ala	Pro	Arg	Leu	Ser	Ser	Gly	
145					150					155					160	
Arg	Glu	Val	Arg	Arg	Leu	Phe	Ser	Leu	Lys	Ile	Tyr	Pro	Phe	Gln	Asp	
				165					170					175		
Pro	Ser	Leu	Gly	Ala	Asp	Pro	His	Met	Val	Pro	Ala	Cys	Ser	Ser	Ser	
			180					185					190			
Arg	His	Asp	Lys	Ala	Trp	Arg	Leu	Cys	Val	His	Thr	Ser	Gly	Ala	Ala	
		195					200					205				
Cys	Ala	Ser	Pro	Ala	Gly	Val	Glu	Val	Arg	Cys	Thr	Ala	Val			
	210					215					220					

<210> 519  
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 <213> homo sapiens



65

70

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 <212> PRT  
 <213> homo sapiens

<400> 528

Leu	Thr	Tyr	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Gly	Arg	Ser	
1				5					10					15		
Leu	Gly	Phe	Ile	Arg	Ser	Val	Gly	Thr	Leu	Phe	Arg	Ser	Glu	Ala	Pro	
			20					25					30			
Pro	Ser	His	Gly	Val	Gly	Asp	Ser	Gly	Gly	Arg	Gly	Asn	Pro	Ser	Glu	
		35					40					45				
His	Pro	Gly	Gly	Cys	Val	Val	Ser	Met	Tyr	Phe	Ala	Leu	Pro	His	Leu	
	50					55					60					
Phe	His	Gly	Val	Pro	Cys	Gln	Gly	Gln	Ala	Leu	Ile	Cys	Gly	Glu	Gly	
65					70					75					80	
Ser	Lys	Gln	Arg	Arg	Arg	Pro	Phe	Arg	Gly	Gly	Glu	Arg	Ala	Val	Ala	
				85					90					95		
Pro	Arg	Thr	Pro	Ser	Pro	Ala	His	Asp	Ile	Pro	Glu	Lys	Glu	Thr	Lys	
			100					105					110			
Ile	Lys	Pro	Arg	Gly	Leu	Ser	Thr									
		115					120									

<210> 529  
 <211> 90  
 <212> PRT  
 <213> homo sapiens

<400> 529



Pro 1	Leu	Leu	Lys	Gly 5	Lys	Lys	Leu	Ser	Ala 10	Ala	Leu	Thr	Asn	Leu 15	Ser
Phe	Phe	Phe	Phe 20	Phe	Phe	Phe	Phe	Phe 25	Gly	Lys	Lys	Pro	Trp 30	Leu	Tyr
Ser	Leu	Cys 35	Gly	Asp	Thr	Val	Pro 40	Phe	Arg	Gly	Pro	Ser 45	Gln	Pro	Trp
Gly	Gly 50	Gly	Gln	Trp	Trp	Ala 55	Trp	Glu	Ser	Gln	Arg 60	Ala	Ser	Trp	Arg
Val 65	Arg	Arg	Leu	His	Val 70	Phe	Cys	Ser	Ser	Pro 75	Ser	Phe	Pro	Trp	Gly 80
Pro	Leu	Pro	Gly	Ser 85	Ser	Thr	Asn	Met	Trp 90						

<210> 530  
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 <212> PRT  
 <213> homo sapiens

<400> 530

Asn 1	Lys	Ala	Pro	Gly 5	Pro	Phe	Tyr	Val	Gly 10	Ala	Pro	Leu	Lys	Tyr 15	Gly
Met	Val	Val	Gly 20	Arg	Glu	Ala	Val	Ala 25	Gln	Gln	Ser	Leu	Ser 30	Pro	Asp
Tyr	Gln	Leu 35	Trp	Gly	Gly	Phe	Gln 40	Gly	Ala	Arg	Ser	Arg 45	Leu	Gly	Ser
Ser 50	Ser	His	Arg	His	Val	Gly 55	Gly	Gly	Arg	Lys	Tyr 60	Leu	Gln	Gly	Gly
Thr 65	Val	Ser	Glu	Glu	Gln 70	Asp	Gly	Arg	Gly	Phe 75	Ser	Ala	Cys	Tyr	Gly 80
Ile	Leu	Phe	Lys	Glu 85	Met	Gly	Val	Lys	Pro 90	Gly	Thr	Val	Ala	His 95	Ala

<210> 531  
 <211> 497  
 <212> PRT  
 <213> homo sapiens

<400> 531

Thr 1	Pro	Ala	Leu	Val 5	Gln	Arg	Phe	Arg	Glu 10	Gly	Gly	Ser	Gly	Ala 15	Pro
Glu	Gln	Ala	Glu 20	Cys	Val	Glu	Leu	Leu 25	Leu	Ala	Leu	Gly	Glu 30	Pro	Ala
Glu	Glu	Leu 35	Cys	Glu	Glu	Phe	Leu 40	Ala	His	Ala	Arg	Gly 45	Arg	Leu	Glu
Lys	Glu 50	Leu	Arg	Asn	Leu	Glu 55	Ala	Glu	Leu	Gly	Pro 60	Ser	Pro	Pro	Ala

Pro 65	Asp	Val	Leu	Glu	Phe 70	Thr	Asp	His	Gly	Gly 75	Ser	Gly	Phe	Val	Gly 80
Gly	Leu	Cys	Gln	Val 85	Ala	Ala	Ala	Tyr	Gln 90	Glu	Leu	Phe	Ala	Ala 95	Gln
Gly	Pro	Ala	Gly 100	Ala	Glu	Lys	Leu	Ala 105	Ala	Phe	Ala	Arg	Gln 110	Leu	Gly
Ser	Arg	Tyr 115	Phe	Ala	Leu	Val	Glu 120	Arg	Arg	Leu	Ala	Gln 125	Glu	Gln	Gly
Gly 130	Gly	Asp	Asn	Ser	Leu	Leu 135	Val	Arg	Ala	Leu	Asp 140	Arg	Phe	His	Arg
Arg 145	Leu	Arg	Ala	Pro	Gly 150	Ala	Leu	Leu	Ala	Ala 155	Ala	Gly	Leu	Ala	Asp 160
Ala	Ala	Thr	Glu	Ile 165	Val	Glu	Arg	Val	Ala 170	Arg	Glu	Arg	Leu	Gly 175	His
His	Leu	Gln	Gly 180	Leu	Arg	Ala	Ala	Phe 185	Leu	Gly	Cys	Leu	Thr 190	Asp	Val
Arg	Gln	Ala 195	Leu	Ala	Ala	Pro	Arg 200	Val	Ala	Gly	Lys	Glu 205	Gly	Pro	Gly
Leu	Ala 210	Glu	Leu	Leu	Ala	Asn 215	Val	Ala	Ser	Ser	Ile 220	Leu	Ser	His	Ile
Lys 225	Ala	Ser	Leu	Ala	Ala 230	Val	His	Leu	Phe	Thr 235	Ala	Lys	Glu	Val	Ser 240
Phe	Ser	Asn	Lys	Pro 245	Tyr	Phe	Arg	Gly	Glu 250	Phe	Cys	Ser	Gln	Gly 255	Val
Arg	Glu	Gly	Leu 260	Ile	Val	Gly	Phe	Val 265	His	Ser	Met	Cys	Gln 270	Thr	Ala
Gln	Ser	Phe 275	Cys	Asp	Ser	Pro	Gly 280	Glu	Lys	Gly	Gly	Ala 285	Thr	Pro	Pro
Ala	Leu 290	Leu	Leu	Leu	Leu	Ser 295	Arg	Leu	Cys	Leu	Asp 300	Tyr	Glu	Thr	Ala
Thr 305	Ile	Ser	Tyr	Ile	Leu 310	Thr	Leu	Thr	Asp	Glu 315	Gln	Phe	Leu	Val	Gln 320
Asp	Gln	Phe	Pro	Val 325	Thr	Pro	Val	Ser	Thr 330	Leu	Cys	Ala	Glu	Ala 335	Arg
Glu	Thr	Ala 340	Arg	Arg	Leu	Leu	Thr	His 345	Tyr	Val	Lys	Val	Gln 350	Gly	Leu
Val	Ile	Ser 355	Gln	Met	Leu	Arg	Lys 360	Ser	Val	Glu	Thr	Arg 365	Asp	Trp	Leu
Ser	Thr 370	Leu	Glu	Pro	Arg	Asn 375	Val	Arg	Ala	Val	Met 380	Lys	Arg	Val	Val
Glu 385	Asp	Thr	Thr	Ala	Ile 390	Asp	Val	Gln	Val	Gly 395	Leu	Leu	Tyr	Glu	Glu 400

Gly	Val	Arg	Lys	Ala 405	Gln	Ser	Ser	Asp	Ser 410	Ser	Lys	Arg	Thr	Phe 415	Ser
Val	Tyr	Ser	Ser 420	Ser	Arg	Gln	Gln	Gly 425	Arg	Tyr	Ala	Pro	Ser 430	Tyr	Thr
Pro	Ser	Ala 435	Pro	Met	Asp	Thr	Asn 440	Leu	Leu	Ser	Asn	Ile 445	Gln	Lys	Leu
Phe	Ser 450	Glu	Arg	Ile	Asp	Val 455	Phe	Ser	Pro	Val	Glu 460	Phe	Asn	Lys	Val
Ser 465	Val	Leu	Thr	Gly	Ile 470	Ile	Lys	Ile	Ser	Leu 475	Lys	Thr	Leu	Ala	Gly 480
Ser	Val	Cys	Gly	Leu 485	Arg	Thr	Phe	Leu	Ala 490	Leu	Cys	Gly	Leu	Gln 495	Gln

Gly

<210> 532  
 <211> 153  
 <212> PRT  
 <213> homo sapiens

<400> 532

Cys 1	Gly	Ser	Gly	Trp 5	Ser	Trp	Pro	His	Trp 10	Pro	Ala	Thr	Arg	Pro 15	Gly
Gln	Gly	Pro	Pro 20	Ser	Gln	Pro	Arg	Glu 25	Val	Leu	Pro	Ala	Pro 30	Gly	Gly
Arg	Leu	Ser 35	Gly	Ser	Pro	Gly	Arg 40	Pro	Pro	Gly	Asp	Pro 45	Ala	Gly	Gly
Gly	Pro 50	Gly	Ala	Arg	Gly	Pro 55	Leu	Val	Pro	Arg	Ser 60	Pro	Trp	Gln	Arg
Leu 65	Arg	Ala	Arg	Gln	Arg 70	Pro	Ala	Gly	Pro	Arg 75	Glu	Pro	Ala	Ser	Ala 80
Gly	Gly	Ser	Gly	Pro 85	Ala	Pro	Ala	Pro	Ala 90	Val	Ser	Cys	His	His 95	His
Pro	Ala	Pro	Ala 100	Pro	Ala	Ala	Ala	Pro 105	Pro	Ala	Gln	Asn	Ser 110	Gly	Cys
Pro	Ala	Ala 115	Gly	Arg	Arg	Pro	Pro 120	Ala	Ser	Arg	His	Leu 125	Leu	Gly	Pro
Gly	Pro 130	Gln	Thr	Ala	Pro	Gly 135	Arg	Pro	Pro	Pro	Pro 140	Gly	Arg	Gly	Arg
Pro 145	Arg	Ser	His	Cys	Leu 150	His	Gly	Arg							

<210> 533  
 <211> 221  
 <212> PRT  
 <213> homo sapiens

<400> 533

Tyr 1	Asp	Gln	Ala	Leu 5	His	Leu	His	Val	Val 10	Gly	Gln	Gln	Pro	Pro 15	Arg
Arg	Phe	Pro	Gly 20	Leu	Cys	Thr	Gln	Arg 25	Ala	His	Gly	Arg	His 30	Trp	Glu
Leu	Ile	Leu 35	His	Gln	Lys	Leu	Phe 40	Ile	Ser	Glu	Ser	Glu 45	Asp	Val	Gly
Asp	Gly 50	Gly	Arg	Leu	Val	Val 55	Gln	Ala	Glu	Ala	Gly 60	Glu	Gln	Gln	Glu
Gln 65	Gly	Arg	Trp	Cys	Gly 70	Thr	Pro	Leu	Leu	Pro 75	Arg	Ala	Val	Ala	Glu 80
Ala	Leu	Ser	Arg	Leu 85	Ala	His	Arg	Val	Asp 90	Glu	Ala	His	Asp	Glu 95	Ala
Leu	Thr	Asp	Thr 100	Leu	Thr	Ala	Glu	Leu 105	Thr	Pro	Glu	Val	Gly 110	Leu	Val
Gly	Glu	Gly 115	His	Leu	Phe	Gly	Gly 120	Glu	Lys	Val	His	Cys 125	Cys	Gln	Arg
Gly	Leu 130	Asn	Val	Ala	Gln	Asp 135	Gly	Ala	Gly	His	Ile 140	Gly	Gln	Gln	Leu
Gly 145	Gln	Ala	Arg	Ala	Leu 150	Leu	Pro	Ser	His	Ala 155	Arg	Cys	Cys	Gln	Arg 160
Leu	Ala	Asp	Val	Cys 165	Gln	Ala	Ala	Gln	Glu 170	Gly	Arg	Pro	Glu	Thr 175	Leu
Gln	Val	Val	Ala 180	Gln	Ala	Leu	Ala	Gly 185	His	Ser	Phe	His	Asp 190	Leu	Arg
Gly	Ser	Val 195	Cys	Glu	Pro	Gly	Ser 200	Gly	Gln	Gln	Gly	Pro 205	Gly	Ser	Pro
Gln	Ala 210	Pro	Val	Glu	Ala	Val 215	Gln	Arg	Pro	His	Gln 220	Gln			

<210> 534

<211> 52

<212> PRT

<213> homo sapiens

<400> 534

Pro 1	Ser	Ile	Leu	Ile 5	Pro	Met	Thr	Pro	Gly 10	Gly	Phe	Phe	Ser	Val 15	Met
Val	Arg	Ala	Lys 20	Thr	Gly	Ser	Thr	His 25	Arg	Cys	Ser	Pro	Ala 30	Val	Tyr
Pro	Leu	Met 35	Arg	Arg	Ile	Pro	Cys 40	Trp	Arg	Ile	Leu	Ile 45	Gly	Arg	Gln
Glu	Thr 50	Thr	Gly												

<210> 535

1. *How many of you are going to the beach this summer?*  
 2. *How many of you are going to the beach this summer?*  
 3. *How many of you are going to the beach this summer?*  
 4. *How many of you are going to the beach this summer?*  
 5. *How many of you are going to the beach this summer?*  
 6. *How many of you are going to the beach this summer?*  
 7. *How many of you are going to the beach this summer?*  
 8. *How many of you are going to the beach this summer?*  
 9. *How many of you are going to the beach this summer?*  
 10. *How many of you are going to the beach this summer?*

[illegible][illegible]

Ser 1	Gly	Cys	Val	Pro 5	Ser	His	Glu	Glu	Asp 10	Ser	Met	Leu	Glu	Asp 15	Ser
His	Arg	Gln	Ala 20	Arg	Asn	His	Arg	Leu 25	Val	Ile	Ile	Arg	Asn 30	Pro	Val
Val	His	Leu 35	Gly	Gln	Ala	Pro	Leu 40	Ala	Thr	Pro	His	Arg 45	Pro	Gln	Ile
Arg	Ser 50	Leu	Thr	Ile	Gln	Ser 55									

[illegible]

<210> 538  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 538

Glu 1	Pro	Ala	Asp	Ser 5	Gln	Ala	Arg	Gly	Arg 10	Gln	Cys	Leu	Leu	Leu 15	Leu
His	Gln	Val	Gln 20	Gly	Ile	Trp	Leu	Lys 25	Ala	Cys	Ile	Phe	Pro 30	Gly	His
Lys	Leu	Pro 35	Glu	Pro	Leu	Lys	Trp 40	Glu	Ala	Arg	Gln	Phe 45	Gln	Thr	Asn
Leu	Phe 50	Ser	Thr	His	His	Ser 55	Thr	Phe	Lys	Val	Cys 60	Leu	Leu	Leu	Leu
Pro 65	Val	His	Pro	Pro	Ser 70	Leu	Gln	Phe	Phe	His 75	Ser	Leu	Thr	Ser	Glu 80
Arg	Val	Pro	Gly	Gly 85	Ser	Met	Val	Asn	Lys 90	Leu	Thr	Cys	Met	Leu 95	Gln
Lys	Lys	Lys	Lys	Lys 100											

<210> 539  
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 <212> PRT  
 <213> homo sapiens

<400> 539

Tyr 1	Ser	Leu	Cys	Ser 5	Gln	Cys	Val	Ser	Ala 10	Pro	Leu	Thr	Leu	Asn 15	Arg
His	Arg	Ser	Arg 20	Arg	Lys	Arg	Lys	Trp 25	Trp	Ile	Ala	Gln	Leu 30	Glu	Pro
Gly	Asp	Cys 35	Tyr	Asp	Cys	Leu	Asp 40	Leu	Cys	Gly	His	Arg 45	Ala	Ser	Gln
Pro 50	Pro	Gln	Thr	Leu	Ser	Leu 55	Glu	Cys	Gly	Gly	Thr 60	Gln	Cys	Arg	Phe
Pro 65	Gly	Gly	Leu	Ser	Pro 70	Arg	Pro	Ser	Pro	Cys 75	Pro	Pro	Ser	Ser	Ser 80
Gly	Leu	Leu	Phe	Tyr 85	Arg	Phe	Phe	Leu	Val 90	Ser	Phe	Leu	Gly	Leu 95	Leu
Phe	Thr	Glu	Gly 100	Thr	Ala	Ala	Leu	Gly 105	Phe	Leu	Val	Thr	Ser 110	Ala	Leu
Leu	Gly	Ser 115	Asp	Gly	Ser	Ala	Ser 120	Ala	Ser	Trp	Asp	Leu 125	Gly	Met	Gly
Thr	Met 130	Met	Ala	Ser	Thr	Gln 135	Met	Ser	Trp	Lys	Met 140	Ala	Pro	Arg	Lys

Ser 145	Pro	Tyr	Arg	Ser	Arg 150	Phe	Ser	Arg	Lys	Val 155	Gly	Ser	Gly	Thr	Ser 160
Gly	Gly	Glu	Lys	Ser 165	Arg	Ser	Glu	Ala	Met 170	Ala	Gln	Val	Ala	Cys 175	Cys
Leu	Thr	Ser	Leu 180	Leu	Thr	His	His	Ser 185	Leu	Glu	Pro	Thr	Pro 190	Ala	Pro
Pro	Arg	Arg 195	Ser	Pro	Arg										

<210> 540  
 <211> 147  
 <212> PRT  
 <213> homo sapiens

<400> 540

Lys 1	Lys	Asn	Ser	Ser 5	Ala	Leu	Ile	Phe	Leu 10	Glu	Glu	Ala	Ala	Asp 15	Phe
Gly	Cys	Gln	Ile 20	Ser	Leu	Arg	Asn	Gly 25	His	Phe	Leu	Arg	Cys 30	Phe	Phe
Leu	Thr	Glu 35	Ser	Val	Asp	Lys	Leu 40	Ile	Lys	Arg	Leu	Ser 45	His	Phe	Lys
Ile	Thr 50	Pro	Lys	Ser	Ser	Ser 55	Thr	Val	Phe	Phe	Phe 60	Phe	Ser	Phe	Cys
Phe 65	Lys	Ile	Thr	Asn	Gln 70	Val	Arg	Ser	Pro	Thr 75	Ser	Ser	Ser	Met	Asn 80
Ser	Phe	Val	Thr	Glu 85	Leu	Leu	Ser	Val	Cys 90	Ser	Pro	His	Cys	Ala 95	Leu
Asn	Thr	Val	Ser 100	Ala	Ala	Pro	Val	Cys 105	Pro	Leu	Phe	Arg	Lys 110	Glu	Ser
Ile	Phe	Asn 115	Thr	Phe	Thr	Ile	Cys 120	Thr	Pro	Trp	Asn	Leu 125	His	Met	Leu
Thr	Ser 130	Tyr	Tyr	Lys	Pro	Thr 135	His	Pro	Gln	Leu	Ser 140	Ser	Gly	Thr	Gly
His 145	Pro	Leu													

<210> 541  
 <211> 138  
 <212> PRT  
 <213> homo sapiens

<400> 541

Lys 1	Asn	Asp	Arg	Phe 5	Pro	Trp	Thr	Ser	Leu 10	Pro	Gly	Leu	Lys	Gly 15	Ala
Leu	Ile	Lys	Leu 20	Phe	Thr	Glu	His	Val 25	Ala	Glu	Lys	His	Ile 30	Tyr	Gly
Leu	Met	Pro	Leu	Leu	Leu	Glu	Ala	Gln	Ser	Thr	Pro	Phe	Gln	Val	Thr

35						40				45					
Pro	Ser	Thr	Met	Ala	Asn	Ile	Val	Lys	Gly	Leu	Tyr	Thr	Leu	Arg	Pro
	50					55					60				
Glu	Trp	Val	Gln	Met	Ala	Pro	Thr	Leu	Phe	Ser	Lys	Phe	Ile	Pro	Asn
65					70					75					80
Ile	Leu	Pro	Pro	Ala	Val	Glu	Ser	Glu	Leu	Ser	Glu	Tyr	Ala	Ala	Gln
				85					90					95	
Asp	Gln	Lys	Phe	Gln	Arg	Glu	Leu	Ile	Gln	Asn	Gly	Phe	Thr	Arg	Gly
			100					105					110		
Asp	Gln	Ser	Arg	Lys	Arg	Ala	Gly	Asp	Glu	Leu	Ala	Tyr	Asn	Ser	Ser
		115					120					125			
Ser	Ala	Cys	Ala	Ser	Ser	Arg	Gly	Tyr	Arg						
	130					135									

<210> 542

<211> 179

<212> PRT

<213> homo sapiens

<400> 542

Lys	Ala	Cys	Ile	Pro	Ser	Asp	Gln	Ser	Gly	Phe	Arg	Trp	Leu	Gln	Leu
1				5					10					15	
Tyr	Phe	Leu	Asn	Leu	Phe	Gln	Thr	Phe	Ser	Leu	Arg	Arg	Trp	Asn	Leu
			20					25					30		
Asn	Phe	Leu	Asn	Met	Leu	Leu	Lys	Ile	Arg	Asn	Phe	Lys	Glu	Asn	Leu
		35					40					45			
Tyr	Arg	Met	Val	Leu	Gln	Gly	Val	Thr	Ser	Pro	Gly	Arg	Glu	Leu	Gly
	50					55					60				
Met	Ser	Trp	Leu	Ile	Ile	Ala	Arg	Gln	His	Val	Gln	Val	Pro	Gly	Gly
65					70					75					80
Thr	Asp	Ser	Glu	Cys	Ile	Glu	Tyr	Ala	Phe	Leu	Pro	Glu	Lys	Arg	Thr
				85					90					95	
His	Trp	Ser	Cys	Arg	Asp	Cys	Ile	Gln	Ser	Thr	Val	Gly	Ala	Ala	His
			100					105					110		
Thr	Gln	Glu	Leu	Cys	His	Lys	Ala	Val	His	Gly	Arg	Gly	Cys	Trp	Thr
		115					120					125			
Ser	Tyr	Leu	Val	Cys	Asn	Phe	Lys	Thr	Lys	Thr	Lys	Lys	Lys	Lys	Asn
	130					135					140				
Ser	Ala	Ala	Arg	Leu	Gly	Gly	Asp	Phe	Glu	Met	Gly	Gln	Ser	Phe	Asn
145					150					155					160
Glu	Phe	Ile	Tyr	Arg	Phe	Cys	Glu	Glu	Lys	Ala	Ser	Gln	Lys	Val	Thr
				165					170					175	
Ile	Ser	Lys													

<210> 543



<211> 92  
 <212> PRT  
 <213> homo sapiens

<400> 543

Ile	Gln	Phe	Leu	Glu	Ala	Ala	Phe	Ala	Val	Phe	Leu	His	Cys	Met	Arg	
1				5					10					15		
Phe	Gly	Asn	Glu	Cys	Arg	Asn	Leu	Leu	Trp	Ala	Phe	Thr	Phe	Leu	Cys	
			20					25					30			
Gln	Phe	Gly	Phe	Tyr	Cys	Leu	Asn	Leu	Met	Leu	Thr	Trp	Arg	Gly	Asp	
		35					40					45				
Gly	Gly	Gln	Cys	Cys	Cys	Gly	Ala	Ser	Ser	Glu	Ser	Val	Cys	Gly	Glu	
	50					55					60					
Leu	Cys	Cys	Ala	Asp	Val	Ala	Val	Gly	Gly	Gln	Val	Arg	Gly	Ser	Ala	
65					70					75					80	
Pro	Ser	Trp	Lys	Lys	Ser	Cys	Leu	Arg	Val	Tyr	Val					
				85					90							

<210> 544  
 <211> 99  
 <212> PRT  
 <213> homo sapiens

<400> 544

Lys	Pro	Asn	Trp	His	Arg	Lys	Val	Asn	Ala	His	Ser	Lys	Phe	Leu	His	
1				5					10					15		
Ser	Phe	Pro	Asn	Arg	Ile	Gln	Cys	Lys	Lys	Thr	Ala	Lys	Ala	Ala	Ser	
			20					25					30			
Arg	Asn	Cys	Ile	Tyr	Trp	Pro	Leu	Pro	Glu	Gln	Gln	Ala	Ala	Met	Pro	
		35					40					45				
Ala	Pro	Trp	Pro	Pro	Glu	Leu	Asp	Ala	Cys	Cys	Ala	Asp	Val	Leu	Thr	
	50					55					60					
Leu	Met	Arg	Met	Leu	Gly	Tyr	Gly	Ser	Asp	Ser	Glu	Glu	Ile	His	Leu	
65					70					75					80	
Ser	Tyr	Ser	Ser	Leu	Glu	Arg	Ser	Ser	Cys	Val	Phe	Asn	Met	Lys	His	
				85					90					95		
Phe	Ile	Trp														

<210> 545  
 <211> 96  
 <212> PRT  
 <213> homo sapiens

<400> 545

Gln	Ser	Gln	Asn	Thr	Lys	Val	Phe	Val	Pro	Ile	Arg	Ile	Tyr	Thr	Asp	
1				5					10					15		
Pro	Leu	Thr	Lys	Val	Leu	Leu	Ile	Met	Gln	Phe	Ala	Ser	Ser	Pro	Ser	
			20					25					30			

Ser	Trp	Leu	Gly	Ser	Ser	Pro	Ile	Trp	His	Asp	His	Ile	Lys	Arg	Thr
		35					40					45			
Pro	Ser	Asp	Met	Ile	Ser	Ser	Lys	Lys	Val	Pro	Ser	Leu	Leu	Pro	Asp
	50					55					60				
His	Gln	Arg	Pro	His	Gln	His	Asn	Thr	Thr	Leu	Arg	Ile	Gln	Ile	His
65					70					75					80
Cys	Trp	Pro	His	Asn	Ser	Thr	Val	Pro	His	Leu	Leu	Ser	Arg	Ser	Ala
				85					90					95	

<210> 546  
 <211> 108  
 <212> PRT  
 <213> homo sapiens

<400> 546

Gly	Arg	Asp	Ala	Gly	Gln	Ser	Glu	Pro	Trp	Leu	Ser	Thr	Ser	Gly	Cys
1				5					10					15	
Cys	Ala	Trp	Gly	Gly	Cys	Ala	Pro	Gly	Ala	Arg	Gly	Cys	Trp	Gly	Pro
			20					25					30		
Gly	Pro	Pro	Ser	Leu	Gly	Val	Gly	Arg	Lys	Pro	Gly	Cys	Arg	Val	Ser
		35					40					45			
Ala	Ser	Ser	Val	Pro	Glu	Arg	Trp	Ile	Ala	Trp	Ser	Pro	Arg	Pro	Ser
	50					55					60				
Glu	Ala	Ser	Ala	Thr	Phe	Arg	Gly	Ala	Pro	Lys	Ser	Ile	Leu	Thr	Ala
65					70					75					80
Arg	Leu	Trp	Ala	Ser	Ala	Trp	Arg	Pro	Gln	His	Arg	Gly	Ser	Gln	Asn
				85					90					95	
Glu	Arg	Pro	Trp	Ser	Ser	Ser	Met	Lys	Thr	Ser	Gly				
			100					105							

<210> 547  
 <211> 117  
 <212> PRT  
 <213> homo sapiens

<400> 547

Pro	Gly	Arg	Arg	Ala	Lys	Arg	Ala	Met	Ala	Val	Tyr	Val	Gly	Met	Leu
1				5					10					15	
Arg	Leu	Gly	Arg	Leu	Cys	Ala	Gly	Ser	Ser	Gly	Val	Leu	Gly	Ala	Arg
			20					25					30		
Ala	Ala	Leu	Ser	Arg	Ser	Trp	Gln	Glu	Ala	Arg	Leu	Gln	Gly	Val	Arg
		35					40					45			
Phe	Leu	Ser	Ser	Arg	Glu	Val	Asp	Arg	Met	Val	Ser	Thr	Pro	Ile	Gly
	50					55					60				
Gly	Leu	Ser	Tyr	Val	Gln	Gly	Cys	Thr	Lys	Lys	His	Leu	Asn	Ser	Lys
65					70					75					80

Thr	Val	Gly	Gln	Cys 85	Leu	Glu	Thr	Thr	Ala 90	Gln	Arg	Val	Pro	Glu 95	Arg
Glu	Ala	Leu	Val 100	Val	Leu	His	Glu	Asp 105	Val	Arg	Leu	Thr	Phe 110	Ala	Gln
Leu	Lys	Glu 115	Glu	Trp											

<210> 548  
 <211> 117  
 <212> PRT  
 <213> homo sapiens

<400> 548

Pro 1	Leu	Leu	Leu	Glu 5	Leu	Gly	Lys	Gly	Gln 10	Pro	Asp	Val	Phe	Met 15	Glu
Asp	Asp	Gln	Gly 20	Leu	Ser	Phe	Trp	Asp 25	Pro	Leu	Cys	Cys	Gly 30	Leu	Gln
Ala	Leu	Ala 35	His	Ser	Leu	Ala	Val 40	Lys	Met	Leu	Phe	Gly 45	Ala	Pro	Leu
Asn 50	Val	Ala	Glu	Ala	Ser	Asp 55	Gly	Arg	Gly	Asp	His 60	Ala	Ile	His	Leu
Ser 65	Gly	Thr	Glu	Glu	Ala 70	Asp	Thr	Leu	Gln	Pro 75	Gly	Phe	Leu	Pro	Thr 80
Pro	Arg	Glu	Gly	Gly 85	Pro	Gly	Pro	Gln	His 90	Pro	Arg	Ala	Pro	Gly 95	Ala
Gln	Pro	Pro	Gln 100	Ala	Gln	His	Pro	Asp 105	Val	Asp	Ser	His	Gly 110	Ser	Leu
Cys	Pro	Ala 115	Ser	Arg											

<210> 549  
 <211> 68  
 <212> PRT  
 <213> homo sapiens

<400> 549

Arg 1	Leu	Ser	Gly	Pro 5	Ala	Ala	Asn	Pro	Arg 10	Gly	Ala	Ala	Gly	Trp 15	Arg
Ala	Ala	Gly	Ala 20	Gln	Glu	Leu	Gly	Met 25	Ser	Tyr	Lys	Pro	Met 30	Arg	Pro
Trp	Leu	Pro 35	Ser	Ser	Thr	Pro	Trp 40	Ser	Ala	Arg	His	Pro 45	Leu	Gly	Pro
Gly	Ala 50	Pro	Arg	Phe	Pro	Asp 55	Arg	Glu	Ala	Cys	Ala 60	Cys	Ala	Val	Arg
Gly 65	Cys	Ser	Val												

<210> 550

<211> 68  
<212> PRT  
<213> homo sapiens

<400> 550

Gly 1	His	Cys	Ser	Pro 5	Ala	Arg	Arg	Thr	Arg 10	Thr	Pro	Pro	Cys	Gln 15	Gly
Thr	Gly	Val	Pro 20	Arg	Ala	Pro	Gly	Gly 25	Ala	Trp	Gln	Thr	Arg 30	Gly	Cys
Cys	Trp	Ala 35	Ala	Arg	Gly	Ala	Trp 40	Val	Cys	Arg	Thr	Ser 45	Pro	Thr	Pro
Gly	Arg 50	Gln	Arg	His	Ala	Ser 55	Arg	Pro	Leu	Leu	Gly 60	Gly	Trp	Leu	Arg
Gly 65	Arg	Ser	Ala												

<210> 551  
<211> 68  
<212> PRT  
<213> homo sapiens

<400> 551

Asp 1	Thr	Ala	Ala	Pro 5	His	Gly	Ala	Arg	Ala 10	Arg	Leu	Pro	Val	Arg 15	Glu
Pro	Gly	Cys	Pro 20	Gly	Pro	Gln	Gly	Val 25	Pro	Gly	Arg	Pro	Gly 30	Gly	Ala
Ala	Gly	Gln 35	Pro	Gly	Ala	His	Gly 40	Phe	Val	Gly	His	Pro 45	Gln	Leu	Leu
Gly	Ala 50	Ser	Gly	Thr	Pro	Ala 55	Gly	Arg	Ser	Ser	Gly 60	Val	Gly	Cys	Gly
Ala 65	Ala	Gln	Pro												

<210> 552  
<211> 32  
<212> PRT  
<213> homo sapiens

<400> 552

Ser 1	Pro	Ile	Ser	Ile 5	Thr	Glu	Thr	Gln	Gln 10	Phe	Ser	Asn	Asn	Leu 15	Ile
His	Thr	Ile	Thr 20	Cys	Leu	Leu	Arg	Met 25	Ala	Leu	Tyr	Leu	Phe 30	Ser	Leu

<210> 553  
<211> 33  
<212> PRT  
<213> homo sapiens

<400> 553

Ile	Thr	Leu	Gln	Pro	Ile	Ser	Gln	Asn	Met	Phe	Leu	Leu	Leu	Asn	Asn
1				5					10					15	
Thr	Gln	Leu	Phe	Tyr	Leu	Cys	Val	Leu	Phe	Met	Pro	Asp	His	Gln	Tyr
			20					25					30		

Gln

<210> 554  
 <211> 43  
 <212> PRT  
 <213> homo sapiens

<400> 554

Ser	Phe	Tyr	Phe	Gly	Trp	Ser	His	Tyr	Asn	Glu	Asn	Lys	Tyr	Asn	Ala
1				5					10					15	
Ile	Leu	Asn	Arg	Gln	Val	Met	Val	Cys	Ile	Lys	Leu	Leu	Leu	Asn	Cys
			20					25					30		
Cys	Val	Ser	Val	Ile	Asp	Ile	Gly	Asp	Gln	Ala					
		35					40								

<210> 555  
 <211> 85  
 <212> PRT  
 <213> homo sapiens

<400> 555

Cys	Phe	Thr	His	Trp	Asn	Val	Phe	Pro	Arg	Leu	Trp	Met	Thr	Ser	Phe
1				5					10					15	
Leu	Met	Glu	Arg	Val	Gln	Glu	Gly	Trp	Lys	Thr	Pro	Gly	Phe	Lys	Leu
			20					25					30		
Ser	Ile	Pro	His	Met	Gly	Phe	Ser	Ile	Ile	Phe	Arg	Pro	Glu	Ala	Ala
		35					40					45			
Arg	Pro	Glu	Val	Arg	Leu	His	Leu	Ser	Ala	Leu	Phe	Val	Leu	Leu	Leu
	50					55					60				
Ala	Thr	Leu	Gly	Phe	Leu	Leu	Gly	Thr	Met	Cys	Gly	Cys	Gly	Met	Cys
65					70					75					80
Glu	Gln	Lys	Gly	Gly											
				85											

<210> 556  
 <211> 106  
 <212> PRT  
 <213> homo sapiens

<400> 556

Phe	Asn	Asp	Gly	Lys	Thr	Trp	Gln	Leu	Lys	Lys	Thr	Leu	Val	Thr	Asn
1				5					10					15	
Gly	Gly	Phe	Leu	Leu	Phe	Phe	Pro	His	Pro	Pro	Phe	Cys	Ser	His	Met
			20					25					30		
Pro	Gln	Pro	His	Met	Val	Pro	Ser	Arg	Asn	Pro	Lys	Val	Ala	Arg	Ser

		35					40					45				
Ser	Thr	Lys	Arg	Ala	Asp	Lys	Cys	Arg	Arg	Thr	Ser	Gly	Arg	Ala	Ala	
	50					55					60					
Ser	Gly	Leu	Lys	Met	Ile	Glu	Lys	Pro	Met	Trp	Gly	Met	Leu	Ser	Leu	
65					70					75					80	
Asn	Pro	Gly	Val	Phe	His	Pro	Ser	Trp	Thr	Leu	Ser	Ile	Arg	Lys	Glu	
				85					90					95		
Val	Ile	His	Asn	Arg	Gly	Lys	Thr	Phe	Gln							
			100					105								

<210> 557  
 <211> 109  
 <212> PRT  
 <213> homo sapiens

<400> 557

Asn	Ile	Asn	Tyr	Ile	Glu	Ile	Ile	Phe	Leu	Phe	Leu	Leu	Leu	Ile	Ser	
1				5					10					15		
Pro	Leu	Gly	Pro	His	Arg	Leu	Ser	Pro	Ala	Gln	Leu	Ala	Gln	Leu	Ala	
			20					25					30			
Gln	Leu	Ala	His	Ser	Pro	Gln	Val	Ser	Arg	Arg	His	Arg	Ala	Leu	Thr	
		35					40					45				
Met	Val	Gly	Trp	His	Gly	Val	Ser	Asn	Val	Ala	Asn	Ser	Ser	His	His	
	50					55					60					
Pro	His	Pro	His	Ser	Pro	Ser	Gln	Arg	Pro	Leu	Val	Val	Gly	Pro	Ala	
65					70					75					80	
Val	Phe	Gln	Lys	Gly	Leu	Thr	Cys	Thr	Asn	Leu	Arg	Gln	Thr	Tyr	Ala	
				85					90					95		
Pro	Phe	Ser	Val	Ser	Leu	Ala	Ser	Pro	Ser	Trp	Glu	Asp				
			100					105								

<210> 558  
 <211> 50  
 <212> PRT  
 <213> homo sapiens

<400> 558

Leu	Gly	Ile	Phe	Val	Ala	Tyr	Arg	Asn	Gln	Leu	Gly	Val	Pro	Ser	Leu	
1				5					10					15		
Met	Arg	Cys	Ser	Trp	Lys	Ala	Ile	Tyr	Ala	Arg	Gly	Gly	Phe	Thr	Phe	
			20					25					30			
Val	Ala	Pro	Pro	Phe	Ile	Asp	Pro	Ser	Ala	Phe	Lys	Lys	Leu	Glu	Cys	
		35					40					45				
Glu	Asn															
	50															

<210> 559  
 <211> 44

<212> PRT  
<213> homo sapiens

<400> 559

Phe	Arg	Leu	Pro	Phe	Leu	Thr	Trp	His	Phe	Cys	Ser	Leu	Gln	Glu	Pro
1				5					10					15	
Ala	Trp	Cys	Thr	Phe	Ser	Tyr	Glu	Met	Gln	Leu	Glu	Ser	His	Leu	Cys
			20					25					30		
Lys	Arg	Trp	Phe	His	Phe	Cys	Arg	Ser	Ser	Ile	His				
		35					40								

<210> 560  
<211> 45  
<212> PRT  
<213> homo sapiens

<400> 560

Arg	Val	Asn	Glu	Trp	Arg	Ser	Asp	Lys	Ser	Glu	Thr	Thr	Ser	Cys	Ile
1				5					10					15	
Asn	Gly	Phe	Pro	Ala	Ala	Ser	His	Lys	Arg	Arg	Tyr	Thr	Lys	Leu	Val
			20					25					30		
Pro	Val	Ser	Tyr	Lys	Asn	Ala	Lys	Leu	Arg	Met	Gly	Val			
		35					40					45			

<210> 561  
<211> 34  
<212> PRT  
<213> homo sapiens

<400> 561

Met	Arg	Ser	Arg	Leu	Pro	Cys	Glu	Gly	Leu	Val	Ala	Arg	His	Pro	Arg
1				5					10					15	
Glu	Leu	Arg	Val	Pro	Ser	Val	Arg	Phe	Trp	Ile	Asp	Trp	Pro	Trp	Val
			20					25					30		
Leu	Thr														

<210> 562  
<211> 67  
<212> PRT  
<213> homo sapiens

<400> 562

Val	Ser	Thr	His	Gly	Gln	Ser	Ile	Gln	Lys	Arg	Thr	Glu	Gly	Thr	Arg
1				5					10					15	
Ser	Ser	Arg	Gly	Cys	Arg	Ala	Thr	Ser	Pro	Ser	His	Gly	Asn	Arg	Leu
			20					25					30		
Leu	Ile	Gln	Glu	Ser	Phe	Pro	Gln	Asn	Pro	Pro	Arg	Ala	Arg	Phe	Gln
		35					40					45			
Gly	His	Pro	Leu	Gly	Arg	Gln	Ser	Arg	Gln	Gln	Pro	Phe	Thr	Glu	Ala
	50					55					60				

Met Ser Gln  
65

<210> 563  
<211> 50  
<212> PRT  
<213> homo sapiens

<400> 563

Ala	Pro	Met	Ala	Ser	Gln	Ser	Arg	Ser	Ala	Leu	Arg	Ala	Arg	Val	Ala
1				5					10					15	
His	Ala	Gly	Ala	Val	Pro	Pro	Ala	Leu	His	Thr	Ala	Ile	Asp	Ser	Ser
			20					25					30		
Phe	Arg	Asn	His	Phe	Leu	Lys	Thr	His	Gln	Gly	Leu	Gly	Ser	Lys	Gly
		35					40					45			
Thr	Arg														
	50														

<210> 564  
<211> 54  
<212> PRT  
<213> homo sapiens

<400> 564

Tyr	Ser	Ile	Ile	Phe	Glu	Gln	Phe	Phe	Lys	Cys	Lys	Ser	Val	Ser	Tyr
1				5					10					15	
Ser	Glu	Cys	Val	Ser	Glu	Val	Ile	Lys	Asp	Ile	Ser	Gln	Arg	Tyr	Trp
			20					25					30		
Pro	Ile	Ser	Leu	Cys	Asn	Gln	Arg	Asn	Ser	Val	Ser	Arg	Leu	Leu	Leu
		35					40					45			
Cys	Val	Ile	Cys	Gly	Ser										
	50														

<210> 565  
<211> 57  
<212> PRT  
<213> homo sapiens

<400> 565

Cys	Thr	Met	Val	Asn	Val	Asp	Asn	Thr	Val	Ser	Phe	Leu	Ser	Ser	Phe
1				5					10					15	
Leu	Asn	Val	Asn	Leu	Tyr	Leu	Thr	Gln	Ser	Val	Cys	Leu	Lys	Leu	Leu
			20					25					30		
Arg	Thr	Phe	Pro	Asn	Val	Thr	Gly	Pro	Phe	Pro	Phe	Val	Ile	Arg	Gly
		35					40					45			
Ile	Leu	Phe	Gln	Asp	Tyr	Cys	Cys	Val							
	50					55									

<210> 566  
<211> 49



<212> PRT  
<213> homo sapiens

<400> 566

Glu 1	Lys	Cys	Gln	Pro 5	His	Ser	Leu	Ile	Leu 10	Leu	Trp	Pro	Phe	Asn 15	Phe
Ile	Leu	Ile	Lys 20	Ser	His	Arg	Ser	His 25	Thr	Thr	Ile	Ile	Leu 30	Lys	Gln
Asn	Ser	Ser 35	Asp	Tyr	Lys	Gly	Lys 40	Trp	Ala	Ser	Asn	Val 45	Gly	Lys	Cys
Pro															

<210> 567  
<211> 94  
<212> PRT  
<213> homo sapiens

<400> 567

Gly 1	Glu	Gly	Arg	Val 5	Trp	Asn	Pro	Glu	Gly 10	Ser	Lys	Ser	Arg	His 15	Trp
Pro	Asp	His	Pro 20	Ala	Pro	Trp	Ala	Pro 25	Ser	Pro	Arg	Gln	Glu 30	Gln	Leu
Phe	Ser	Ile 35	Pro	Ser	Gln	Thr	Ser 40	Ser	Ile	Phe	Ile	Thr 45	Met	Thr	Phe
Arg	Glu 50	Val	Ser	Gln	Ala	Ser 55	Ser	Arg	Cys	Pro	Thr 60	Ile	Pro	Ser	Gly
Gly 65	Lys	Arg	Gln	Glu	Asn 70	Ser	Pro	Arg	Val	Pro 75	Val	Met	Leu	Leu	Ser 80
Pro	Ser	Gln	Phe	Arg 85	Leu	Ser	Arg	Thr	Ser 90	Tyr	Leu	Gln	Pro		

<210> 568  
<211> 89  
<212> PRT  
<213> homo sapiens

<400> 568

Gly 1	Leu	Thr	Leu	Lys 5	Lys	Gly	Thr	Phe	Pro 10	Arg	Gly	Pro	Glu	Ile 15	Gln
Ala	Asp	Pro	Asn 20	Leu	Thr	Pro	Cys	Ser 25	Arg	Thr	Gln	Ala	His 30	Arg	Pro
Leu	Asn	Ser 35	Asn	Pro	Thr	Ser	Pro 40	Pro	Pro	Pro	Pro	Thr 45	Pro	Asp	Phe
Leu 50	Ile	Ser	Trp	Asn	Ala	Phe 55	Gln	Asp	Trp	Lys	Ser 60	Pro	Gln	Gly	Ser
Ser 65	Glu	Pro	Ile	Leu	Ser 70	Pro	Ala	Arg	Ile	Ser 75	Ser	Met	His	Pro	Gly 80

His Ala Phe His Ile Ser Arg Asn Lys  
85

<210> 569  
<211> 89  
<212> PRT  
<213> homo sapiens

<400> 569

Asp 1	Val	Leu	Asp	Ser 5	Leu	Asn	Trp	Asp	Gly 10	Glu	Ser	Ser	Met	Thr 15	Gly
Thr	Arg	Gly	Glu 20	Phe	Ser	Cys	Leu	Phe 25	Pro	Pro	Glu	Gly	Ile 30	Val	Gly
His	Leu	Glu 35	Leu	Ala	Trp	Glu	Thr 40	Ser	Leu	Lys	Val	Ile 45	Val	Ile	Lys
Ile	Glu 50	Leu	Val	Trp	Glu	Gly 55	Met	Glu	Asn	Ser	Cys 60	Ser	Cys	Leu	Gly
Leu 65	Gly	Ala	Gln	Gly	Ala 70	Gly	Trp	Ser	Gly	Gln 75	Cys	Leu	Asp	Leu	Leu 80
Pro	Ser	Gly	Phe	His 85	Thr	Arg	Pro	Ser							

<210> 570  
<211> 73  
<212> PRT  
<213> homo sapiens

<400> 570

Lys 1	Ser	Ile	Ala	His 5	Ser	Val	Ile	Gly	Tyr 10	Phe	His	Asp	Phe	Lys 15	Trp
Phe	Tyr	Glu	Glu 20	Thr	Glu	Ser	Ser	Asp 25	Asp	Val	Glu	Val	Leu 30	Thr	Leu
Lys	Lys	Phe 35	Lys	Gly	Asp	Leu	Ala 40	Tyr	Arg	Arg	Gln	Glu 45	Tyr	Gln	Val
Glu	Phe 50	Asn	Ile	Trp	Cys	Leu 55	Lys	Trp	Ala	Leu	Val 60	Leu	Ser	Val	Met
Ala 65	Tyr	Val	Asn	Asn	Ser 70	Val	Pro	Ser							

<210> 571  
<211> 40  
<212> PRT  
<213> homo sapiens

<400> 571

Ser 1	Ala	Asp	Ser	Gln 5	Glu	Ile	Gln	Arg	Arg 10	Pro	Gly	Leu	Gln	Thr 15	Thr
Arg	Val	Ser	Gly 20	Arg	Ile	Gln	His	Met 25	Val	Leu	Glu	Val	Gly 30	Ser	Cys

Phe	Ile	Ser	Tyr	Gly	Ile	Cys	Lys
		35					40

<210> 572  
 <211> 60  
 <212> PRT  
 <213> homo sapiens

<400> 572

Asn	Lys	Ser	Pro	Leu	Gln	Ala	Pro	Tyr	Val	Glu	Phe	Tyr	Leu	Ile	Leu
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Leu	Ser	Ser	Val	Gly	Gln	Val	Ser	Phe	Glu	Phe	Leu	Glu	Ser	Gln	His
			20					25					30		
Phe	Asn	Ile	Ile	Thr	Ala	Phe	Cys	Phe	Phe	Ile	Lys	Pro	Leu	Glu	Ile
		35					40					45			
Met	Lys	Ile	Ala	Tyr	Tyr	Arg	Val	Ser	Tyr	Ala	Phe				
	50					55					60				

<210> 573  
 <211> 318  
 <212> PRT  
 <213> homo sapiens

<400> 573

Gly	Asn	Leu	Ser	Leu	Glu	Ser	Leu	Cys	Asn	Leu	Tyr	Asn	Trp	Arg	Tyr
1				5					10					15	
Lys	Asn	Leu	Gly	Asn	Leu	Pro	His	Val	Gln	Leu	Leu	Pro	Glu	Phe	Ser
			20					25					30		
Thr	Ala	Asn	Ala	Gly	Leu	Leu	Tyr	Asp	Phe	Gln	Leu	Ile	Asn	Val	Glu
		35					40					45			
Asp	Phe	Gln	Gly	Val	Gly	Glu	Ser	Glu	Pro	Asn	Pro	Tyr	Phe	Tyr	Gln
	50					55					60				
Asn	Leu	Gly	Glu	Ala	Glu	Tyr	Val	Val	Ala	Leu	Phe	Met	Tyr	Met	Cys
65					70					75					80
Leu	Leu	Gly	Tyr	Pro	Ala	Asp	Lys	Ile	Ser	Ile	Leu	Thr	Thr	Tyr	Asn
				85					90					95	
Gly	Gln	Lys	His	Leu	Ile	Arg	Asp	Ile	Ile	Asn	Arg	Arg	Cys	Gly	Asn
			100					105					110		
Asn	Pro	Leu	Ile	Gly	Arg	Pro	Asn	Lys	Val	Thr	Thr	Val	Asp	Arg	Phe
		115					120					125			
Gln	Gly	Gln	Gln	Asn	Asp	Tyr	Ile	Leu	Leu	Ser	Leu	Val	Arg	Thr	Arg
	130					135					140				
Ala	Val	Gly	His	Leu	Arg	Asp	Val	Arg	Arg	Leu	Val	Val	Ala	Met	Ser
145					150					155					160
Arg	Ala	Arg	Leu	Gly	Leu	Tyr	Ile	Phe	Ala	Arg	Val	Ser	Leu	Phe	Gln
				165					170					175	
Asn	Cys	Phe	Glu	Leu	Thr	Pro	Ala	Phe	Ser	Gln	Leu	Thr	Ala	Arg	Pro

			180					185					190			
Leu	His	Leu	His	Ile	Ile	Pro	Thr	Glu	Pro	Phe	Pro	Thr	Thr	Arg	Lys	
		195					200					205				
Asn	Gly	Glu	Arg	Pro	Ser	His	Glu	Val	Gln	Ile	Ile	Lys	Asn	Met	Pro	
	210					215					220					
Gln	Met	Ala	Asn	Phe	Val	Tyr	Asn	Met	Tyr	Met	His	Leu	Ile	Gln	Thr	
225					230					235					240	
Thr	His	His	Tyr	His	Gln	Thr	Leu	Leu	Gln	Leu	Pro	Pro	Ala	Met	Val	
				245					250					255		
Glu	Glu	Gly	Glu	Glu	Val	Gln	Asn	Gln	Glu	Thr	Glu	Leu	Glu	Thr	Glu	
			260					265					270			
Glu	Glu	Ala	Met	Thr	Val	Gln	Ala	Asp	Ile	Ile	Pro	Ser	Pro	Thr	Asp	
		275					280					285				
Thr	Ser	Cys	Arg	Gln	Glu	Thr	Pro	Ala	Phe	Glu	Arg	Glu	Ser	Arg	Pro	
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Gly	Gly	Glu	Gly	Ala	Ile	Ala	Leu	Gly	Gly	Leu	Gly	Cys	Phe			
305					310					315						

<210> 574  
 <211> 67  
 <212> PRT  
 <213> homo sapiens

<400> 574

Lys	Thr	Pro	Lys	Pro	Pro	Gln	Arg	Asn	Cys	Pro	Phe	Pro	Thr	Gly	Ala	
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Ala	Leu	Thr	Leu	Lys	Gly	Trp	Ser	Phe	Leu	Thr	Ala	Ala	Gly	Val	Cys	
			20					25					30			
Trp	Thr	Gly	Tyr	Asp	Val	Ser	Leu	Asn	Ser	His	Gly	Leu	Phe	Phe	Cys	
		35					40					45				
Phe	Gln	Leu	Cys	Phe	Leu	Ile	Leu	Asn	Phe	Leu	Thr	Leu	Phe	Tyr	His	
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Ser	Arg	Trp														
65																

<210> 575  
 <211> 155  
 <212> PRT  
 <213> homo sapiens

<400> 575

Ser	Leu	Met	Ile	Met	Met	Cys	Ser	Leu	Tyr	Gln	Met	His	Val	His	Val	
1				5					10					15		
Val	Tyr	Lys	Val	Cys	His	Leu	Gly	His	Ile	Phe	Tyr	Tyr	Leu	Tyr	Phe	
			20					25					30			
Met	Arg	Trp	Ser	Leu	Ser	Ile	Leu	Ser	Ser	Ser	Trp	Glu	Arg	Phe	Cys	
		35					40					45				

Trp	Asn	Tyr	Met	Gln	Met	Lys	Gly	Ala	Ser	Cys	Glu	Leu	Thr	Glu	Ser
	50					55					60				
Trp	Ser	Gln	Phe	Lys	Thr	Val	Leu	Glu	Glu	Gly	Tyr	Ser	Gly	Glu	Asp
65					70					75					80
Ile	Lys	Ser	Lys	Ser	Gly	Ser	Arg	His	Gly	His	Tyr	Gln	Ala	Thr	Asp
				85					90					95	
Ile	Pro	Gln	Met	Ala	His	Cys	Pro	Gly	Ser	Tyr	Gln	Arg	Lys	Lys	Asn
			100					105					110		
Ile	Val	Ile	Leu	Leu	Thr	Leu	Lys	Ser	Ile	Asn	Ser	Cys	His	Leu	Val
		115					120					125			
Trp	Ser	Ser	Asn	Gln	Trp	Ile	Val	Ser	Thr	Ser	Ser	Ile	Asp	Asp	Val
	130					135					140				
Ala	Asn	Lys	Met	Leu	Leu	Ala	Ile	Ile	Cys	Cys					
145					150					155					

<210> 576  
 <211> 57  
 <212> PRT  
 <213> homo sapiens

<400> 576

Asp	His	Leu	Gly	Phe	Ile	Ser	Thr	Lys	Met	Arg	Thr	Asn	His	Gly	Val
1				5					10					15	
Arg	Lys	Gly	Ser	Leu	Glu	Glu	His	Lys	Asn	Leu	Lys	Ala	Leu	Gly	Gly
			20					25					30		
Tyr	His	Tyr	Tyr	Ile	Ser	Tyr	Phe	His	Arg	Ser	Asp	Leu	Ala	Lys	Leu
		35					40					45			
Cys	Ile	Leu	Ser	Leu	Leu	Thr	Phe	Ile							
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<210> 577  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 577

Phe	Lys	Phe	Phe	Leu	Met	Thr	Ile	Phe	Leu	Gln	Asn	Phe	Glu	Arg	Lys
1				5					10					15	
Met	Cys	Ser	Phe	Cys	Cys	Ile	Leu	Cys	Lys	Lys	Thr	Ala	Asn	Arg	Gly
			20					25					30		
Lys	Arg	Thr	Leu	Gln	Ile	Lys	Thr	Ile	Leu	Val	Ser	Phe	Pro	Gln	Arg
		35					40					45			

<210> 578  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 578

Leu 1	Tyr	Phe	Phe	Lys 5	Thr	Leu	Lys	Glu	Lys 10	Cys	Val	Leu	Phe	Ala 15	Ala
Ser	Phe	Val	Arg 20	Arg	Leu	Pro	Thr	Glu 25	Glu	Lys	Gly	Leu	Tyr 30	Lys	Leu
Arg	Pro	Ser 35	Trp	Phe	His	Phe	His 40	Lys	Asp	Glu	Asn	Lys 45	Ser	Trp	Cys

<210> 579  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 579

Gly 1	Ser	Phe	Pro	Asn 5	Thr	Met	Ile	Cys	Ser 10	His	Leu	Cys	Gly	Asn 15	Glu
Thr	Lys	Met	Val 20	Leu	Ile	Cys	Lys	Val 25	Leu	Phe	Pro	Leu	Leu 30	Ala	Val
Phe	Leu	Gln 35	Arg	Met	Gln	Gln	Lys 40	Glu	His	Ile	Phe	Leu 45	Ser	Lys	Phe

<210> 580  
 <211> 48  
 <212> PRT  
 <213> homo sapiens

<400> 580

His 1	Cys	Arg	Ile	Leu 5	Gln	Gly	Leu	Ser	Pro 10	Leu	Val	Gly	Arg	Glu 15	Lys
Thr	Thr	Gln	Val 20	Met	Arg	Asn	Phe	Tyr 25	Ser	Phe	Gln	Glu	Leu 30	Glu	Glu
Gln	Leu	Leu 35	Ile	Lys	Phe	His	Ala 40	Leu	Val	Thr	Lys	Tyr 45	Phe	Tyr	Ser

<210> 581  
 <211> 59  
 <212> PRT  
 <213> homo sapiens

<400> 581

Ile 1	Met	Pro	Arg	Ala 5	Pro	Leu	Tyr	Arg	Ile 10	Pro	Leu	Asn	Cys	Asn 15	Tyr
Val	Leu	Leu	Lys 20	Ser	Gln	Leu	Val	Lys 25	Glu	Glu	Leu	Met	Val 30	Ser	Val
Phe	Val	Gly 35	Asn	Thr	Cys	Asn	Thr 40	Ala	Glu	Phe	Tyr	Lys 45	Gly	Phe	Leu
Leu	Trp 50	Trp	Ala	Gly	Lys	Lys 55	Pro	Leu	Lys	Ser					

<210> 582  
 <211> 44

<212> PRT  
<213> homo sapiens

<400> 582

Gly	Thr	Leu	Arg	Pro	Arg	Ser	Ser	Asp	Val	Leu	Pro	Ile	Tyr	Leu	Cys
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Phe	Thr	Thr	Cys	Leu	Leu	Ser	Leu	Thr	Pro	Asn	Ile	Phe	Thr	Tyr	Phe
			20					25					30		
Ser	Asn	Ser	Ala	Cys	His	Lys	Phe	Ala	Ala	Ser	Pro				
		35					40								

<210> 583

<211> 46

<212> PRT

<213> homo sapiens

<400> 583

Asn	Val	Asp	Ser	Cys	Gln	Thr	His	Ser	Leu	Ala	Leu	Ile	Pro	Pro	Leu
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Leu	Ser	Ser	Ser	Asp	Ile	Val	Asn	Asn	Asp	Lys	Gln	Leu	Leu	Cys	Thr
			20					25					30		
Glu	Cys	Phe	Phe	Met	Cys	Cys	Ser	His	Phe	Ile	His	Met	Tyr		
		35					40					45			

<210> 584

<211> 41

<212> PRT

<213> homo sapiens

<400> 584

Leu	Tyr	Met	Cys	Ile	Lys	Cys	Glu	Gln	His	Ile	Lys	Lys	His	Ser	Val
1				5					10					15	
His	Ser	Ser	Cys	Leu	Ser	Leu	Leu	Thr	Ile	Ser	Leu	Leu	Glu	Arg	Arg
			20					25					30		
Gly	Gly	Ile	Arg	Ala	Arg	Leu	Cys	Val							
		35					40								

<210> 585

<400> 585

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<210> 586

<400> 586

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<210> 587

<400> 587

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<210> 588

<211> 112

<212> PRT

<213> homo sapiens

<400> 588

Gly 1	Lys	Pro	Leu	Val 5	Leu	His	Ala	Thr	Pro 10	Leu	Ser	Arg	Cys	Pro 15	Leu
Pro	Leu	His 20	Pro	Thr	Arg	Ser	Leu	Ile 25	Leu	Arg	Pro	Ser	Leu 30	His	Leu
Ser	Asp	Pro 35	Ser	Phe	His	His	Tyr 40	Leu	Gln	Arg	Cys	Ser 45	Tyr	Tyr	Ala
Pro	Val 50	Tyr	Arg	Gly	Cys	Pro 55	Thr	Met	Thr	Val	Pro 60	Ser	Gln	Ser	Asn
Tyr 65	Ser	Ser	Gly	Pro	Lys 70	Val	Trp	Leu	Ser	Arg 75	Ala	Pro	Leu	Pro	Arg 80
Arg	Gly	Arg	Pro	Phe 85	Gln	Ala	Leu	Pro	Gly 90	Trp	Asn	Trp	Cys	Arg 95	Arg
Ser	Leu	Gly	Cys 100	Ile	Val	Arg	Pro	Gly 105	Val	Gly	Val	Ala	Ser 110	Leu	Leu

<210> 589

<211> 76

<212> PRT

<213> homo sapiens

<400> 589

Gly 1	Arg	Ser	Arg	Glu 5	Ala	Pro	Ala	Gly	Trp 10	Pro	Lys	Ser	Thr	Lys 15	Pro
Pro	Ser	Ala	Arg 20	Glu	Asn	Pro	Trp	Phe 25	Ser	Met	Pro	His	Leu 30	Ser	Pro
Gly	Ala	Leu 35	Cys	Leu	Phe	Thr	Pro 40	Gln	Glu	Ala	Leu	Ser 45	Tyr	Val	Leu
Leu	Ser 50	Ile	Tyr	Arg	Thr	Pro 55	Val	Ser	Ile	Thr	Ile 60	Ser	Arg	Asp	Val
Ala 65	Ile	Met	Arg	Pro	Ser 70	Thr	Gly	Gly	Ala	Arg 75	Arg				

<210> 590

<211> 97

<212> PRT

<213> homo sapiens

<400> 590

Ala 1	Gly	Leu	Asp	Gln 5	Lys	Glu	Glu	Leu	Arg 10	Gly	Val	Arg	Gln	His 15	Gln
His	Gln	Gly	Val 20	Arg	Tyr	Thr	Arg	Gly 25	Ser	Ser	Asp	Thr	Ser 30	Ser	Ser
Pro	Glu	Gly 35	Leu	Gly	Met	Ala	Cys 40	His	Ala	Gly	Ala	Met 45	Glu	Arg	Val
Lys	Ala 50	Lys	Pro	Trp	Asp	Pro 55	Lys	Ser	Asn	Leu	Thr 60	Ala	Lys	Ala	Pro





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<210> 594  
 <211> 41  
 <212> PRT  
 <213> homo sapiens

<400> 594

Ser	Gly	Asp	Val	Cys	Thr	Glu	Ser	His	Cys	Gly	Leu	Ser	Arg	Val	Lys
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Glu	Lys	Glu	Gln	Gln	Glu	Leu	Ser	Leu	Gly	Arg	Trp	Arg	Arg	Gly	Gly
			20					25					30		
Ile	Asp	Gln	Ala	Arg	Pro	Trp	Pro	Trp							
		35					40								

<210> 595  
 <211> 47  
 <212> PRT  
 <213> homo sapiens

<400> 595

Phe	Lys	Val	Gly	Leu	Trp	Lys	Gly	Asp	Ile	Val	Glu	Gly	Glu	Arg	Ala
1				5					10					15	
Val	Leu	Tyr	Thr	Tyr	Lys	Trp	Tyr	Thr	Pro	Phe	Ile	His	Gly	Gly	Gln
			20					25					30		
Arg	Ser	Ser	Asp	Gln	Val	Thr	Tyr	Val	Gln	Lys	Val	Thr	Val	Ala	
		35					40					45			

<210> 596  
 <211> 44  
 <212> PRT  
 <213> homo sapiens

<400> 596

Ser	Val	Leu	Thr	Thr	Ser	Gln	Arg	Leu	Ser	Ser	His	Phe	Lys	Ser	Gln
1				5					10					15	
Ile	Pro	Thr	Arg	Ala	Lys	Val	Leu	Leu	Asp	Leu	Phe	His	Pro	Phe	Ser
			20					25					30		
Thr	Ser	Leu	Ser	Ser	Thr	Leu	Ala	Ala	Pro	Ser	Pro				
		35					40								

<210> 597  
 <211> 1651  
 <212> DNA  
 <213> homo sapiens

<400> 597

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<212> DNA

<213> homo sapiens

<400> 598

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<212> DNA

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<212> DNA

<213> homo sapiens

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<211> 1322

<212> DNA

<213> homo sapiens

<400> 613

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<212> DNA

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<212> DNA

<213> homo sapiens

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<210> 616

<211> 2278

<212> DNA

<213> homo sapiens

<400> 616

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<210> 617

<211> 931

<212> DNA

<213> homo sapiens

<400> 617

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931

<210> 618

<211> 447

<212> PRT

<213> homo sapiens

<400> 618

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			20					25					30		



Thr	Asn	Tyr	Pro	Val	Glu	Cys	Thr	Glu	Gly	Ser	Ala	Gly	Pro	Gln	Ser
		35					40					45			
Leu	Pro	Leu	Pro	Ile	Leu	Glu	Pro	Val	Lys	Asn	Pro	Cys	Ser	Val	Lys
	50					55					60				
Asp	Gln	Thr	Pro	Leu	Gln	Leu	Ser	Val	Glu	Asp	Thr	Thr	Ser	Pro	Asn
65					70					75					80
Thr	Lys	Pro	Cys	Pro	Pro	Thr	Pro	Thr	Thr	Pro	Glu	Thr	Trp	Gly	Gly
				85					90					95	
Gly	Gly	Gly	Gly	Ala	Pro	Ser	Ser	Thr	Pro	Cys	Ser	Ala	His	Leu	Thr
			100					105					110		
Pro	Ser	Ser	Leu	Phe	Pro	Ser	Ser	Leu	Glu	Ser	Ser	Ser	Glu	Gln	Lys
		115					120					125			
Phe	Tyr	Asn	Phe	Val	Ile	Leu	His	Ala	Arg	Ala	Asp	Glu	His	Ile	Ala
	130					135					140				
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Thr	Phe	Cys	Glu	Asp	Phe	Gln	Val	Pro	Gly	Arg	Gly	Glu	Leu	Ser	Cys
				165					170					175	
Leu	Gln	Asp	Ala	Ile	Asp	His	Ser	Ala	Phe	Ile	Ile	Leu	Leu	Leu	Thr
			180					185					190		
Ser	Asn	Phe	Asp	Cys	Arg	Leu	Ser	Leu	His	Gln	Val	Asn	Gln	Ala	Met
		195					200					205			
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	210					215					220				
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225					230					235					240
Leu	Leu	Ser	Gly	Leu	Val	Arg	Leu	Asp	Glu	His	Ser	Gln	Ile	Phe	Ala
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Ala	Met	Trp	Arg	Lys	Glu	Gln	Asp	Thr	Arg	Ala	Leu	Arg	Glu	Gln	Ser
		275					280					285			
Gln	His	Leu	Asp	Gly	Glu	Arg	Met	Gln	Ala	Ala	Ala	Leu	Asn	Ala	Ala
	290					295					300				
Tyr	Ser	Ala	Tyr	Leu	Gln	Ser	Tyr	Leu	Ser	Tyr	Gln	Ala	Gln	Met	Glu
305					310					315					320
Gln	Leu	Gln	Val	Ala	Phe	Gly	Ser	His	Met	Ser	Phe	Gly	Thr	Gly	Ala
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Pro	Tyr	Gly	Val	Arg	Met	Pro	Phe	Gly	Gly	Gln	Gly	Pro	Leu	Gly	Ala
			340					345					350		
Pro	Pro	Pro	Phe	Pro	Thr	Trp	Pro	Gly	Cys	Pro	Gln	Pro	Pro	Pro	Leu
		355					360					365			

His	Ala	Trp	Gln	Ala	Gly	Thr	Pro	Pro	Pro	Pro	Ser	Pro	Gln	Pro	Ala
	370					375					380				
Ala	Phe	Pro	Gln	Ser	Leu	Pro	Phe	Pro	Gln	Ser	Pro	Ala	Phe	Pro	Thr
385					390					395					400
Ala	Ser	Pro	Ala	Pro	Pro	Gln	Ser	Pro	Gly	Leu	Gln	Pro	Leu	Ile	Ile
				405					410					415	
His	His	Ala	Gln	Met	Val	Gln	Leu	Gly	Leu	Asn	Asn	His	Met	Trp	Asn
			420					425					430		
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<210> 619

<211> 205

<212> PRT

<213> homo sapiens

<400> 619

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Glu	Leu	Leu	Val	Leu	Pro	Gly	Thr	Asp	Gly	Ala	Ala	Pro	Gly	Gly	Phe
			20					25					30		
Trp	Glu	Pro	His	Val	Ile	Trp	Asp	Trp	Gly	Ala	Leu	Trp	Gly	Gln	Asn
		35					40					45			
Ala	Leu	Trp	Gly	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Ala	Thr	Leu	Ser	His
	50					55					60				
Leu	Ala	Gly	Val	Pro	Ala	Ala	Ala	Thr	Pro	Ala	Arg	Met	Ala	Gly	Trp
65					70					75					80
His	Pro	Pro	Thr	Ala	Leu	Pro	Thr	Ala	Ser	Ser	Leu	Ser	Thr	Val	Thr
				85					90					95	
Ala	Leu	Pro	Ala	Val	Pro	Ser	Leu	Pro	Tyr	Gly	Leu	Thr	Arg	Thr	Pro
			100					105					110		
Ser	Glu	Pro	Arg	Ala	Ala	Thr	Pro	His	Tyr	Pro	Pro	Arg	Thr	Asp	Gly
		115					120					125			
Thr	Ala	Gly	Ala	Glu	Gln	Pro	His	Val	Glu	Pro	Glu	Arg	Val	Pro	Gly
	130					135					140				
Ala	Arg	Gly	Gln	Asp	Ala	Gly	Gly	Arg	Met	Thr	Ala	Cys	Pro	Cys	Leu
145					150					155					160
Thr	Thr	Trp	Gly	Thr	Pro	Leu	Asp	Pro	Gly	Ile	Gly	Gln	Asp	Pro	Ile
				165					170					175	
Glu	His	Pro	Gly	Leu	Pro	Cys	Ala	Leu	Trp	Thr	Val	Glu	Asp	Glu	Val
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<210> 620

<211> 409  
 <212> PRT  
 <213> homo sapiens

<400> 620

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Pro	Glu	Trp	Asn 20	Glu	Ser	Met	His	Ser 25	Leu	Arg	Ile	Ser	Val 30	Gly	Gly
Leu	Pro	Val 35	Leu	Ala	Ser	Met	Thr 40	Lys	Ala	Ala	Asp	Pro 45	Arg	Phe	Arg
Pro	Arg 50	Trp	Lys	Val	Ile	Leu 55	Thr	Phe	Phe	Val	Gly 60	Ala	Ala	Ile	Leu
Trp 65	Leu	Leu	Cys	Ser	His 70	Arg	Pro	Ala	Pro	Gly 75	Arg	Pro	Pro	Thr	His 80
Asn	Ala	His	Asn	Trp 85	Arg	Leu	Gly	Gln	Ala 90	Pro	Ala	Asn	Trp	Tyr 95	Asn
Asp	Thr	Tyr	Pro 100	Leu	Ser	Pro	Pro	Gln 105	Arg	Thr	Pro	Ala	Gly 110	Ile	Arg
Tyr	Arg	Ile 115	Ala	Val	Ile	Ala	Asp 120	Leu	Asp	Thr	Glu	Pro 125	Thr	Ala	Gln
Asp	Glu 130	Asn	Thr	Trp	Arg	Ser 135	Asp	Leu	Lys	Lys	Gly 140	Tyr	Leu	Thr	Leu
Ser 145	Asp	Ser	Gly	Asp	Lys 150	Val	Ala	Val	Glu	Trp 155	Asp	Lys	Asp	His	Gly 160
Val	Leu	Glu	Ser	His 165	Leu	Ala	Glu	Lys	Gly 170	Arg	Gly	Met	Glu	Leu 175	Ser
Asp	Leu	Ile	Val 180	Phe	Asn	Gly	Lys	Leu 185	Tyr	Ser	Val	Asp	Asp 190	Arg	Thr
Gly	Val	Val 195	Tyr	Gln	Ile	Glu	Gly 200	Ser	Lys	Ala	Val	Pro 205	Trp	Val	Ile
Leu	Ser 210	Asp	Gly	Asp	Gly	Thr 215	Val	Glu	Lys	Gly	Phe 220	Lys	Ala	Glu	Trp
Leu 225	Ala	Val	Lys	Asp	Glu 230	Arg	Leu	Tyr	Val	Gly 235	Gly	Leu	Gly	Lys	Glu 240
Trp	Thr	Thr	Thr	Thr 245	Gly	Asp	Val	Val	Asn 250	Glu	Asn	Pro	Glu	Trp 255	Val
Lys	Val	Val	Gly 260	Tyr	Lys	Gly	Ser	Val 265	Asp	His	Glu	Asn	Trp 270	Val	Ser
Asn	Tyr	Asn 275	Ala	Leu	Arg	Ala	Ala 280	Ala	Gly	Ile	Gln	Pro 285	Pro	Ala	Asn
Leu	Ile 290	His	Glu	Ser	Ala	Cys 295	Trp	Ser	Asp	Thr	Leu 300	Gln	Arg	Trp	Phe

Phe 305	Leu	Pro	Arg	Arg	Ala 310	Ser	Gln	Glu	Arg	Tyr 315	Ser	Glu	Lys	Asp	Asp 320
Glu	Arg	Lys	Gly	Ala 325	Asn	Leu	Leu	Leu	Ser 330	Ala	Ser	Pro	Asp	Phe 335	Gly
Asp	Ile	Ala	Val 340	Ser	His	Val	Gly	Ala 345	Val	Val	Pro	Thr	His 350	Gly	Phe
Ser	Ser	Phe 355	Lys	Phe	Ile	Pro	Asn 360	Thr	Asp	Asp	Gln	Ile 365	Ile	Val	Ala
Leu	Lys 370	Ser	Glu	Glu	Asp	Ser 375	Gly	Arg	Val	Ala	Ser 380	Tyr	Ile	Met	Ala
Phe 385	Thr	Leu	Asp	Gly	Arg 390	Phe	Leu	Leu	Pro	Glu 395	Thr	Lys	Ile	Gly	Ser 400
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<210> 621

<211> 249

<212> PRT

<213> homo sapiens

<400> 621

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Glu	Leu	Asp	Ala 20	Phe	Val	Phe	His	Ala 25	Ser	Asp	Leu	Gly	Leu 30	Arg	Gln
Gln	Glu	Ala 35	Pro	Val	Gln	Arg	Glu 40	Gly	His	Asp	Val	Gly 45	Gly	Asp	Ser
Ala 50	Ala	Val	Leu	Leu	Gly	Phe 55	Glu	Gly	His	Asn	Asp 60	Leu	Val	Val	Gly
Val 65	Gly	Asp	Glu	Leu	Glu 70	Gly	Arg	Glu	Ala	Val 75	Ser	Gly	Asp	His	Arg 80
Pro	Asp	Val	Ala	His 85	Ser	Asp	Val	Ala	Glu 90	Val	Arg	Gly	Gly	Ala 95	Gln
Gln	Gln	Val	Gly 100	Ala	Leu	Ala	Leu	Val 105	Val	Leu	Leu	Ala	Val 110	Ala	Leu
Leu	Ala	Gly 115	Ala	Ala	Arg	Gln	Glu 120	Glu	Pro	Ala	Leu	Gln 125	Arg	Val	Thr
Pro	Ala 130	Gly	Arg	Leu	Met	Asp 135	Glu	Val	Ser	Trp	Arg 140	Leu	Asp	Ala	Gly
Ser 145	Ser	Pro	Gln	Gly	Val 150	Val	Val	Gly	His	Pro 155	Val	Leu	Val	Val	His 160
Ala	Ala	Leu	Val	Ala 165	His	His	Leu	His	Pro 170	Leu	Arg	Val	Leu	Val 175	His
His	Ile	Thr	Arg 180	Ser	Gly	Arg	Pro	Leu 185	Leu	Ala	Gln	Ala	Ala 190	His	Val

Gln	Thr	Leu	Val	Leu	His	Cys	Gln	Pro	Phe	Gly	Leu	Glu	Ala	Phe	Leu
		195					200					205			
His	Gly	Ala	Val	Ala	Val	Gly	Gln	Asn	His	Pro	Gly	His	Gly	Phe	Ala
	210					215					220				
Ala	Phe	Asp	Leu	Val	Asp	Asp	Pro	Arg	Pro	Val	Ile	His	Gly	Val	Glu
225					230					235					240
Phe	Pro	Ile	Glu	Asn	Asn	Gln	Val	Gly							
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<210> 622

<211> 255

<212> PRT

<213> homo sapiens

<400> 622

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			20					25					30		
Gly	Gln	Glu	Val	Val	Pro	Ala	Glu	Pro	Gly	Val	Pro	Ala	Pro	Gln	His
		35					40					45			
Ala	Glu	Pro	Val	Ala	Ala	Ala	Gly	Ala	Ala	Gln	Gln	Leu	Gln	Thr	Glu
	50					55					60				
Glu	Gln	Pro	Gly	Leu	Gln	Arg	Leu	Arg	Leu	Gly	Pro	Val	Arg	Gly	Ala
65					70					75					80
Ala	Arg	Gly	Gly	Asp	Ala	Arg	Val	Arg	Gly	Pro	Arg	Gly	Asp	Arg	Arg
				85					90					95	
Val	Asn	Pro	Glu	Ser	Ala	Arg	Ala	Leu	Leu	Pro	Gly	Asp	Pro	Gln	Gly
			100					105					110		
Pro	Gly	Thr	Ala	Ala	Pro	Arg	Ala	Leu	Gly	Leu	Pro	Pro	Arg	Cys	Glu
		115					120					125			
Pro	Val	Gly	Ala	Pro	Leu	Ala	Ala	Leu	Ala	Leu	Ala	Arg	Glu	Arg	Arg
	130					135					140				
Glu	Arg	Gly	Arg	Phe	Pro	Arg	Pro	Cys	Lys	Cys	Leu	Phe	Phe	Asn	Ser
145					150					155					160
Ser	Gln	Cys	Glu	Leu	Cys	Cys	Glu	Cys	Val	Arg	Gly	Gly	Ala	Pro	Ala
				165					170					175	
Leu	Ser	Arg	Arg	Arg	Val	Ala	Thr	Pro	Cys	Pro	Cys	Pro	Met	Val	Cys
			180					185					190		
Asn	Ser	Asp	Phe	Ala	His	Arg	Ser	Thr	Val	Pro	Pro	Ser	Ala	His	Pro
		195					200					205			
Phe	Thr	Leu	Thr	Pro	Thr	Leu	Ser	Leu	Asn	Thr	Phe	Ile	Ile	Val	Arg
	210					215					220				
Arg	Gly	Arg	Trp	Asp	Phe	Gly	Arg	Ser	Ala	Ala	Ala	Thr	Ala	Ser	Gly

225					230					235					240
Gly	Leu	Ile	Phe	Ile	Phe	Ala	Leu	Arg	Trp	Leu	Lys	Ala	Phe	Ile	
				245					250					255	

<210> 623  
 <211> 196  
 <212> PRT  
 <213> homo sapiens

<400> 623

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			20					25					30		
Thr	Ile	Ile	Lys	Val	Phe	Ser	Glu	Ser	Val	Gly	Val	Ser	Val	Asn	Gly
		35					40					45			
Cys	Ala	Leu	Gly	Gly	Thr	Val	Glu	Arg	Cys	Ala	Lys	Ser	Glu	Leu	Gln
	50					55					60				
Thr	Ile	Gly	Gln	Gly	His	Gly	Val	Ala	Thr	Arg	Arg	Arg	Leu	Ser	Ala
65					70					75					80
Gly	Ala	Pro	Pro	Arg	Thr	His	Ser	Gln	Gln	Ser	Ser	His	Trp	Glu	Glu
				85					90					95	
Leu	Lys	Asn	Lys	His	Leu	Gln	Gly	Arg	Gly	Lys	Arg	Pro	Arg	Ser	Arg
			100					105					110		
Arg	Ser	Arg	Ala	Arg	Ala	Ser	Ala	Ala	Arg	Gly	Ala	Pro	Thr	Gly	Ser
		115					120					125			
Gln	Arg	Gly	Gly	Ser	Pro	Ser	Ala	Arg	Gly	Ala	Ala	Val	Pro	Gly	Pro
	130					135					140				
Cys	Gly	Ser	Pro	Gly	Ser	Arg	Ala	Arg	Ala	Leu	Ser	Gly	Phe	Thr	Arg
145					150					155					160
Arg	Ser	Pro	Arg	Gly	Pro	Arg	Thr	Arg	Ala	Ser	Pro	Pro	Arg	Ala	Ala
				165					170					175	
Pro	Leu	Thr	Gly	Pro	Ser	Arg	Ser	Arg	Trp	Ser	Pro	Gly	Cys	Ser	Ser
			180					185					190		
Val	Cys	Ser	Cys												
		195													

<210> 624  
 <211> 242  
 <212> PRT  
 <213> homo sapiens

<400> 624

Val	Glu	Ser	His	Arg	Arg	Ala	His	Thr	His	Thr	Thr	Val	Arg	Ser	Pro
1				5					10					15	
Glu	Thr	Ala	Arg	Gly	Trp	Lys	Pro	Trp	Pro	His	Arg	Leu	Ser	Arg	Tyr
			20					25					30		

Val	His	Ser	Pro	Gly	Arg	Gln	Pro	His	Gly	His	Gly	Gln	His	Leu	Cys
		35					40					45			
Phe	Cys	Ser	Gly	Arg	Arg	Ala	Phe	Gly	Gly	His	Pro	Arg	Gln	Gly	Ala
	50					55					60				
Arg	Ala	Ser	Leu	Leu	Ala	Leu	Gly	Leu	Glu	Asn	Ser	Pro	Gly	Gly	Ser
	65				70					75					80
Ser	Pro	Glu	Glu	Arg	Leu	Gly	Arg	Leu	Ala	Val	Ala	Gly	Pro	Pro	Arg
				85					90					95	
Gly	Ala	Gln	Asn	Val	Ser	Gln	Ala	Gly	Pro	Glu	Ala	Glu	Ala	Pro	Pro
			100					105					110		
Leu	Arg	Phe	Gly	His	Ala	Trp	Gly	Ala	Gln	Thr	Pro	Arg	Leu	Gly	Ala
		115					120					125			
Pro	Gly	Pro	Trp	Thr	Pro	Leu	Pro	Thr	Leu	Pro	Ser	His	Ile	Pro	Pro
	130					135					140				
Phe	Trp	Ser	Gln	Thr	Pro	Ala	Gln	Arg	Lys	Glu	Gly	Phe	Thr	Glu	Glu
	145				150					155					160
Gly	Gln	Gly	Arg	Ala	Trp	Pro	Gln	Gly	Gly	Asp	Glu	Asp	Ile	Ser	Gly
				165					170					175	
Pro	Gly	Ser	Cys	Arg	Leu	Leu	Trp	Glu	Glu	Glu	Pro	Cys	Val	Cys	Lys
			180					185					190		
Leu	Leu	Gly	Leu	Ala	Ala	Arg	Pro	Thr	Ala	Gly	Pro	Ser	Leu	Asp	Pro
		195					200					205			
Cys	Thr	Trp	Pro	Ser	Ser	Cys	Pro	Leu	Ala	Ala	Pro	Gly	Leu	Gly	Thr
	210					215					220				
Gly	Ile	Glu	Pro	Arg	Gly	Leu	Gly	Trp	Leu	Gly	Gln	Gly	Arg	Asp	Arg
	225				230					235					240

Glu Gly

<210> 625

<211> 216

<212> PRT

<213> homo sapiens

<400> 625

Gly	Leu	Val	Met	Pro	Gly	Glu	Leu	Arg	Arg	Pro	Gly	Leu	Gly	Pro	Gln
1				5					10					15	
Ala	His	Gly	Leu	Pro	Ser	Pro	Leu	Cys	Pro	Pro	Ile	Phe	Pro	Leu	Phe
			20					25					30		
Gly	Pro	Arg	His	Gln	His	Lys	Glu	Arg	Arg	Gly	Ser	Gln	Arg	Lys	Ala
		35					40					45			
Arg	Ala	Glu	Pro	Gly	Pro	Arg	Glu	Gly	Met	Arg	Thr	Phe	Pro	Val	Gln
	50					55					60				
Val	Ala	Ala	Gly	Cys	Ser	Gly	Arg	Lys	Ser	His	Ala	Ser	Val	Asn	Cys
	65				70					75					80

Trp	Gly	Trp	Arg	Pro 85	Ala	Pro	Leu	Gln	Gly 90	Pro	Ala	Leu	Thr	Pro 95	Ala	
Arg	Gly	His	Pro 100	Ala	Ala	Leu	Trp	Leu 105	Pro	Leu	Ala	Leu	Ala 110	Gln	Ala	
Ser	Ser	Leu 115	Glu	Gly	Trp	Ala	Gly 120	Trp	Ala	Arg	Ala	Gly 125	Thr	Gly	Arg	
Gly	Ser 130	Thr	Ser	Asp	Pro	Asp 135	Val	Gly	Trp	Leu	Cys 140	Pro	Pro	Arg	Arg	
Glu 145	Ala	Gln	Gln	Thr	Ser 150	Tyr	Thr	Lys	Ala	Lys 155	Ser	Thr	Ile	Gly	Glu 160	
Pro	Arg	Ser	His	Phe 165	Met	Gly	Arg	Arg	Pro 170	Arg	Pro	Gln	Gly	Pro 175	Gln	
Ser	Lys	Ala	Arg 180	Gly	Arg	Phe	Ile	Pro 185	Glu	Asp	Ser	Pro	Pro 190	Gly	Ala	
Ala	Pro	Ala 195	Trp	Gly	Gly	Val	Ser 200	Arg	Pro	Leu	Gly	Cys 205	Leu	Ser	Val	
Cys	Gly 210	Thr	Pro	Trp	Ser	Thr 215	Pro									

<210> 626

<211> 299

<212> PRT

<213> homo sapiens

<400> 626

Pro 1	Gly	Ile	Ser	Val 5	Ser	Val	Asp	Lys	Met 10	Glu	Ser	Ser	Pro	Phe 15	Asn	
Arg	Arg	Gln	Trp 20	Thr	Ser	Leu	Ser	Leu 25	Arg	Val	Thr	Ala	Lys 30	Glu	Leu	
Ser	Leu	Val 35	Asn	Lys	Asn	Lys	Ser 40	Ser	Ala	Ile	Val	Glu 45	Ile	Phe	Ser	
Lys	Tyr 50	Gln	Lys	Ala	Ala	Glu 55	Glu	Thr	Asn	Met	Glu 60	Lys	Lys	Arg	Ser	
Asn 65	Thr	Glu	Asn	Leu	Ser 70	Gln	His	Phe	Arg	Lys 75	Gly	Thr	Leu	Thr	Val 80	
Leu	Lys	Lys	Lys	Trp 85	Glu	Asn	Pro	Gly	Leu 90	Gly	Ala	Glu	Ser	His 95	Thr	
Asp	Ser	Leu	Arg 100	Asn	Ser	Ser	Thr	Glu 105	Ile	Arg	His	Arg	Ala 110	Asp	His	
Pro	Pro	Ala 115	Glu	Val	Thr	Ser	His 120	Ala	Ala	Ser	Gly	Ala 125	Lys	Ala	Asp	
Gln	Glu 130	Glu	Gln	Ile	His	Pro 135	Arg	Ser	Arg	Leu	Arg 140	Ser	Pro	Pro	Glu	
Ala	Leu	Val	Gln	Gly	Arg	Tyr	Pro	His	Ile	Lys	Asp	Gly	Glu	Asp	Leu	



145					150					155					160
Lys	Asp	His	Ser	Thr	Glu	Ser	Lys	Lys	Met	Glu	Asn	Cys	Leu	Gly	Glu
				165					170					175	
Ser	Arg	His	Glu	Val	Glu	Lys	Ser	Glu	Ile	Ser	Glu	Asn	Thr	Asp	Ala
			180					185					190		
Ser	Gly	Lys	Ile	Glu	Lys	Tyr	Asn	Val	Pro	Leu	Asn	Arg	Leu	Lys	Met
		195					200					205			
Met	Phe	Glu	Lys	Gly	Glu	Pro	Thr	Gln	Thr	Lys	Ile	Leu	Arg	Ala	Gln
	210					215					220				
Ser	Arg	Ser	Ala	Ser	Gly	Arg	Lys	Ile	Ser	Glu	Asn	Ser	Tyr	Ser	Leu
225					230					235					240
Asp	Asp	Leu	Glu	Ile	Gly	Pro	Gly	Gln	Leu	Ser	Ser	Ser	Thr	Phe	Asp
				245					250					255	
Ser	Glu	Lys	Asn	Glu	Ser	Arg	Arg	Asn	Leu	Glu	Leu	Pro	Arg	Leu	Ser
			260					265					270		
Glu	Thr	Ser	Ile	Lys	Asp	Arg	Met	Ala	Lys	Tyr	Gln	Ala	Ala	Val	Ser
		275					280					285			
Lys	Gln	Ser	Ser	Ser	Pro	Thr	Ile	Pro	Met	Ser					
	290					295									

<210> 627  
 <211> 94  
 <212> PRT  
 <213> homo sapiens

<400> 627

Asp	Ser	Ala	Pro	Ser	Pro	Gly	Phe	Ser	His	Phe	Phe	Phe	Asn	Thr	Val
1				5					10					15	
Arg	Val	Pro	Phe	Leu	Lys	Cys	Trp	Glu	Arg	Phe	Ser	Val	Leu	Leu	Leu
			20					25					30		
Phe	Phe	Ser	Met	Phe	Val	Ser	Ser	Ala	Ala	Phe	Trp	Tyr	Leu	Glu	Asn
		35					40					45			
Ile	Ser	Thr	Ile	Ala	Asp	Asp	Leu	Phe	Leu	Leu	Thr	Arg	Glu	Ser	Ser
	50					55					60				
Leu	Ala	Val	Thr	Leu	Asn	Asp	Ser	Glu	Val	His	Cys	Arg	Leu	Leu	Asn
65					70					75					80
Gly	Asp	Asp	Ser	Ile	Leu	Ser	Thr	Asp	Thr	Glu	Ile	Pro	Gly		
				85					90						

<210> 628  
 <211> 765  
 <212> PRT  
 <213> homo sapiens

<400> 628

Ile	Arg	Pro	Val	Val	Gln	Leu	Thr	Ala	Ile	Glu	Ile	Leu	Ala	Trp	Gly
1				5					10					15	

Leu	Arg	Asn	Met	Lys	Asn	Phe	Gln	Met	Ala	Ser	Ile	Thr	Ser	Pro	Ser
			20					25					30		
Leu	Val	Val	Glu	Cys	Gly	Gly	Glu	Arg	Val	Glu	Ser	Val	Val	Ile	Lys
		35					40					45			
Asn	Leu	Lys	Lys	Thr	Pro	Asn	Phe	Pro	Ser	Ser	Val	Leu	Phe	Met	Lys
	50					55					60				
Val	Phe	Leu	Pro	Lys	Glu	Glu	Leu	Tyr	Met	Pro	Pro	Leu	Val	Ile	Lys
					70					75					80
Val	Ile	Asp	His	Arg	Gln	Phe	Gly	Arg	Lys	Pro	Val	Val	Gly	Gln	Cys
				85					90					95	
Thr	Ile	Glu	Arg	Leu	Asp	Arg	Phe	Arg	Cys	Asp	Pro	Tyr	Ala	Gly	Lys
			100					105					110		
Glu	Asp	Ile	Val	Pro	Gln	Leu	Lys	Ala	Ser	Leu	Leu	Ser	Ala	Pro	Pro
		115					120					125			
Cys	Arg	Asp	Ile	Val	Ile	Glu	Met	Glu	Asp	Thr	Lys	Pro	Leu	Leu	Ala
	130					135					140				
Ser	Lys	Leu	Thr	Glu	Lys	Glu	Glu	Glu	Ile	Val	Asp	Trp	Trp	Ser	Lys
	145				150					155					160
Phe	Asp	Ala	Ser	Ser	Gly	Glu	His	Glu	Lys	Cys	Gly	Gln	Tyr	Ile	Gln
				165					170					175	
Lys	Gly	Tyr	Ser	Lys	Leu	Lys	Ile	Tyr	Asn	Cys	Glu	Leu	Glu	Asn	Val
			180					185					190		
Ala	Glu	Phe	Glu	Gly	Leu	Thr	Asp	Phe	Ser	Asp	Thr	Phe	Lys	Leu	Tyr
		195					200					205			
Arg	Gly	Lys	Ser	Asp	Glu	Asn	Glu	Asp	Pro	Ser	Val	Val	Gly	Glu	Phe
	210					215					220				
Lys	Gly	Ser	Phe	Arg	Ile	Tyr	Pro	Leu	Pro	Asp	Asp	Pro	Ser	Val	Pro
	225				230					235					240
Ala	Pro	Pro	Arg	Gln	Phe	Arg	Glu	Leu	Pro	Asp	Ser	Val	Pro	Gln	Glu
				245					250					255	
Cys	Thr	Val	Arg	Ile	Tyr	Ile	Val	Arg	Gly	Leu	Glu	Leu	Gln	Pro	Gln
			260					265					270		
Asp	Asn	Asn	Gly	Leu	Cys	Asp	Pro	Tyr	Ile	Lys	Ile	Thr	Leu	Gly	Lys
		275					280					285			
Lys	Val	Ile	Glu	Asp	Arg	Asp	His	Tyr	Ile	Pro	Asn	Thr	Leu	Asn	Pro
	290					295					300				
Val	Phe	Gly	Arg	Met	Tyr	Glu	Leu	Ser	Cys	Tyr	Leu	Pro	Gln	Glu	Lys
	305				310					315					320
Asp	Leu	Lys	Ile	Ser	Val	Tyr	Asp	Tyr	Asp	Thr	Phe	Thr	Arg	Asp	Glu
				325					330					335	
Lys	Val	Gly	Glu	Thr	Ile	Ile	Asp	Leu	Glu	Asn	Arg	Phe	Leu	Ser	Arg
			340					345					350		

Phe	Gly	Ser 355	His	Cys	Gly	Ile	Pro 360	Glu	Glu	Tyr	Cys	Val 365	Ser	Gly	Val
Asn	Thr 370	Trp	Arg	Asp	Gln	Leu 375	Arg	Pro	Thr	Gln	Leu 380	Leu	Gln	Asn	Val
Ala 385	Arg	Phe	Lys	Gly	Phe 390	Pro	Gln	Pro	Ile	Leu 395	Ser	Glu	Asp	Gly	Ser 400
Arg	Ile	Arg	Tyr	Gly 405	Gly	Arg	Asp	Tyr	Ser 410	Leu	Asp	Glu	Phe	Glu 415	Ala
Asn	Lys	Ile	Leu 420	His	Gln	His	Leu	Gly 425	Ala	Pro	Glu	Glu	Arg 430	Leu	Ala
Leu	His	Ile 435	Leu	Arg	Thr	Gln	Gly 440	Leu	Val	Pro	Glu	His 445	Val	Glu	Thr
Arg	Thr 450	Leu	His	Ser	Thr	Phe 455	Gln	Pro	Asn	Ile	Ser 460	Gln	Gly	Lys	Leu
Gln 465	Met	Trp	Val	Asp	Val 470	Phe	Pro	Lys	Ser	Leu 475	Gly	Pro	Pro	Gly	Pro 480
Pro	Phe	Asn	Ile	Thr 485	Pro	Arg	Lys	Ala	Lys 490	Lys	Tyr	Tyr	Leu	Arg 495	Val
Ile	Ile	Trp	Asn 500	Thr	Lys	Asp	Val	Ile 505	Leu	Asp	Glu	Lys	Ser 510	Ile	Thr
Gly	Glu	Glu 515	Met	Ser	Asp	Ile	Tyr 520	Val	Lys	Gly	Trp	Ile 525	Pro	Gly	Asn
Glu	Glu 530	Asn	Lys	Gln	Lys	Thr 535	Asp	Val	His	Tyr	Arg 540	Ser	Leu	Asp	Gly
Glu 545	Gly	Asn	Phe	Asn	Trp 550	Arg	Phe	Val	Phe	Pro 555	Phe	Asp	Tyr	Leu	Pro 560
Ala	Glu	Gln	Leu	Cys 565	Ile	Val	Ala	Lys	Lys 570	Glu	His	Phe	Trp	Ser 575	Ile
Asp	Gln	Thr	Glu 580	Phe	Arg	Ile	Pro	Pro 585	Arg	Leu	Ile	Ile	Gln 590	Ile	Trp
Asp	Asn	Asp 595	Lys	Phe	Ser	Leu	Asp 600	Asp	Tyr	Leu	Gly	Phe 605	Leu	Glu	Leu
Asp	Leu 610	Arg	His	Thr	Ile	Ile 615	Pro	Ala	Lys	Ser	Pro 620	Glu	Lys	Cys	Arg
Leu 625	Asp	Met	Ile	Pro	Asp 630	Leu	Lys	Ala	Met	Asn 635	Pro	Leu	Lys	Ala	Lys 640
Thr	Ala	Ser	Leu	Phe 645	Glu	Gln	Lys	Ser	Met 650	Lys	Gly	Trp	Trp	Pro 655	Cys
Tyr	Ala	Glu	Lys 660	Asp	Gly	Ala	Arg	Val 665	Met	Ala	Gly	Lys	Val 670	Glu	Met
Thr	Leu	Glu 675	Ile	Leu	Asn	Glu	Lys 680	Glu	Ala	Asp	Glu	Arg 685	Pro	Ala	Gly

Lys	Gly	Arg	Asp	Glu	Pro	Asn	Met	Asn	Pro	Lys	Leu	Asp	Leu	Pro	Asn
	690					695					700				
Arg	Pro	Glu	Thr	Ser	Phe	Leu	Trp	Phe	Thr	Asn	Pro	Cys	Lys	Thr	Met
705					710					715					720
Lys	Phe	Ile	Val	Trp	Arg	Arg	Phe	Lys	Trp	Val	Ile	Ile	Gly	Leu	Leu
				725					730					735	
Phe	Leu	Leu	Ile	Leu	Leu	Leu	Phe	Val	Ala	Val	Leu	Leu	Tyr	Ser	Leu
			740					745					750		
Pro	Asn	Tyr	Leu	Ser	Met	Lys	Ile	Val	Lys	Pro	Asn	Val			
		755					760					765			

<210> 629

<211> 289

<212> PRT

<213> homo sapiens

<400> 629

Glu	Thr	Gln	Val	Val	Ile	Gln	Arg	Lys	Leu	Val	Ile	Val	Pro	Tyr	Leu
1				5					10					15	
Asn	Asp	Gln	Pro	Gly	Trp	Asp	Ser	Lys	Phe	Arg	Leu	Val	Asn	Thr	Pro
			20					25					30		
Glu	Met	Leu	Phe	Phe	Arg	Asn	Asp	Thr	Glu	Leu	Phe	Gly	Trp	Lys	Val
		35					40					45			
Val	Lys	Arg	Glu	Asn	Lys	Ser	Pro	Val	Lys	Ile	Pro	Phe	Thr	Ile	Gln
	50					55					60				
Arg	Ser	Val	Met	Asp	Ile	Cys	Phe	Leu	Phe	Val	Phe	Phe	Ile	Ala	Arg
65					70					75					80
Asn	Pro	Ala	Phe	Asp	Val	Asp	Val	Thr	His	Phe	Leu	Ser	Cys	Asp	Ala
				85					90					95	
Phe	Leu	Val	Gln	Asp	Asn	Val	Leu	Gly	Val	Pro	Asp	Asp	His	Thr	Gln
			100					105					110		
Val	Val	Phe	Leu	Gly	Phe	Pro	Gly	Cys	Asp	Val	Glu	Arg	Arg	Ala	Trp
		115					120					125			
Trp	Pro	Gln	Thr	Leu	Gly	Glu	Asn	Ile	His	Pro	His	Leu	Lys	Phe	Ser
	130					135					140				
Leu	Gly	Asn	Val	Gly	Leu	Glu	Gly	Ala	Val	Gln	Ser	Pro	Cys	Phe	His
145				150						155					160
Val	Leu	Arg	Asp	Gln	Pro	Leu	Ser	Pro	Glu	Asp	Val	Lys	Ser	Lys	Pro
				165					170					175	
Leu	Phe	Arg	Gly	Pro	Glu	Val	Leu	Val	Gln	Asp	Phe	Val	Gly	Phe	Lys
			180					185					190		
Phe	Ile	Gln	Ala	Val	Val	Ser	Ser	Ser	Ile	Ser	Asp	Ser	Thr	Pro	Ile
		195				200						205			
Phe	Gly	Lys	Asp	Gly	Leu	Trp	Glu	Ala	Phe	Glu	Ser	Gly	Asp	Ile	Leu

210						215						220				
Lys	Gln	Leu	Cys	Trp	Ser	Gln	Leu	Ile	Ser	Pro	Gly	Ile	Asp	Ser	Arg	
225					230					235					240	
Asn	Thr	Val	Leu	Leu	Trp	Tyr	Ala	Ala	Val	Gly	Pro	Lys	Ala	Gly	Lys	
				245					250					255		
Glu	Ser	Val	Phe	Gln	Ile	Asn	Asn	Cys	Phe	Ser	Tyr	Phe	Phe	Ile	Pro	
			260					265					270			
Gly	Lys	Gly	Val	Ile	Ile	Ile	Asp	Arg	Asn	Phe	Gln	Val	Phe	Phe	Leu	
		275					280					285				

Arg

<210> 630  
 <211> 824  
 <212> PRT  
 <213> homo sapiens

<400> 630

Arg	Val	Ser	Val	Leu	Ala	Ala	Ala	Ser	Ser	Ala	Leu	Pro	Val	Ala	Pro
1				5					10					15	
Arg	Glu	Ala	Gly	Val	Thr	Asn	Trp	Pro	Ala	Gly	Cys	Val	Pro	Glu	Val
			20					25					30		
Arg	Ser	Thr	Gly	Glu	Lys	Glu	Val	Ala	Lys	Thr	Leu	His	Arg	Arg	Ser
		35					40					45			
Arg	Pro	Glu	Trp	Cys	Gly	Ala	Arg	Asp	Pro	Pro	Ala	Met	Leu	Leu	Phe
	50					55					60				
Val	Leu	Thr	Cys	Leu	Leu	Ala	Val	Phe	Pro	Ala	Ile	Ser	Thr	Lys	Ser
65					70					75					80
Pro	Ile	Phe	Gly	Pro	Glu	Glu	Val	Asn	Ser	Val	Glu	Gly	Asn	Ser	Val
				85					90					95	
Ser	Ile	Thr	Cys	Tyr	Tyr	Pro	Pro	Thr	Ser	Val	Asn	Arg	His	Thr	Arg
			100					105					110		
Lys	Tyr	Trp	Cys	Arg	Gln	Gly	Ala	Arg	Gly	Gly	Cys	Ile	Thr	Leu	Ile
		115					120					125			
Ser	Ser	Glu	Gly	Tyr	Val	Ser	Ser	Lys	Tyr	Ala	Gly	Arg	Ala	Asn	Leu
	130					135					140				
Thr	Asn	Phe	Pro	Glu	Asn	Gly	Thr	Phe	Val	Val	Asn	Ile	Ala	Gln	Leu
145					150					155					160
Ser	Gln	Asp	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu	Gly	Ile	Asn	Ser
				165					170					175	
Arg	Gly	Leu	Ser	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser	Gln	Gly	Pro	Gly
			180					185					190		
Leu	Leu	Asn	Asp	Thr	Lys	Val	Tyr	Thr	Val	Asp	Leu	Gly	Arg	Thr	Val
		195					200					205			
Thr	Ile	Asn	Cys	Pro	Phe	Lys	Thr	Glu	Asn	Ala	Gln	Lys	Arg	Lys	Ser

210					215					220					
Leu 225	Tyr	Lys	Gln	Ile	Gly 230	Leu	Tyr	Pro	Val	Leu 235	Val	Ile	Asp	Ser	Ser 240
Gly	Tyr	Val	Asn	Pro 245	Asn	Tyr	Thr	Gly	Arg 250	Ile	Arg	Leu	Asp	Ile 255	Gln
Gly	Thr	Gly	Gln 260	Arg	Leu	Phe	Ser	Val 265	Val	Ile	Asn	Gln	Leu 270	Arg	Leu
Ser	Asp	Ala 275	Gly	Gln	Tyr	Leu	Cys 280	Gln	Ala	Gly	Asp	Asp 285	Ser	Asn	Ser
Asn	Lys 290	Lys	Asn	Ala	Asp	Leu 295	Gln	Val	Leu	Lys	Pro 300	Glu	Pro	Glu	Leu
Val 305	Tyr	Glu	Asp	Leu	Arg 310	Gly	Ser	Val	Thr	Phe 315	His	Cys	Ala	Leu	Gly 320
Pro	Glu	Val	Ala	Asn 325	Val	Ala	Lys	Phe	Leu 330	Cys	Arg	Gln	Ser	Ser 335	Gly
Glu	Asn	Cys	Asp 340	Val	Val	Val	Asn	Thr 345	Leu	Gly	Lys	Arg	Ala 350	Pro	Ala
Phe	Glu	Gly 355	Arg	Ile	Leu	Leu	Asn 360	Pro	Gln	Asp	Lys	Asp 365	Gly	Ser	Phe
Ser	Val 370	Val	Ile	Thr	Gly	Leu 375	Arg	Lys	Glu	Asp	Ala 380	Gly	Arg	Tyr	Leu
Cys 385	Gly	Ala	His	Ser	Asp 390	Gly	Gln	Leu	Gln	Glu 395	Gly	Ser	Pro	Ile	Gln 400
Ala	Trp	Gln	Leu	Phe 405	Val	Asn	Glu	Glu	Ser 410	Thr	Ile	Pro	Arg	Ser 415	Pro
Thr	Val	Val	Lys 420	Gly	Val	Ala	Gly	Gly 425	Ser	Val	Ala	Val	Leu 430	Cys	Pro
Tyr	Asn	Arg 435	Lys	Glu	Ser	Lys	Ser 440	Ile	Lys	Tyr	Trp	Cys 445	Leu	Trp	Glu
Gly	Ala 450	Gln	Asn	Gly	Arg	Cys 455	Pro	Leu	Leu	Val	Asp 460	Ser	Glu	Gly	Trp
Val 465	Lys	Ala	Gln	Tyr	Glu 470	Gly	Arg	Leu	Ser	Leu 475	Leu	Glu	Glu	Pro	Gly 480
Asn	Gly	Thr	Phe	Thr 485	Val	Ile	Leu	Asn	Gln 490	Leu	Thr	Ser	Arg	Asp 495	Ala
Gly	Phe	Tyr	Trp 500	Cys	Leu	Thr	Asn	Gly 505	Asp	Thr	Leu	Trp	Arg 510	Thr	Thr
Val	Glu	Ile 515	Lys	Ile	Ile	Glu	Gly 520	Glu	Pro	Asn	Leu	Lys 525	Val	Pro	Gly
Asn	Val 530	Thr	Ala	Val	Leu	Gly 535	Glu	Thr	Leu	Lys	Val 540	Pro	Cys	His	Phe
Pro	Cys	Lys	Phe	Ser	Ser	Tyr	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	Asn

545					550					555					560
Thr	Gly	Cys	Gln	Ala 565	Leu	Pro	Ser	Gln	Asp 570	Glu	Gly	Pro	Ser	Lys 575	Ala
Phe	Val	Asn	Cys 580	Asp	Glu	Asn	Ser	Arg 585	Leu	Val	Ser	Leu	Thr 590	Leu	Asn
Leu	Val	Thr 595	Arg	Ala	Asp	Glu	Gly 600	Trp	Tyr	Trp	Cys	Gly 605	Val	Lys	Gln
Gly	His 610	Phe	Tyr	Gly	Glu	Thr 615	Ala	Ala	Val	Tyr	Val 620	Ala	Val	Glu	Glu
Arg 625	Lys	Ala	Ala	Gly	Ser 630	Arg	Asp	Val	Ser	Leu 635	Ala	Lys	Ala	Asp	Ala 640
Ala	Pro	Asp	Glu	Lys 645	Val	Leu	Asp	Ser	Gly 650	Phe	Arg	Glu	Ile	Glu 655	Asn
Lys	Ala	Ile	Gln 660	Asp	Pro	Arg	Leu	Phe 665	Ala	Glu	Glu	Lys	Ala 670	Val	Ala
Asp	Thr	Arg 675	Asp	Gln	Ala	Asp	Gly 680	Ser	Arg	Ala	Ser	Val 685	Asp	Ser	Gly
Ser	Ser 690	Glu	Glu	Gln	Gly	Gly 695	Ser	Ser	Arg	Ala	Leu 700	Val	Ser	Thr	Leu
Val 705	Pro	Leu	Gly	Leu	Val 710	Leu	Ala	Val	Gly	Ala 715	Val	Ala	Val	Gly	Val 720
Ala	Arg	Ala	Arg	His 725	Arg	Lys	Asn	Val	Asp 730	Arg	Val	Ser	Ile	Arg 735	Ser
Tyr	Arg	Thr	Asp 740	Ile	Ser	Met	Ser	Asp 745	Phe	Glu	Asn	Ser	Arg 750	Glu	Phe
Gly	Ala	Asn 755	Asp	Asn	Met	Gly	Ala 760	Ser	Ser	Ile	Thr	Gln 765	Glu	Thr	Ser
Leu	Gly 770	Gly	Lys	Glu	Glu	Phe 775	Val	Ala	Thr	Thr	Glu 780	Ser	Thr	Thr	Glu
Thr 785	Lys	Glu	Pro	Lys	Lys 790	Ala	Lys	Arg	Ser	Ser 795	Lys	Glu	Glu	Ala	Glu 800
Met	Ala	Tyr	Lys	Asp 805	Phe	Leu	Leu	Gln	Ser 810	Ser	Thr	Val	Ala	Ala 815	Glu
Ala	Gln	Asp	Gly 820	Pro	Gln	Glu	Ala								

<210> 631

<211> 267

<212> PRT

<213> homo sapiens

<400> 631

Ala	Asp	Ile	Ala	Gly	Pro	Arg	Cys	Leu	Pro	Leu	Phe	Asn	Cys	His	Ile
1				5					10					15	

Asp	Gly	Cys	Ser 20	Leu	Ser	Ile	Glu	Val 25	Ala	Leu	Leu	His	Ser 30	Thr	Pro
Val	Pro	Ala 35	Leu	Ile	Ser	Pro	Gly 40	His	Gln	Val	Gln	Gly 45	Gln	Gly	Asp
Lys	Pro 50	Ala	Val	Leu	Val	Thr 55	Val	His	Glu	Gly	Leu 60	Ala	Gly	Ala	Phe
Val 65	Leu	Ala	Gly	Gln	Gly 70	Leu	Ala	Ala	Arg	Val 75	Ile	Pro	Leu	Ala	Pro 80
Val	Phe	Leu	Val	Arg 85	Gly	Glu	Phe	Ala	Trp 90	Lys	Val	Thr	Gly	Asp 95	Leu
Glu	Ser	Leu	Ser 100	Gln	His	Ser	Arg	Asp 105	Ile	Pro	Trp	Tyr	Leu 110	Glu	Val
Trp	Phe	Ser 115	Phe	Asp	Asn	Leu	Asp 120	Leu	His	Gly	Gly	Pro 125	Pro	Glu	Ser
Ile	Ala 130	Val	Gly	Gln	Thr	Pro 135	Val	Glu	Ala	Gly	Val 140	Pro	Ala	Gly	Glu
Leu 145	Val	Glu	Asp	Asp	Ser 150	Glu	Gly	Ala	Val	Ala 155	Trp	Leu	Leu	Gln	Gln 160
Gly	Glu	Ala	Ala	Leu 165	Val	Leu	Gly	Leu	Asn 170	Pro	Pro	Leu	Ala	Val 175	His
Gln	Gln	Gly	Ala 180	Ala	Ala	Ile	Leu	Gly 185	Pro	Phe	Pro	Glu	Thr 190	Pro	Val
Leu	Asp	Ala 195	Phe	Ala	Phe	Leu	Thr 200	Val	Val	Gly	Ala	Glu 205	His	Gly	His
Arg	Ala 210	Ser	Cys	His	Pro	Leu 215	His	His	Ser	Gly	Ala 220	Ala	Gly	Asn	Arg
Gly 225	Leu	Leu	Ile	Asp	Glu 230	Glu	Leu	Pro	Gly	Leu 235	Asp	Arg	Arg	Ala	Phe 240
Leu	Gln	Leu	Thr	Ile 245	Arg	Met	Gly	Ser	Thr 250	Gln	Val	Ala	Pro	Cys 255	Ile
Leu	Leu	Pro	Gln 260	Ala	Cys	Asp	His	His 265	Thr	Glu					

<210> 632

<211> 140

<212> PRT

<213> homo sapiens

<400> 632

Gly 1	Glu	Thr	Arg	Val 5	His	Ser	Gln	Gln	Gly 10	Gly	Gly	Ile	Lys	Ala 15	Pro
Ser	Trp	Asp	Trp 20	Phe	Phe	Arg	Glu	Pro 25	Gly	Pro	Leu	Val	Lys 30	Gly	Leu
Leu	Gly	His 35	Val	Lys	Gln	Tyr	Leu 40	Glu	Gln	Pro	Arg	Pro 45	Trp	Gly	Tyr



Gln	Val	Glu	Arg	Arg	Glu	Gly	Arg	Arg	Leu	Pro	Cys	Thr	His	Leu	Pro
	50					55					60				
Trp	Trp	Ala	Gly	Phe	Ser	Leu	Leu	Gly	Ser	Thr	Leu	Pro	Pro	Ser	Val
65					70					75					80
His	Asp	Thr	Asp	Pro	Arg	Ala	Ser	Pro	Cys	Pro	Arg	Pro	Ser	Tyr	Arg
				85					90					95	
Leu	Leu	Phe	Gln	Asp	Ile	Thr	Asp	Asn	Pro	Glu	Arg	Met	Glu	Lys	Gly
			100					105					110		
Gly	Ala	Trp	Val	Pro	Ala	Val	Ser	Gly	Gln	Lys	Glu	Val	Ala	Cys	Gly
		115					120					125			
Asn	Leu	Arg	Ser	Pro	His	Pro	Arg	Phe	Pro	Lys	Arg				
	130					135					140				

<210> 633

<211> 127

<212> PRT

<213> homo sapiens

<400> 633

Val	Phe	Pro	Cys	His	Leu	Val	Gly	Ala	Gly	Pro	Thr	Pro	Ala	Thr	Thr
1				5					10					15	
Ser	Gly	Thr	Ala	Lys	Gly	Ser	Thr	Arg	Cys	Asp	Tyr	Pro	Gly	Pro	Cys
			20					25					30		
Trp	Gln	Leu	Arg	Ile	Pro	Gly	Thr	Cys	Ser	Asp	Pro	Val	Ser	Gly	Ser
		35					40					45			
Ser	Glu	Ser	Gln	Glu	Pro	Arg	Met	Arg	Ala	Leu	Cys	Ser	Pro	Ser	Ser
	50					55					60				
Lys	Thr	Gln	Gly	Ser	Pro	Pro	Arg	Lys	Gly	Ala	His	Val	Pro	Gln	Arg
65					70					75					80
Gly	Trp	Leu	Pro	Gly	Cys	Tyr	Leu	Phe	Tyr	Pro	Thr	Ser	Ala	Ala	Glu
				85					90					95	
Ser	Gln	Gly	Glu	Thr	Ala	Ser	His	Pro	Lys	Pro	Leu	Gly	Phe	Ser	Arg
			100					105					110		
Glu	Lys	Asn	Leu	Ser	Gln	Lys	His	Asp	Leu	Phe	Ser	Gly	Cys	Lys	
		115					120					125			

<210> 634

<211> 140

<212> PRT

<213> homo sapiens

<400> 634

His	His	Gln	Lys	His	Met	Gln	Gly	Lys	Gly	Ser	Tyr	Trp	Ala	Ser	Gly
1				5					10					15	
Leu	Leu	Ser	Pro	Trp	Leu	Gly	Arg	Lys	Gly	Arg	Glu	Asp	Gly	Trp	Gly
			20					25					30		

Ser	Leu	Phe	Gly	Ile	Asp	Asp	Val	His	Glu	Phe	Gly	Leu	Glu	Gly	Ser
		35					40					45			
Thr	Thr	His	Lys	Glu	Ala	Ile	His	Ile	Arg	Leu	Ala	Gly	Gln	Leu	Leu
	50					55					60				
Ala	Gly	Cys	Pro	Ser	His	Arg	Ala	Ser	Ile	Asn	Asp	Thr	Gly	Ala	Leu
65					70					75					80
Ser	His	Arg	Ile	Arg	Asp	Val	Gly	Leu	Gln	Pro	Ser	Ser	Glu	Leu	Leu
				85					90					95	
Val	Tyr	Phe	Leu	Gly	Leu	Leu	Gly	Cys	Cys	Ser	Leu	Ala	Ser	Thr	Asn
			100					105					110		
Gly	Pro	His	Arg	Leu	Ile	Gly	Gln	Asp	Asp	Leu	Ala	Pro	Val	Leu	His
		115					120					125			
Val	Ile	Cys	Asp	Asp	Leu	Leu	Val	Trp	Trp	Glu	Gly				
	130					135					140				

<210> 635  
 <211> 101  
 <212> PRT  
 <213> homo sapiens

<400> 635

Lys	Val	Ile	Ala	Asp	Asn	Val	Lys	Asp	Trp	Ser	Lys	Val	Val	Leu	Ala
1				5					10					15	
Tyr	Glu	Pro	Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Pro	Gln
			20					25					30		
Gln	Ala	Gln	Glu	Val	His	Glu	Lys	Leu	Arg	Gly	Trp	Leu	Lys	Ser	Asn
		35					40					45			
Val	Ser	Asp	Ala	Val	Ala	Gln	Ser	Thr	Arg	Ile	Ile	Tyr	Gly	Gly	Ser
	50					55					60				
Val	Thr	Gly	Ala	Thr	Cys	Lys	Glu	Leu	Ala	Ser	Gln	Pro	Asp	Val	Asp
65					70					75					80
Gly	Phe	Leu	Val	Gly	Gly	Ala	Ser	Leu	Lys	Pro	Glu	Phe	Val	Asp	Ile
				85					90					95	
Ile	Asn	Ala	Lys	Gln											
			100												

<210> 636  
 <211> 329  
 <212> PRT  
 <213> homo sapiens

<400> 636

Asp	Ser	Ile	Phe	Pro	Leu	Trp	Ala	Val	Leu	Ala	Leu	Ser	Pro	Pro	Gly
1				5					10					15	
Ile	Arg	Val	Arg	Met	Lys	Lys	Ser	Ser	Val	Ser	Gly	Met	Thr	Ala	Ala
			20					25					30		
Gly	Trp	Val	Val	Trp	Gly	Glu	Ala	Glu	Gly	Lys	Ala	Ala	Leu	Arg	Leu

35						40					45				
Gly	Val	Glu	Phe	Leu	Glu	Val	Trp	Gly	Gly	Gly	Arg	Val	Phe	Asn	Leu
	50					55					60				
Glu	Lys	Ser	Gln	Pro	Ala	Arg	Ala	Glu	Arg	Glu	Cys	Glu	Arg	Gly	Ser
65					70					75					80
Ser	Glu	Gly	Ala	Arg	Asn	Gly	Val	Gly	Gly	Ser	Gly	Gly	Arg	Ser	Val
				85					90					95	
Ala	Val	Ala	Leu	Val	His	Gln	His	Gly	Val	Arg	Leu	Leu	Gly	Asp	Leu
			100					105					110		
Gln	Gln	Arg	Val	His	Val	Gly	Ala	Ala	Pro	Ala	Pro	Gln	Val	Ala	Gly
		115					120					125			
Leu	Pro	Pro	Leu	Arg	Ala	Ala	Leu	Val	Val	Val	Gly	Ala	His	Leu	His
	130					135					140				
His	Leu	Gly	Gly	Leu	Glu	His	Phe	His	Leu	Ala	Leu	Ala	Asp	Leu	Leu
145					150					155					160
Asp	Val	Glu	Gly	Glu	Gly	Trp	His	Leu	Val	Asp	Arg	Gly	Leu	Gly	Ala
				165					170					175	
Arg	Val	His	His	Val	Val	Gly	Arg	Glu	Gly	Phe	Ala	Gln	Leu	Val	Pro
			180					185					190		
Arg	Arg	Leu	Gln	Phe	Leu	Ala	Pro	Leu	Gly	Gly	His	Gln	Ala	Arg	Ala
		195					200					205			
Gln	Leu	Val	His	Ala	Leu	Leu	Gln	Gly	Val	Pro	Arg	Leu	Leu	Gln	Val
	210					215					220				
Phe	Leu	Gly	Leu	Glu	Ala	Arg	Leu	Leu	Gln	Val	Leu	Ala	Gly	Thr	His
225					230					235					240
Leu	Gly	Leu	Leu	His	Leu	Leu	Leu	Gly	Glu	Gly	Leu	Leu	Glu	Val	Val
				245					250					255	
His	Ala	Pro	Gln	Ala	Leu	Arg	Leu	Ile	Arg	Ser	Ala	Arg	Asp	Ser	Ser
			260					265					270		
Ile	Thr	Ser	Ser	Thr	Ser	Thr	Ala	Ser	Ser	Asp	Glu	Ser	Ser	Ser	Ala
		275					280					285			
Ala	Ala	Ser	Ser	Ser	Gly	Arg	Ser	Pro	Ser	Pro	Ser	Ser	Ser	Pro	Ser
	290					295					300				
Phe	Ser	Gly	Ser	Ala	Ser	Asp	Ser	Phe	Ser	Asp	Leu	Leu	Met	Leu	Ser
305					310					315					320
Leu	Ala	Gly	Ser	Phe	Thr	Ser	Ser	Trp							
				325											

<210> 637  
 <211> 263  
 <212> PRT  
 <213> homo sapiens

<400> 637

Gly 1	Arg	Leu	Pro	Gly 5	Tyr	Pro	Asp	Arg	Arg 10	Gly	Pro	Gly	Ala	Ser 15	Ser
Ala	Gly	Ala	Gln 20	Ala	Ala	Glu	Glu	Pro 25	Ser	Gly	Ala	Gly	Ser 30	Glu	Glu
Leu	Ile	Lys 35	Ser	Asp	Gln	Val	Asn 40	Gly	Val	Leu	Val	Leu 45	Ser	Leu	Leu
Asp	Lys 50	Ile	Ile	Gly	Ala	Val 55	Asp	Gln	Ile	Gln	Leu 60	Thr	Gln	Ala	Gln
Leu 65	Glu	Glu	Arg	Gln	Ala 70	Glu	Met	Glu	Gly	Ala 75	Val	Gln	Ser	Ile	Gln 80
Gly	Glu	Leu	Ser	Lys 85	Leu	Gly	Lys	Ala	His 90	Ala	Thr	Thr	Ser	Asn 95	Thr
Val	Ser	Lys	Leu 100	Leu	Glu	Lys	Val	Arg 105	Lys	Val	Ser	Val	Asn 110	Val	Lys
Thr	Val	Arg 115	Gly	Ser	Leu	Glu	Arg 120	Gln	Ala	Gly	Gln	Ile 125	Lys	Lys	Leu
Glu	Val 130	Asn	Glu	Ala	Glu	Leu 135	Leu	Arg	Arg	Arg	Asn 140	Phe	Lys	Val	Met
Ile 145	Tyr	Gln	Asp	Glu	Val 150	Lys	Leu	Pro	Ala	Lys 155	Leu	Ser	Ile	Ser	Lys 160
Ser	Leu	Lys	Glu	Ser 165	Glu	Ala	Leu	Pro	Glu 170	Lys	Glu	Gly	Glu	Glu 175	Leu
Gly	Glu	Gly	Glu 180	Arg	Pro	Glu	Glu	Asp 185	Ala	Ala	Ala	Leu	Glu 190	Leu	Ser
Ser	Asp	Glu 195	Ala	Val	Glu	Val	Glu 200	Glu	Val	Ile	Glu	Glu 205	Ser	Arg	Ala
Glu	Arg 210	Ile	Lys	Arg	Arg	Ala 215	Cys	Gly	Ala	Trp	Thr 220	Thr	Ser	Arg	Arg
Pro 225	Ser	Pro	Arg	Arg	Arg 230	Trp	Arg	Arg	Pro	Arg 235	Cys	Val	Pro	Ala	Arg 240
Thr	Trp	Arg	Arg	Arg 245	Ala	Ser	Arg	Pro	Arg 250	Lys	Thr	Trp	Arg	Arg 255	Arg
Gly	Thr	Pro	Trp 260	Arg	Ser	Ala									

<210> 638

<211> 205

<212> PRT

<213> homo sapiens

<400> 638

Ser 1	Gly	Asp	Leu	Arg 5	Leu	Leu	Val	Asp	Thr 10	Ser	Lys	Val	Gln	Glu 15	Ala
Trp	Val	Pro	Ser 20	Gln	Asp	Thr	His	His 25	Thr	Gln	Glu	Leu	Leu 30	Ala	Val

Gln	Gly	Ser 35	Leu	Val	Ser	Gly	Tyr 40	Arg	Pro	Gly	Gly	Gly 45	Phe	Gly	Ala
Ala	Pro 50	Val	His	Glu	Asp	Pro 55	His	Leu	Leu	Gly	Pro 60	Ala	Ser	Arg	Gly
Ala 65	Pro	Glu	Thr	Ala	Ala 70	Phe	Phe	Phe	Phe	Phe 75	Phe	Phe	Phe	Phe	Pro 80
Glu	Gln	His	Leu	Arg 85	Val	Gly	Leu	Leu	Leu 90	Leu	Pro	Pro	Arg	Leu 95	Ser
Pro	Arg	Pro	Gly 100	Pro	Ala	Trp	Pro	Val 105	Pro	Asn	Pro	Val	Gly 110	Trp	Pro
Gly	His	Leu 115	His	Gln	Gly	Gly	Gln 120	Leu	Leu	Ala	Gly	Thr 125	Asn	Lys	Pro
Phe	His 130	Leu	Ala	Met	Val	Val 135	Val	Phe	Ser	Met	Asp 140	Arg	Gly	Pro	Glu
Thr 145	Arg	Ala	Gly	Arg	Gly 150	Arg	Glu	His	Thr	Ser 155	Leu	Gly	Val	Gly	Thr 160
Ser	Leu	Xxx	Thr	Pro 165	Gln	Gln	Leu	Xxx	Gly 170	Pro	Arg	Xxx	Xxx	Phe 175	Pro
Xxx	Ala	Val	Gln 180	Ala	Ser	Pro	Xxx	Pro 185	Gly	Val	Cys	Ser	Leu 190	Ala	Trp
Val	Glu	Leu 195	Cys	His	Ile	Xxx	Asp 200	Lys	Gln	Xxx	Gly	Gly 205			

<210> 639

<211> 171

<212> PRT

<213> homo sapiens

<400> 639

Pro 1	Val	Thr	Pro	Arg 5	Asp	Xxx	Pro	Gly	Ala 10	Gly	Gly	Gly	Ser	Xxx 15	Glu
Gly	Pro	Met	Gln 20	His	Pro	Gly	Gln	Ser 25	Arg	Pro	Xxx	Pro	Leu 30	Ala	Xxx
Pro	Ala	Pro 35	Xxx	Trp	Xxx	Leu	Met 40	Ala	Pro	Cys	Gly	Ala 45	Leu	Thr	Cys
Trp	Ala 50	Arg	Leu	Xxx	Leu	Gly 55	Leu	Ser	Ala	Pro	Xxx 60	Leu	Leu	Ile	Xxx
Asp 65	Val	Thr	Glu	Leu	Asp 70	Pro	Ser	Gln	Ala	Ala 75	His	Ser	Trp	Thr	Trp 80
Ala	Ser	Leu	His	Cys 85	Xxx	Gly	Lys	Xxx	Xxx 90	Pro	Arg	Ala	Xxx	Lys 95	Leu
Leu	Arg	Gly	Xxx 100	Glu	Ala	Gly	Ala	His 105	Pro	Gln	Ala	Ser	Val 110	Phe	Ser
Ala	Pro	Pro	Cys	Pro	Arg	Phe	Arg	Ala	Ser	Val	His	Arg	Glu	His	His

		115					120					125				
His	His	Gly	Gln	Val	Glu	Gly	Phe	Ile	Ser	Pro	Cys	Gln	Gln	Leu	Ser	
	130					135					140					
Ser	Leu	Val	Gln	Val	Ala	Trp	Pro	Ala	His	Trp	Ile	Gly	Asp	Gly	Pro	
145					150					155					160	
Gly	Trp	Ala	Arg	Ser	Gly	Ala	Gln	Ser	Gly	Arg						
				165					170							

<210> 640  
 <211> 161  
 <212> PRT  
 <213> homo sapiens

<400> 640

Ile	Ser	Arg	Asn	Glu	Gly	Val	Leu	Val	Arg	Gly	Pro	Lys	Ser	Pro	Arg	
1				5					10					15		
Ser	Leu	Leu	Arg	Ser	His	Ser	Glu	Pro	Pro	Ala	Leu	Val	Leu	Trp	Arg	
			20					25					30			
Asp	His	Arg	Leu	Val	Pro	Gly	Thr	Asp	Tyr	Cys	Lys	Asp	Thr	Ala	Leu	
		35					40					45				
Val	Pro	Thr	Glu	Lys	Asn	Thr	Gly	Gln	Gln	Glu	His	Thr	Phe	Ser	Gln	
	50					55					60					
Tyr	Leu	Ala	Thr	Pro	His	Ser	Glu	Leu	Thr	Ile	Thr	His	Gly	Lys	Trp	
65					70					75					80	
Val	His	Ser	Ser	Leu	Trp	Ser	Asp	Pro	Ala	Gly	Leu	Gly	Arg	Gln	Glu	
				85					90					95		
Gln	His	Ser	Ser	Ser	Ser	Leu	Ser	Pro	Arg	Gln	Arg	Glu	Ser	Leu	Asn	
			100					105					110			
Cys	Lys	Arg	Ser	Gly	Ala	Tyr	Thr	Val	Arg	Glu	Lys	Glu	Lys	Gly	Gly	
		115					120					125				
Arg	Lys	Gly	Phe	Ser	Pro	Arg	Pro	Pro	Arg	Asp	Ala	His	Arg	Glu	Gly	
	130					135					140					
Gly	Lys	Glu	Arg	Glu	Lys	Ser	Val	Leu	Glu	Ser	Glu	Ala	Thr	Leu	Ser	
145					150					155					160	

Lys

<210> 641  
 <211> 127  
 <212> PRT  
 <213> homo sapiens

<400> 641

Cys	Ala	Tyr	Arg	Thr	Glu	Lys	Trp	Lys	Ser	His	Thr	Val	Pro	Cys	Ser	
1				5					10					15		
Pro	Glu	Val	Lys	Leu	Val	Leu	Thr	Leu	Ala	Leu	Arg	Ala	Phe	Ser	Ser	
			20					25					30			

Met	Glu	Pro	Leu	Gly	Leu	Gly	Arg	Lys	Ala	Arg	Val	Ser	Ala	His	Arg
		35					40					45			
His	Thr	Ser	Tyr	Leu	Gln	Asp	Ile	Asp	Cys	Leu	Cys	Arg	Gly	Ser	Thr
	50					55					60				
Gly	Gln	Pro	Thr	Ala	Asn	Thr	Ala	Ala	Ser	Leu	Val	Ser	Ala	Ser	Leu
65					70					75					80
Leu	Pro	Val	His	Pro	Gly	Asp	Tyr	Ser	Trp	Ile	Asn	Leu	Pro	Lys	Asn
				85					90					95	
Ser	Ala	Phe	Ile	Met	Ser	Leu	Phe	Cys	Ser	Lys	Thr	Gln	Asn	Gly	Ser
			100					105					110		
Leu	Pro	Pro	Arg	Gly	Arg	Pro	Ser	His	His	Cys	Ile	Pro	Asn	Arg	
		115					120					125			

<210> 642  
 <211> 136  
 <212> PRT  
 <213> homo sapiens

<400> 642

Trp	Gly	Xxx	Gly	Arg	Val	Arg	Val	Xxx	Gly	Trp	Xxx	Arg	Lys	Pro	Met
1				5					10					15	
Lys	Xxx	Gly	Ile	Pro	Pro	Glu	Xxx	His	Gly	Pro	Ile	Thr	Ala	Asp	Gly
			20					25					30		
His	Arg	Xxx	Leu	Xxx	Xxx	Leu	Pro	Pro	Xxx	Gly	Xxx	Arg	Cys	Xxx	Xxx
		35					40					45			
Ala	Asp	Pro	Lys	Gly	Xxx	Gly	Leu	Xxx	Ala	Leu	Phe	Xxx	Lys	Xxx	Pro
	50					55					60				
Pro	Xxx	Glu	Xxx	Cys	Leu	Leu	Ser	Xxx	Xxx	Pro	Xxx	Xxx	Pro	Val	Thr
65					70					75					80
His	Arg	Ala	Gly	Met	Glu	Phe	Asn	Gly	Xxx	Phe	Trp	Xxx	Xxx	Thr	Leu
				85					90					95	
Val	His	Gly	Gln	Thr	Ser	Leu	Leu	Xxx	Gly	Tyr	Xxx	Thr	Arg	Leu	Lys
			100					105					110		
Xxx	Lys	Ile	Val	Cys	Cys	His	Ser	Ser	Gly	Xxx	Trp	Ser	Val	Cys	Gly
		115					120					125			
Leu	His	Arg	Phe	His	Arg	Asn	Gln								
	130					135									

<210> 643  
 <211> 132  
 <212> PRT  
 <213> homo sapiens

<400> 643

Gly	Arg	Xxx	Ser	Arg	Ala	Trp	Gly	Leu	Gly	Cys	Pro	Ser	Leu	Leu	Ser
1				5					10					15	
Pro	Ile	Ser	Leu	Arg	Leu	Pro	Val	Pro	Pro	Pro	Arg	Pro	Pro	Asn	Leu

20						25						30			
Arg	Pro	Pro	Ala	Thr	Pro	Gly	Ala	Pro	Thr	Xxx	Pro	Xxx	Gln	Asn	Thr
		35					40					45			
Ala	Xxx	Leu	Lys	Xxx	Leu	Leu	Glu	Leu	Ser	Xxx	Xxx	Leu	Ser	Gly	Leu
	50					55					60				
Gly	Leu	Met	Gly	Xxx	Arg	Ala	Gly	Thr	Cys	Thr	Trp	Val	Ala	Xxx	Glu
65					70					75					80
Ala	His	Glu	Asp	Xxx	Asp	Thr	Pro	Arg	Val	Pro	Trp	Thr	Xxx	Tyr	Xxx
				85					90					95	
Arg	Trp	Ser	Ser	Xxx	Pro	Xxx	Ala	Ile	Ala	Thr	Xxx	Gly	Xxx	Ser	Leu
			100					105					110		
Xxx	Xxx	Gly	Arg	Pro	Gln	Arg	Glu	Xxx	Pro	Xxx	Arg	Val	Val	Xxx	Lys
		115					120					125			
Xxx	Thr	Thr	Xxx												
	130														

<210> 644  
 <211> 131  
 <212> PRT  
 <213> homo sapiens

<400> 644

Gly	Val	Glu	Thr	Thr	Ala	Asn	Ser	Ser	Thr	Ser	Leu	Arg	Ser	Thr	Thr
1				5					10					15	
Leu	Glu	Lys	Glu	Val	Pro	Val	Ile	Phe	Ile	His	Pro	Leu	Asn	Thr	Gly
			20					25					30		
Leu	Phe	Arg	Ile	Lys	Ile	Gln	Gly	Ala	Thr	Gly	Lys	Phe	Asn	Met	Val
		35					40					45			
Ile	Pro	Leu	Val	Asp	Gly	Met	Ile	Val	Ser	Arg	Arg	Ala	Leu	Gly	Phe
	50					55					60				
Leu	Val	Arg	Gln	Thr	Val	Ile	Asn	Ile	Cys	Arg	Arg	Lys	Arg	Leu	Glu
65					70					75					80
Ser	Asp	Ser	Tyr	Ser	Pro	Pro	Met	Ser	Ala	Gly	Asn	Arg	Lys	Ser	Pro
				85					90					95	
Thr	Leu	Ser	Thr	Ser	Thr	Gly	Thr	Ser	Ser	Trp	Ser	Gln	Ser	Phe	Ile
			100					105					110		
Leu	His	Phe	Ser	Arg	Arg	Leu	Asp	Ser	Arg	Thr	Ala	Val	Leu	Arg	Pro
		115					120					125			
Leu	Asn	Phe													
	130														

<210> 645  
 <211> 86  
 <212> PRT  
 <213> homo sapiens

<400> 645



Leu 1	Thr	Asn	Met	Ser 5	Asp	His	Leu	Phe	Gly 10	Trp	Leu	Leu	Leu	Glu 15	Met
Ala	Val	Val	Met 20	Phe	Ser	Gly	Leu	Cys 25	Gln	Pro	Thr	Asp	Pro 30	Cys	Gln
Val	Leu	Glu 35	Ile	Leu	Leu	Leu	Pro 40	Arg	Cys	Tyr	Phe	Ser 45	Ala	Gly	Ile
Lys	Leu 50	Leu	Xxx	Val	Ala	Arg 55	Pro	Arg	Thr	Ser	Lys 60	Asp	Ser	Cys	Tyr
Ser 65	Ala	Thr	Val	Tyr	Thr 70	Ala	His	Leu	Ser	Tyr 75	Ser	His	Val	Leu	Ser 80
Ser	Leu	Val	Arg	Leu 85	Phe										

<210> 646  
 <211> 96  
 <212> PRT  
 <213> homo sapiens  
 <400> 646

Lys 1	Ala	Pro	Asn	Pro 5	Ser	Val	Leu	His	Thr 10	Val	Arg	Met	Gln	Leu 15	Ile
Ala	Asp	Arg	Cys 20	Cys	Glu	Leu	Tyr	Ile 25	Cys	Lys	Arg	Cys	Phe 30	Thr	Thr
Ser	Ala	Gly 35	Phe	Ile	Thr	Ala	Ser 40	Trp	Ser	Arg	Val	Ala 45	Ile	Leu	Pro
Ala	Ile 50	Pro	Ala	Lys	Gln	Thr 55	Pro	Glu	Asn	Tyr	Pro 60	Leu	Arg	Ser	Gly
Val 65	Leu	Arg	Lys	Phe	Leu 70	Glu	Pro	Lys	Ile	Arg 75	Arg	Asn	Pro	Gly	Leu 80
Ser	Phe	Leu	Arg	Ser 85	Lys	Met	Tyr	Tyr	Gln 90	Leu	Arg	Pro	Gly	Glu 95	His

<210> 647  
 <211> 92  
 <212> PRT  
 <213> homo sapiens  
 <400> 647

Ser 1	Ser	Ala	Cys	Arg 5	Cys	Thr	Thr	Arg	Ser 10	Thr	Gly	Gln	Gln	Ser 15	Ala
Ala	Ser	Gly	Arg 20	Cys	Gly	Gly	Pro	Arg 25	Gly	Trp	Gly	Pro	Ser 30	Thr	Gly
Ala	Thr	Pro 35	Arg	Gln	Leu	Thr	Met 40	Asn	Ile	Pro	Phe	Gln 45	Ser	Ile	His
Phe	Ile 50	Thr	Tyr	Glu	Phe	Leu 55	Gln	Glu	Gln	Val	Asn 60	Pro	His	Arg	Thr

Tyr	Asn	Pro	Gln	Ser	His	Ile	Ile	Ser	Gly	Gly	Leu	Ala	Gly	Ala	Leu
65					70					75					80
Ala	Ala	Ala	Ala	Arg	Gly	Pro	Leu	Asp	Val	Leu	Arg				
				85					90						

<210> 648

<211> 280

<212> PRT

<213> homo sapiens

<400> 648

Ala	Val	Gly	Ser	Ala	Ala	Leu	Phe	Lys	Asp	Gly	Gly	Gly	Gly	Thr	Ser
1				5					10					15	
Ala	Ala	Glu	Ala	Gly	Ala	Ala	Gly	Gln	Arg	Leu	Arg	Ser	Val	Asn	Cys
			20					25					30		
Leu	Ala	Tyr	Asp	Glu	Ala	Ile	Met	Ala	Gln	Gln	Asp	Arg	Ile	Gln	Gln
		35					40					45			
Glu	Ile	Ala	Val	Gln	Asn	Pro	Leu	Val	Ser	Glu	Arg	Leu	Glu	Leu	Ser
	50					55					60				
Val	Leu	Tyr	Lys	Glu	Tyr	Ala	Glu	Asp	Asp	Asn	Ile	Tyr	Gln	Gln	Lys
65					70					75					80
Ile	Lys	Asp	Leu	His	Lys	Lys	Tyr	Ser	Tyr	Ile	Arg	Lys	Thr	Arg	Pro
				85					90					95	
Asp	Gly	Asn	Cys	Phe	Tyr	Arg	Ala	Phe	Gly	Phe	Ser	His	Leu	Glu	Ala
			100					105					110		
Leu	Leu	Asp	Asp	Ser	Lys	Glu	Leu	Gln	Arg	Phe	Lys	Ala	Val	Ser	Ala
		115					120					125			
Lys	Ser	Lys	Glu	Asp	Leu	Val	Ser	Gln	Gly	Phe	Thr	Glu	Phe	Thr	Ile
	130					135					140				
Glu	Asp	Phe	His	Asn	Thr	Phe	Met	Asp	Leu	Ile	Glu	Gln	Val	Glu	Lys
145					150					155					160
Gln	Thr	Ser	Val	Ala	Asp	Leu	Leu	Ala	Ser	Phe	Asn	Asp	Gln	Ser	Thr
				165					170					175	
Ser	Asp	Tyr	Leu	Val	Val	Tyr	Leu	Arg	Leu	Leu	Thr	Ser	Gly	Tyr	Leu
			180					185					190		
Gln	Arg	Glu	Ser	Lys	Phe	Phe	Glu	His	Phe	Ile	Glu	Gly	Gly	Arg	Thr
		195					200					205			
Val	Lys	Glu	Phe	Cys	Gln	Gln	Glu	Val	Glu	Pro	Met	Cys	Lys	Glu	Ser
	210					215					220				
Asp	His	Ile	His	Ile	Ile	Ala	Leu	Ala	Gln	Ala	Leu	Ser	Val	Ser	Ile
225					230					235					240
Gln	Val	Glu	Tyr	Met	Asp	Arg	Gly	Glu	Gly	Gly	Thr	Thr	Asn	Pro	His
				245					250					255	
Ile	Phe	Pro	Glu	Gly	Ser	Glu	Pro	Lys	Val	Tyr	Leu	Leu	Tyr	Arg	Pro
			260					265					270		

Gly His Tyr Asp Ile Leu Tyr Lys  
275 280

<210> 649  
<211> 244  
<212> PRT  
<213> homo sapiens

<400> 649

Asp 1	His	Leu	Gln	Pro 5	Gln	Lys	Asn	Leu	Cys 10	Thr	Cys	Leu	Ala	Pro 15	Gly
Arg	Gly	Gly	Gln 20	Gln	Gly	Ser	Ser	Gly 25	Leu	Glu	Pro	Ala	Leu 30	Phe	Val
Glu	Asp	Ile 35	Val	Val	Ser	Arg	Pro 40	Val	Glu	Lys	Val	Asp 45	Leu	Gly	Leu
Gly	Ala 50	Leu	Arg	Glu	Asp	Val 55	Arg	Ile	Gly	Gly	Ala 60	Ala	Leu	Ala	Ala
Val 65	His	Val	Leu	His	Leu 70	Asp	Gly	His	Ala	Glu 75	Gly	Leu	Gly	Gln	Arg 80
Asn	Asp	Val	Asp	Val 85	Val	Ala	Leu	Leu	Ala 90	His	Gly	Leu	His	Leu 95	Leu
Leu	Ala	Glu	Leu 100	Leu	Asp	Ser	Pro	Ser 105	Thr	Leu	Asp	Glu	Val 110	Leu	Glu
Glu	Leu	Ala 115	Leu	Ala	Leu	Gln	Val 120	Ala	Arg	Gly	Glu	Gln 125	Pro	Gln	Val
Asp	His 130	Lys	Val	Val	Gly	Gly 135	Ala	Leu	Val	Ile	Glu 140	Gly	Gly	Gln	Gln
Val 145	Gly	Asp	Arg	Gly	Leu 150	Leu	Leu	His	Leu	Leu 155	Asn	Gln	Val	His	Glu 160
Arg	Val	Val	Glu	Ile 165	Leu	Asn	Cys	Glu	Phe 170	Ser	Glu	Ala	Leu	Gly 175	His
Gln	Val	Phe	Leu 180	Ala	Leu	Gly	Arg	His 185	Ser	Leu	Glu	Pro	Leu 190	Gln	Leu
Leu	Ala	Val 195	Ile	Gln	Gln	Cys	Leu 200	Gln	Val	Gly	Glu	Ser 205	Glu	Ser	Pro
Ile	Glu 210	Thr	Val	Ala	Val	Arg 215	Pro	Gly	Leu	Ala	Asp 220	Val	Arg	Val	Leu
Phe 225	Val	Glu	Val	Leu	Asp 230	Leu	Leu	Leu	Ile	Asp 235	Val	Val	Ile	Phe	Ser 240
Ile	Leu	Leu	Val												

<210> 650  
<211> 424  
<212> PRT  
<213> homo sapiens

<400> 650

Leu 1	Thr	Thr	Thr	Cys 5	Val	Ser	Ser	Ser	Ala 10	Pro	Ser	Lys	Thr	Ser 15	Leu
Ile	Met	Asn	Pro 20	His	Ala	Ser	Thr	Asn 25	Gly	Gln	Leu	Ser	Val 30	His	Thr
Pro	Lys	Arg 35	Glu	Ser	Leu	Ser	His 40	Glu	Glu	His	Pro	His 45	Ser	His	Pro
Leu	Tyr 50	Gly	His	Gly	Val	Cys 55	Lys	Trp	Pro	Gly	Cys 60	Glu	Ala	Val	Cys
Glu 65	Asp	Phe	Gln	Ser	Phe 70	Leu	Lys	His	Leu	Asn 75	Ser	Glu	His	Ala	Leu 80
Asp	Asp	Arg	Ser	Thr 85	Ala	Gln	Cys	Arg	Val 90	Gln	Met	Gln	Val	Val 95	Gln
Gln	Leu	Glu	Leu 100	Gln	Leu	Ala	Lys	Asp 105	Lys	Glu	Arg	Leu	Gln 110	Ala	Met
Met	Thr	His 115	Leu	His	Val	Lys	Ser 120	Thr	Glu	Pro	Lys	Ala 125	Ala	Pro	Gln
Pro	Leu 130	Asn	Leu	Val	Ser	Ser 135	Val	Thr	Leu	Ser	Lys 140	Ser	Ala	Ser	Glu
Ala 145	Ser	Pro	Gln	Ser	Leu 150	Pro	His	Thr	Pro	Thr 155	Thr	Pro	Thr	Ala	Pro 160
Leu	Thr	Pro	Val	Thr 165	Gln	Gly	Pro	Ser	Val 170	Ile	Thr	Thr	Thr	Ser 175	Met
His	Thr	Val	Gly 180	Pro	Ile	Arg	Arg	Arg 185	Tyr	Ser	Asp	Lys	Tyr 190	Asn	Val
Pro	Ile	Ser 195	Ser	Ala	Asp	Ile	Ala 200	Gln	Asn	Gln	Glu	Phe 205	Tyr	Lys	Asn
Ala	Glu 210	Val	Arg	Pro	Pro	Phe 215	Thr	Tyr	Ala	Ser	Leu 220	Ile	Arg	Gln	Ala
Ile 225	Leu	Glu	Ser	Pro	Glu 230	Lys	Gln	Leu	Thr	Leu 235	Asn	Glu	Ile	Tyr	Asn 240
Trp	Phe	Thr	Arg	Met 245	Phe	Ala	Tyr	Phe	Arg 250	Arg	Asn	Ala	Ala	Thr 255	Trp
Lys	Asn	Ala	Val 260	Arg	His	Asn	Leu	Ser 265	Leu	His	Lys	Cys	Phe 270	Val	Arg
Val	Glu	Asn 275	Val	Lys	Gly	Ala	Val 280	Trp	Thr	Val	Asp	Glu 285	Val	Glu	Phe
Gln	Lys 290	Arg	Arg	Pro	Gln	Lys 295	Ile	Ser	Gly	Asn	Pro 300	Ser	Leu	Ile	Lys
Asn 305	Met	Gln	Ser	Ser	His 310	Ala	Tyr	Cys	Thr	Pro 315	Leu	Asn	Ala	Ala	Leu 320
Gln	Ala	Ser	Met	Ala	Glu	Asn	Ser	Ile	Pro	Leu	Tyr	Thr	Thr	Ala	Ser

				325					330					335		
Met	Gly	Asn	Pro	Thr	Leu	Gly	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Glu	Glu	
			340					345					350			
Leu	Asn	Gly	Ala	Met	Glu	His	Thr	Asn	Ser	Asn	Glu	Ser	Asp	Ser	Ser	
		355					360					365				
Pro	Gly	Arg	Ser	Pro	Met	Gln	Ala	Val	His	Pro	Val	His	Val	Lys	Glu	
	370					375					380					
Glu	Pro	Leu	Asp	Pro	Glu	Glu	Ala	Glu	Gly	Pro	Leu	Ser	Leu	Val	Thr	
385					390					395					400	
Thr	Ala	Asn	His	Ser	Pro	Asp	Phe	Asp	His	Asp	Arg	Asp	Tyr	Glu	Asp	
				405					410					415		
Glu	Pro	Val	Asn	Glu	Asp	Met	Glu									
			420													

<210> 651  
 <211> 117  
 <212> PRT  
 <213> homo sapiens

<400> 651

Ser	Thr	Asn	Ala	Gly	Cys	Thr	Ala	Val	Arg	Ala	Thr	Ala	Cys	Lys	Arg	
1				5					10					15		
Gln	Arg	Ala	Pro	Ala	Ser	His	Asp	Asp	Pro	Pro	Ala	Cys	Glu	Val	Tyr	
			20					25					30			
Arg	Thr	Gln	Ser	Arg	Pro	Ser	Ala	Leu	Glu	Ser	Gly	Ile	Lys	Cys	His	
		35					40					45				
Ser	Leu	Gln	Val	Arg	Ile	Gly	Gly	Phe	Ser	Thr	Glu	Leu	Thr	Ser	Tyr	
	50					55					60					
Ser	Asn	Asp	Pro	Asn	Arg	Pro	Pro	Asp	Ser	Arg	His	Pro	Arg	Pro	Leu	
65					70					75					80	
Cys	His	His	Asn	His	Gln	His	Ala	His	Gly	Gly	Thr	His	Pro	Gln	Ala	
				85					90					95		
Val	Leu	Arg	Gln	Ile	Gln	Arg	Ala	His	Phe	Val	Ser	Arg	Tyr	Cys	Ala	
			100					105					110			
Glu	Pro	Arg	Ile	Leu												
			115													

<210> 652  
 <211> 426  
 <212> PRT  
 <213> homo sapiens

<400> 652

Pro	Glu	Ala	Gly	Leu	Phe	Ser	Cys	Ser	Glu	Gln	Ser	Asp	Phe	Pro	Glu	
1				5					10					15		
His	Ile	Phe	Ile	Met	Ile	His	Thr	Asn	Leu	Lys	Lys	Lys	Phe	Ser	Cys	
			20					25					30			

Cys	Val	Leu 35	Val	Phe	Leu	Leu	Phe 40	Ala	Val	Ile	Cys	Val 45	Trp	Lys	Glu
Lys	Lys 50	Lys	Gly	Ser	Tyr	Tyr 55	Asp	Ser	Phe	Lys	Leu 60	Gln	Thr	Lys	Glu
Phe 65	Gln	Val	Leu	Lys	Ser 70	Leu	Gly	Lys	Leu	Ala 75	Met	Gly	Ser	Asp	Ser 80
Gln	Ser	Val	Ser	Ser 85	Ser	Ser	Thr	Gln	Asp 90	Pro	His	Arg	Gly	Arg 95	Gln
Thr	Leu	Gly	Ser 100	Leu	Arg	Gly	Leu	Ala 105	Lys	Ala	Lys	Pro	Glu 110	Ala	Ser
Phe	Gln	Val 115	Trp	Asn	Lys	Asp	Ser 120	Ser	Ser	Lys	Asn	Leu 125	Ile	Pro	Arg
Leu	Gln 130	Lys	Ile	Trp	Lys	Asn 135	Tyr	Leu	Ser	Met	Asn 140	Lys	Tyr	Lys	Val
Ser 145	Tyr	Lys	Gly	Pro	Gly 150	Pro	Gly	Ile	Lys	Phe 155	Ser	Ala	Glu	Ala	Leu 160
Arg	Cys	His	Leu	Arg 165	Asp	His	Val	Asn	Val 170	Ser	Met	Val	Glu	Val 175	Thr
Asp	Phe	Pro	Phe 180	Asn	Thr	Ser	Glu	Trp 185	Glu	Gly	Tyr	Leu	Pro 190	Lys	Glu
Ser	Ile	Arg 195	Thr	Lys	Ala	Gly	Pro 200	Trp	Gly	Arg	Cys	Ala 205	Val	Val	Ser
Ser	Ala 210	Gly	Ser	Leu	Lys	Ser 215	Ser	Gln	Leu	Gly	Arg 220	Glu	Ile	Asp	Asp
His 225	Asp	Ala	Val	Leu	Arg 230	Phe	Asn	Gly	Ala	Pro 235	Thr	Ala	Asn	Phe	Gln 240
Gln	Asp	Val	Gly	Thr 245	Lys	Thr	Thr	Ile	Arg 250	Leu	Met	Asn	Ser	Gln 255	Leu
Val	Thr	Thr	Glu 260	Lys	Arg	Phe	Leu	Lys 265	Asp	Ser	Leu	Tyr	Asn 270	Glu	Gly
Ile	Leu	Ile 275	Val	Trp	Asp	Pro	Ser 280	Val	Tyr	His	Ser	Asp 285	Ile	Pro	Lys
Trp	Tyr 290	Gln	Asn	Pro	Asp	Tyr 295	Asn	Phe	Phe	Asn	Asn 300	Tyr	Lys	Thr	Tyr
Arg 305	Lys	Leu	His	Pro	Asn 310	Gln	Pro	Phe	Tyr	Ile 315	Leu	Lys	Pro	Gln	Met 320
Pro	Trp	Glu	Leu	Trp 325	Asp	Ile	Leu	Gln	Glu 330	Ile	Ser	Pro	Glu	Glu 335	Ile
Gln	Pro	Asn	Pro 340	Pro	Ser	Ser	Gly	Met 345	Leu	Gly	Ile	Ile	Ile 350	Met	Met
Thr	Leu	Cys 355	Asp	Gln	Val	Asp	Ile 360	Tyr	Glu	Ser	Leu	Pro 365	Ser	Lys	Arg

Lys	Thr	Asp	Val	Cys	Tyr	Tyr	Tyr	Gln	Lys	Phe	Phe	Asp	Ser	Ala	Cys
	370					375					380				
Thr	Met	Gly	Ala	Tyr	His	Pro	Leu	Leu	Tyr	Glu	Lys	Asn	Leu	Val	Lys
385					390					395					400
His	Leu	Asn	Gln	Gly	Thr	Asp	Glu	Asp	Ile	Tyr	Leu	Leu	Gly	Lys	Ala
				405					410					415	
Thr	Leu	Pro	Gly	Phe	Arg	Thr	Ile	His	Cys						
			420					425							

<210> 653

<211> 139

<212> PRT

<213> homo sapiens

<400> 653

Arg	Cys	Val	Gln	Gly	Ser	His	Phe	Val	Leu	Ser	Arg	Lys	Thr	Ser	Leu
1				5					10					15	
Leu	Leu	Ala	Asn	Pro	Pro	Gly	Ala	Ala	Gly	Pro	Ser	Gly	Pro	Gln	Glu
			20					25					30		
Leu	Ala	Leu	Leu	Ser	Met	Gly	Gly	Lys	Val	Tyr	Trp	Val	Cys	Arg	Pro
		35					40					45			
Arg	Pro	Ile	Phe	Leu	Arg	Met	Ile	Lys	Thr	His	Leu	Cys	Trp	Phe	Met
	50					55					60				
Val	Thr	Cys	Ala	Ala	Gly	Phe	Gly	Asp	Ala	Glu	Val	Cys	Arg	Ser	Ile
65					70					75					80
Ser	Gly	Gly	Leu	Asp	Ala	Val	Leu	Pro	Phe	Ser	Leu	Trp	Cys	Trp	Leu
				85					90					95	
Cys	Gly	Leu	Cys	Gly	Thr	Phe	Cys	Pro	Leu	Ala	Arg	Cys	Thr	Leu	Gly
			100					105					110		
Arg	Gly	Gly	Cys	Gly	Cys	Ser	Ala	Arg	Ser	Val	Ala	Ala	Ala	Arg	Ser
		115					120					125			
Ala	Pro	Thr	Pro	Val	Gly	Ile	Gly	Ser	Leu	Cys					
	130					135									

<210> 654

<211> 243

<212> PRT

<213> homo sapiens

<400> 654

Trp	Arg	Gln	Leu	Ala	Arg	Gly	Trp	Gly	Ala	Leu	Ser	Arg	Ala	Ser	Cys
1				5					10					15	
Pro	Ala	Leu	Pro	Arg	Leu	Ala	Asn	Asn	Thr	Val	Arg	Met	Ala	Lys	Gly
			20					25					30		
Asp	Pro	Lys	Lys	Pro	Lys	Gly	Lys	Met	Ser	Ala	Tyr	Ala	Phe	Phe	Val
		35					40					45			

Gln	Thr	Cys	Arg	Glu	Glu	His	Lys	Lys	Lys	Asn	Pro	Glu	Val	Pro	Val
	50					55					60				
Asn	Phe	Ala	Glu	Phe	Ser	Lys	Lys	Cys	Ser	Glu	Arg	Trp	Lys	Thr	Met
65					70					75					80
Ser	Gly	Lys	Glu	Lys	Ser	Lys	Phe	Asp	Glu	Met	Ala	Lys	Ala	Asp	Lys
				85					90					95	
Val	Arg	Tyr	Asp	Arg	Glu	Met	Lys	Asp	Tyr	Gly	Pro	Ala	Lys	Gly	Gly
			100					105					110		
Lys	Lys	Lys	Lys	Asp	Pro	Asn	Ala	Pro	Lys	Arg	Pro	Pro	Ser	Gly	Phe
		115					120					125			
Phe	Leu	Phe	Cys	Ser	Glu	Phe	Arg	Pro	Lys	Ile	Lys	Ser	Thr	Asn	Pro
	130					135					140				
Gly	Ile	Ser	Ile	Gly	Asp	Val	Ala	Lys	Lys	Leu	Gly	Glu	Met	Trp	Asn
145					150					155					160
Asn	Leu	Asn	Asp	Ser	Glu	Lys	Gln	Pro	Tyr	Ile	Thr	Lys	Thr	Ala	Lys
				165					170					175	
Leu	Lys	Glu	Lys	Tyr	Glu	Lys	Asp	Val	Ala	Asp	Tyr	Lys	Ser	Lys	Gly
			180					185					190		
Lys	Phe	Asp	Gly	Ala	Lys	Gly	Pro	Ala	Lys	Val	Ala	Arg	Lys	Lys	Val
		195					200					205			
Glu	Glu	Glu	Asp	Glu	Glu	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	210					215					220				
Gly	Thr	Tyr	Ser	Arg	Val	Gly	Trp	Trp	Ser	Ser	Pro	Lys	Glu	Gly	Glu
225					230					235					240
Arg	Arg	Asn													

<210> 655  
 <211> 110  
 <212> PRT  
 <213> homo sapiens

<400> 655

Thr	Glu	Gln	Glu	Glu	Ser	Arg	Arg	Trp	Pro	Phe	Gly	Ser	Ile	Arg	Ile
1				5					10					15	
Leu	Leu	Leu	Leu	Ala	Ser	Leu	Ser	Trp	Ser	Ile	Ile	Leu	His	Phe	Pro
			20					25					30		
Ile	Ile	Ala	His	Phe	Ile	Cys	Leu	Cys	His	Phe	Ile	Lys	Phe	Arg	Phe
		35					40					45			
Leu	Phe	Pro	Gly	His	Arg	Leu	Pro	Pro	Leu	Arg	Ala	Leu	Leu	Gly	Lys
	50					55					60				
Phe	Arg	Lys	Ile	Asp	Arg	Asp	Leu	Trp	Val	Phe	Leu	Leu	Met	Phe	Phe
65					70					75					80
Ser	Ala	Cys	Leu	His	Lys	Glu	Gly	Ile	Ser	Gly	His	Leu	Ala	Leu	Trp
				85					90					95	



Phe	Leu	Gly	Val	Thr	Phe	Ser	His	Pro	Asp	Cys	Ile	Val	Arg
			100					105					110

<210> 656

<211> 356

<212> PRT

<213> homo sapiens

<400> 656

Val	Gly	Cys	Ser	His	Ala	Ala	Gln	Leu	His	Ser	Ala	Pro	Glu	Leu	Gln
1				5					10					15	
Thr	Thr	Arg	Gln	Glu	Leu	Ser	His	Ala	Leu	Tyr	Gln	His	Asp	Ala	Ala
			20					25					30		
Cys	Arg	Val	Ile	Ala	Arg	Leu	Thr	Lys	Glu	Val	Thr	Ala	Ala	Arg	Glu
		35					40					45			
Ala	Leu	Ala	Thr	Leu	Lys	Pro	Gln	Ala	Gly	Leu	Ile	Val	Pro	Gln	Ala
	50					55					60				
Val	Pro	Ser	Ser	Gln	Pro	Ser	Val	Val	Gly	Ala	Gly	Glu	Pro	Met	Asp
65					70					75					80
Leu	Gly	Glu	Leu	Val	Gly	Met	Thr	Pro	Glu	Ile	Ile	Gln	Lys	Leu	Gln
				85					90					95	
Asp	Lys	Ala	Thr	Val	Leu	Thr	Thr	Glu	Arg	Lys	Lys	Arg	Gly	Lys	Thr
			100					105					110		
Val	Pro	Glu	Glu	Leu	Val	Lys	Pro	Glu	Glu	Leu	Ser	Lys	Tyr	Arg	Gln
		115					120					125			
Val	Ala	Ser	His	Val	Gly	Leu	His	Ser	Ala	Ser	Ile	Pro	Gly	Ile	Leu
	130					135					140				
Ala	Leu	Asp	Leu	Cys	Pro	Ser	Asp	Thr	Asn	Lys	Ile	Leu	Thr	Gly	Gly
145					150					155					160
Ala	Asp	Lys	Asn	Val	Val	Val	Phe	Asp	Lys	Ser	Ser	Glu	Gln	Ile	Leu
			165						170					175	
Ala	Thr	Leu	Lys	Gly	His	Thr	Lys	Lys	Val	Thr	Ser	Val	Val	Phe	His
			180					185					190		
Pro	Ser	Gln	Asp	Leu	Val	Phe	Ser	Ala	Ser	Pro	Asp	Ala	Thr	Ile	Arg
		195					200					205			
Ile	Trp	Ser	Val	Pro	Asn	Ala	Ser	Cys	Val	Gln	Val	Val	Arg	Ala	His
	210				215						220				
Glu	Ser	Ala	Val	Thr	Gly	Leu	Ser	Leu	His	Ala	Thr	Gly	Asp	Tyr	Leu
225					230					235					240
Leu	Ser	Ser	Ser	Asp	Asp	Gln	Tyr	Trp	Ala	Phe	Ser	Asp	Ile	Gln	Thr
				245					250					255	
Gly	Arg	Val	Leu	Thr	Lys	Val	Thr	Asp	Glu	Thr	Ser	Gly	Cys	Ser	Leu
			260					265					270		
Thr	Cys	Ala	Gln	Phe	His	Pro	Asp	Gly	Leu	Ile	Phe	Gly	Thr	Gly	Thr
		275					280					285			

Met	Asp	Ser	Gln	Ile	Lys	Ile	Trp	Asp	Leu	Lys	Glu	Arg	Thr	Asn	Val
	290					295					300				
Ala	Asn	Phe	Pro	Gly	His	Ser	Gly	Pro	Ile	Thr	Ser	Ile	Ala	Phe	Ser
305					310					315					320
Glu	Asn	Gly	Tyr	Tyr	Leu	Ala	Thr	Ala	Ala	Asp	Asp	Ser	Ser	Val	Lys
				325					330					335	
Leu	Trp	Asp	Leu	Arg	Lys	Leu	Arg	Thr	Leu	Arg	Leu	Cys	Ser	Trp	Ile
			340					345					350		
Thr	Thr	Leu	Arg												
		355													

<210> 657

<211> 240

<212> PRT

<213> homo sapiens

<400> 657

Leu	Ala	Gln	Ile	Pro	Glu	Leu	Asp	Arg	Gly	Val	Ile	Ser	Arg	Cys	Ser
1				5					10					15	
Gln	Val	Val	Thr	Ile	Leu	Arg	Glu	Gly	Asp	Ala	Ser	Asp	Gly	Ala	Arg
			20					25					30		
Val	Ala	Arg	Glu	Val	Gly	His	Ile	Ser	Thr	Phe	Leu	Gln	Val	Pro	Asp
		35					40					45			
Leu	Asp	Leu	Arg	Val	His	Gly	Ser	Cys	Ser	Lys	Asp	Glu	Ser	Val	Arg
	50					55					60				
Val	Glu	Leu	Cys	Thr	Gly	Glu	Arg	Ala	Ala	Gly	Gly	Leu	Ile	Cys	His
65					70					75					80
Leu	Gly	Glu	His	Thr	Pro	Cys	Leu	Asp	Val	Arg	Glu	Ser	Pro	Val	Leu
				85					90					95	
Ile	Ile	Gly	Gly	Ala	Gln	Glu	Ile	Val	Ala	Ser	Gly	Met	Lys	Ala	Glu
			100					105					110		
Ala	Cys	His	Ser	Thr	Leu	Met	Gly	Pro	Asn	His	Leu	Tyr	Thr	Arg	Gly
		115					120					125			
Ile	Gly	Asp	Arg	Pro	Asn	Pro	Asp	Ser	Gly	Ile	Gly	Gly	Ser	Arg	Lys
	130					135					140				
His	Gln	Val	Leu	Gly	Arg	Val	Lys	His	His	Ala	Gly	Asp	Leu	Leu	Gly
145					150					155					160
Met	Ala	Phe	Glu	Gly	Ser	Gln	Asp	Leu	Phe	Arg	Thr	Phe	Val	Lys	His
				165					170					175	
Asn	Asp	Ile	Phe	Ile	Arg	Pro	Thr	Ser	Glu	Asp	Leu	Val	Gly	Val	Gly
			180					185					190		
Arg	Ala	Glu	Val	Gln	Gly	Gln	Asp	Pro	Arg	Asn	Ala	Gly	Thr	Val	Gln
		195					200					205			
Pro	His	Val	Gly	Cys	His	Leu	Pro	Val	Phe	Ala	Glu	Leu	Phe	Trp	Leu

210					215						220					
His	Gln	Leu	Leu	Arg	His	Ser	Leu	Pro	Ser	Leu	Leu	Ala	Leu	Arg	Gly	
225					230					235					240	

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 <211> 162  
 <212> PRT  
 <213> homo sapiens

<400> 658

Glu	His	Asn	Ser	Lys	Ser	Ser	Phe	Ile	Asn	Ile	Lys	Arg	Ala	Tyr	Leu	
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Ala	Lys	Asp	Thr	Gln	Ile	Lys	Glu	Ser	Leu	Trp	Leu	Arg	Thr	Gln	Gly	
			20					25					30			
Arg	Glu	Val	Pro	Gly	Leu	Cys	Pro	Cys	Trp	Ala	Arg	Arg	Arg	Leu	Gly	
		35					40					45				
Thr	Lys	Trp	Glu	Lys	Cys	Trp	Glu	Gly	Leu	Ser	Gly	Arg	Gly	His	Lys	
	50					55					60					
Ser	Ser	Gly	Gly	Gln	His	Cys	Arg	Gln	Val	Met	Gly	Gly	Thr	His	Gly	
65					70					75					80	
Asp	Leu	Ala	Ala	Asn	Ser	Cys	Cys	Gly	Gly	Val	Ser	Leu	Val	Leu	Pro	
				85					90					95		
Pro	Gly	Gly	Pro	Leu	Leu	Gly	Ser	Trp	Arg	Gly	Pro	Thr	Lys	Gly	His	
			100					105					110			
Arg	Thr	Gly	Ser	Pro	Gly	Trp	Leu	Val	Gln	Leu	Gly	Met	Lys	Ala	Arg	
		115					120					125				
Glu	Lys	Arg	Val	Leu	Cys	Ser	Gly	Arg	Ile	Gly	Pro	Asp	Ala	Glu	Ala	
	130					135					140					
Glu	Ala	Leu	Pro	Val	Thr	Cys	Gly	Arg	Ser	Ala	Leu	Ser	Leu	Pro	Gly	
145					150					155					160	
Thr	Leu															

<210> 659  
 <211> 148  
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 <213> homo sapiens

<400> 659

Arg	Leu	Trp	Thr	Ala	Phe	His	Gly	Leu	Arg	Ala	Gly	Asp	Glu	Ala	Thr	
1				5					10					15		
Arg	Arg	Pro	Gly	Leu	Pro	Glu	His	Leu	His	Gly	Pro	Ala	Val	Ser	His	
			20					25					30			
Arg	Gly	Asp	Gly	Gln	Arg	Asp	Pro	Ala	Tyr	Leu	Cys	Trp	Gln	Gln	Glu	
		35					40					45				
Arg	His	Gly	Ala	Pro	Glu	Glu	Arg	Tyr	His	Pro	Cys	Pro	Gly	Pro	Ser	
	50					55					60					

Gln 65	Arg	Val	Pro	Gly	Arg 70	Asp	Arg	Ala	Glu	Arg 75	Pro	His	Val	Thr	Gly 80
Ser	Ala	Ser	Ala	Ser 85	Ala	Ser	Gly	Pro	Ile 90	Arg	Pro	Leu	Gln	Ser 95	Thr
Arg	Phe	Ser	Leu 100	Ala	Phe	Ile	Pro	Ser 105	Cys	Thr	Asn	His	Pro 110	Gly	Leu
Pro	Val	Leu 115	Cys	Pro	Leu	Val	Gly 120	Pro	Leu	Gln	Glu	Pro 125	Arg	Ser	Gly
Pro	Pro 130	Gly	Gly	Ser	Thr	Lys 135	Asp	Thr	Pro	Pro	Gln 140	Gln	Glu	Leu	Ala
Ala 145	Arg	Ser	Pro												

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